

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model
Run on: May 28, 2004, 14:04:04 ; Search time 6849.01 Seconds
(without alignments)
10625.327 Million cell updates/sec

Title: US-10-017-084A-522
Perfect score: 1679
Sequence: 1 gttgttccttcagcaaac.....ataaaagagcaaaaaaaa 1679

Scoring table: IDENTITY_NUC
Gapop 1.0 , Gapext 0.1

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :	GenBank:
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2: gb_hgt.*	
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Pred. No. is the number of results predicted by chance to have a

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5	1679	100.0	1679	6	AX464242 Sequence
6	1679	100.0	1679	6	AX490948 Sequence
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8	1510.9	90.0	1839	6	AX665342 Sequence
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10	1204.5	71.7	2040	10	U16845 Rattus norv
11	1169.2	69.6	1615	10	BC023307 Mus muscu
12	1063.9	63.4	1410	10	AF282980 Mus muscu
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36	757.2	45.1	260206	2	AC113965 Mus muscu
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38	752.8	44.8	208036	2	AC098294 Rattus no
39	752.8	44.8	225433	2	AC106484 Rattus no
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43	737.4	43.9	152686	2	AC018913
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50	709.8	42.3	8461	10	AB035201 Rattus no
51	709.6	42.3	284662	2	AC096608 Rattus no
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62	706.7	42.1	251570	2	AC094463 Rattus no
63	706.6	42.1	18848	4	OCY14852 Oryctolagus
64	706.6	42.1	135672	9	AC000113 Human PAC
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69	C	706.4	42.1	348071	1	EX572100	EX572100 Prochloro
70	C	706.3	42.1	7931	1	AF093576	AF093576 Mus muscu
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73	C	705.9	42.0	145356	9	AC004033	AC004033 Homo sapi
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81	C	705.7	42.0	210907	2	AC101725	AC101725 Mus muscu
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95	C	704.8	42.0	163475	2	AC092619	AC092619 Homo sapi
96	C	704.8	42.0	163778	2	AC010868	AC010868 Homo sapi
97	C	704.8	42.0	192505	9	AL353136	AL353136 Human DNA
98	C	704.8	42.0	193952	2	AC141263	AC141263 Homo sapi
99	C	704.7	42.0	228359	2	AC103081	AC103081 Rattus no
100	C	704.7	42.0	284308	2	AC122955	AC122955 Rattus no

ALIGNMENTS

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RESULT 1
LOCUS AX358872 1679 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 125 from Patent WO0193983.
ACCESSION AX358872
VERSION AX358872.1 GI:18675337
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Deanovys, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 125 13-DEC-2001;
Genentech Inc. (US)
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source Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 1679; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 4.2e-17;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTCGACAAAGCTTGAGAGCAAC 60
Db 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTCGACAAAGCTTGAGAGCAAC 60

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241	QY	CACCTTCCCAAAGCTATGGAACACGTGACCGTCCGCGAGGGAGAGCGCACCTCTCAG	300
241	DB	CACCTTCCCAAAGCTATGGAACACGTGACCGTCCGCGAGGGAGAGCGCACCTCTCAG	300
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301	DB	GTGCACTATTGACAAACCGGGTCAACCGCGGTGGCTTAAACCGCAGCACCATCTCTTA	360
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361	DB	TGCTGGGAATGCAAGTGGTGGCTGGATCTCGGTGTCCTCGGTGCTTCTTGAGCAACCCAAAC	420
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RESULT 3
AX403748 1679 bp DNA linear PAT 14-JUN-2002
LOCUS AX403748
DEFINITION Sequence 103 from Patent WO0077037.
ACCESSION AX403748
VERSION AX403748.1 GI:21437184
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ashkenazi, A., Baker, K., Botstein, D., Desnovers, L., Eaton, D.L.,
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P., Gurney, A., Kljavin, I.J., Mather, J.,
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,
Williams, P.M., Wood, W.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0077037-A 103 21-DEC-2000;
Genentech Inc. (US)
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ORIGIN
Query Match 100.0%; Score 1679; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 4.2e-17;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS
DEFINITION
Sequence 55 from Patent WO0208284.
ACCESSION
AX454470
VERSION
AX454470.1 GI:21713859
KEYWORDS
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SOURCE
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REFERENCE
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AUTHORS
Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL
Patent: WO 0208284-A 55 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
; Paoni, Nicholas P. (US) ; Stephan, Jean-Philippe P. (US) ;
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I. (US)
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DEFINITION Sequence 375 from Patent WO0140466.
ACCESSION AX464242
VERSION AX464242.1 GI:21899137
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E., Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0140466-A 375 07-JUN-2001;
Genentech Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 4.2e-17;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION
ACCESSION AY358331
VERSION AY358331.1 GI:37181786
KEYWORDS FLI_CDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Clark H.F., Garney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I. and Godowski P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1679)
AUTHORS Clark H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Best Local Similarity 100.0%; Pred. No. 4.2e-17;
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DEFINITION AF126426
ACCESSION AF126426
VERSION AF126426.1 GI:7158997
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 1839)
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AUTHORS Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
TITLE Cloning and identification of human neurotrophin full length cDNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1839)
AUTHORS Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
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Qy 192 -----TGGCTG-----197
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RESULT 11

BC023307
LOCUS BC023307
DEFINITION Mus musculus neurotrophin, mRNA (cdna clone MGC:30504
IMAGE:4480983), complete cds.

ACCESSION

BC023307

VERSION

BC023307.1

KEYWORDS

MGC.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 1615)

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krywinski, M.I., Skalska, U., Smalhus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 12477932
 2 (bases 1 to 1615)
 Strausberg, R.
 Direct Submission
 Submitted (05-FEB-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC) Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-x@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 This clone was selected for full length sequencing because it
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Db 180468 CCAGAAACCTATGTTTTCAGACAAATAGGAGAGCTGCTGGGAACTGTACTGCTTGCAG 180527
QY 701 -----G-----G-----CATACC-----CGGAGCAG-----T--CAG 722
Db 180528 TTCTCTGCTCTGTTGTTGTCTCCATCTCCATACACTGGGCGAGGTTCTGCATCCAG 180587
QY 723 GG-----GA-CTACGAG-----TGCA-----G--738
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QY 869 TCAG--C-AGTCCCCTCAGC-----AGAAAT-----C--CAGTGGT-ACAA 903
Db 180871 ACAGGCCAAG-----CAGCTGGAGGTGGTGGATTTTTCAGGCAGGAGTCTCAGAA 180924
QY 904 G-----GATGA-----CAAA--AGACTG-----ATTGAG-----926
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 184716)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 JOURNAL
 REFERENCE
 1 (bases 1 to 184716)
 2 (bases 1 to 184716)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,E.,
 Boguslavsky,L., Bouckgaltier,B., Brown,A., Castle,A., Colangelo,M.,
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 Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
 Zimmer,A. and Zody,M.

TITLE
 JOURNAL
 COMMENT
 Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 7, 2000 this sequence version replaced gi:6649510.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L1344
 Center clone name: 29_L_13

----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 173786 bases at least Q40
 Consensus quality: 178863 bases at least Q30
 Consensus quality: 180884 bases at least Q20
 Insert size: 176000; agarose-fp
 Insert size: 183516; sum-of-contigs
 Quality coverage: 4.6 in Q20 bases; agarose-fp
 Quality coverage: 4.4 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 13 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 1103 1202: gap of 100 bp
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 * 21745 29796: contig of 7952 bp in length
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 * 42716 42815: gap of 100 bp
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 * 54378 69399: contig of 15022 bp in length
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 * 87606 87705: gap of 100 bp
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Qy	92	C-----GAA-----CC-----TGAC 101
Db	161487	CTCAGTCGAGGGAAGCGCACCTGTTTTCCATCTCTTACCAGGGGCATCTCTTAGTCAC 161428
Qy	102	A-----AAA-----AA--GAA--GAA-----113
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Matches 1192; Conservative 0; Mismatches 75; Indels 430; Gaps 82;			
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AUTHORS
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.,
Homo sapiens 187,203 genomic DNA of 11q24
Published Only in Database (1999)
2 (bases 1 to 187203)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.,
Direct Submission
Submitted (03-DEC-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail: hattori@gsc.riken.go.jp,
URL: http://hgp.gsc.riken.go.jp/, Tel: 81-42-778-9923,
Fax: 81-42-778-9324)
On May 31, 2000 this sequence version replaced gi:6997666.

COMMENT

----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humdraft11
Center clone name: RP11-803P2
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 171133 bases at least Q40
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Consensus quality: 182303 bases at least Q20
Insert size: 184603; sum-of-contigs
Quality coverage: 4.41x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
27 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

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54349 68175 contig of 13827 bp in length
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Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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30967 31066: gap of 100 bp
31067 54248: contig of 23182 bp in length
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Qy 598 CACCTGC---ATA---GCACTG-GTAGACACAGGC----- 626
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RESULT 18
AX665344
LOCUS

DEFINITION
Sequence 102 from Patent WO03002765.
ACCESSION
AX665344
VERSION
AX665344.1 GI:29290465

KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM

REFERENCE
1

AUTHORS
Sellar,G.C. and Gabra,H.
TITLE
Cancer
JOURNAL
Patent: WO 03002765-A 102 09-JAN-2003;
Cancer Research Technology Limited (GB)

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source

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Matches 1002; Conservative 0; Mismatches 11; Indels 72; Gaps 14;

AX665344
Sequence 102 from Patent WO03002765.
ACCESSION
AX665344
VERSION
AX665344.1 GI:29290465

KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Sellar,G.C. and Gabra,H.
Cancer
Patent: WO 03002765-A 102 09-JAN-2003;
Cancer Research Technology Limited (GB)
Location/Qualifiers
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Query Match 58.1%; Score 974.7; DB 6; Length 1068;
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Matches 1002; Conservative 0; Mismatches 11; Indels 72; Gaps 14;


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Db 1064 TTGGA 1068

RESULT 19

AX665346 1104 bp DNA linear PAT 26-MAR-2003
LOCUS Sequence 104 from Patent WO03002765.
DEFINITION AX665346
ACCESSION AX665346
VERSION AX665346.1 GI:29290466
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE

1
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 104 09-JAN-2003;
Cancer Research Technology Limited (GB)

FEATURES

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ORIGIN

Query Match 57.8%; Score 971.1; DB 6; Length 1104;
Best Local Similarity 84.3%; Pred. No. 2.2e-05;
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RESULT 22
LOCUSDEFINITION Homo sapiens mRNA; cDNA DKFZp686H1949 (from clone DKFZp686H1949);
complete cds.

ACCESSION BX537377

VERSION BX537377.1 GI:31873255

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (Bases 1 to 6380)
AUTHORS Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.

TITLE

JOURNAL

COMMENT Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp686H1949) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/proj/cDNA/>.

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QY 736 CAGTGCCTCCAATGACGTGGCCCGCCCGTGTGTAAGGAGTAAGGTCAACCGTGAACATA 795
DB 721 CAGCGCGTTGAACGATGTCTGCGCCGATGTGCGAAAGTAAATAACACTGTAAACTA 780
QY 796 TCACCATACATTTCAAGAGCCCAAGGTGACA--GGTGTCCCGTGGGACAAAGGGGACA 853
DB 781 TCTCTCCATATCTCAAAAGCCAA--GAACATGTTGTTTTCAGTCCGTGAGAGGG--CA 836
QY 854 --CTGCAG--TGTGAAGCCCTCAGCAGTCCCTCA--GCAGAAITCCAGTGGTACAAAGATG 908
DB 837 TCTGTG--AGTGTGAAGCCCTCGAGTCCC--CATGGCTGAATTCAGTGGTTCACAGGAG 893
QY 909 ACA--A-----AG--ACTGAT--T--GAAGAAAGAAAGGGGTGAAGTGGAAACAGAC-- 957
DB 894 A--AACCCAGGTAGCCACTGCTGTGATGGAATG--AGGATTTGAAA-----ACAA--AGGCCG 945
QY 958 --TTTCTCTCAAAACTCATCTTCTCAATGCTCTGAAACATGACTATCGGAATCACT 1015
DB 946 CATGTCCATCT--TGACT-----TTCTTCAATGTTTTCAGAAAGATTATGGAACTACT 1000
QY 1016 TGGTGGCCCTCCCAACAAAGCTGGGCCACACCAATGCCAGCATCATGCTATT---TGGTCCA 1072
DB 1001 TGTGTGGCCACGACACAGCTTGGGAACACCAATGCCAGCATCA--C-ATTGTATGGCCT 1057
QY 1073 GGCCTCGTCAGCA--GGTG--AGCAA--CGCACGTGAGAGGGCA--GGC--TGCCTCTG 1125
DB 1058 GAGCAGTCATTTGATGTTGTA--AACTCGGC-C-TCCA-GA--GCACGTGGCTTGTCTCTG 1110
QY 1126 GCT-----G-----CT--GCC-----TCTT-----CT--GGTCT 1145
DB 1111 GCTATCAGGAGACCTCTTAGCCCACTTCTTCATCAAGTTTGTATGAAGAACTCTAGTCC 1170
QY 1146 T-----GCA--CCTGCTTCT--CAAAAT-----TTTGAATG-----GAGTG-----CC 1178
DB 1171 TCTGAGCAACGCTGCTTCTCCATATCACAGACTTTAACTACATCGCGAGAGCAAAACC 1230
QY 1179 A-----CTTC-----CTTC-----CTTC-----CTTC-----CTTC----- 1183
DB 1231 AGCTGGGCTCTTTTGTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTT 1290
QY 1184 -----C-----CCACC-----CGGG-----CGGG----- 1193
DB 1291 TTATTTGTTGTTGTTTATTTTCCAGCTTGAATGAGTGGGTTGGGGCGGGGTGGGC 1350
QY 1194 -----AAA-----AAA-----GG-CTGC-C- 1203
DB 1351 AGGGTTCTACACCGTGTAGGATTAATCATTCATTTGGTGTGTCCAAATAATGGGGTCTGTCTCC 1410
QY 1204 -GCCACC--ACC-----AC--CA-- 1216

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Db 1411 TGCTACCTTGACCCCTCCCTCCCTGCTCTCTCTCATCATCATCTCCCAACAACATC 1470
Qy 1217 -----CCA-ACACACA-----GCAA-----TG-GC-----AA 1237
Db 1471 CTCTGCCATACACAAACAAAGTAAGTTTCATTTGGGCAAAATTTGAGCCTCACATAAA 1530
Qy 1238 CACC-----G-ACAGCAA-----CCAA--T 1254
Db 1531 CACCCTGAAGACACAACTTGACTTATACATAGTGCACAGCAAGAGCTACATCCAGTGT 1590
Qy 1255 C-----A-TAT-----AT-ACAA-----ATG-----A-----AATT 1275
Db 1591 CCTATTACTGTGAATTAATTTCTTAATGACAATGACATATGCCCCCATCATGTTAATT 1650
Qy 1276 A-----GA----- 1278
Db 1651 ATTATCTAATTCCATTAGGTTACGTCCTTTCTTTCTGGGACACTATCTACTATATACC 1710
Qy 1279 -----AGA-----AA-----CA-----C-----AGCC-----TC 1292
Db 1711 ATATCTATAGATTTCAATATAGATGATGTGCCATCTTCTGTAGCCCTCCGCTCTACTC 1770
Qy 1293 A-----TGGACAGAAATTTAGG-----GAGGG-----GAA-----CAA-- 1322
Db 1771 ATTCCTTCCACCATCTG---CAGAGATTTGAAGTTTG-GGGCTATGATGAACCCCAACA 1826
Qy 1323 ---AGAACTATTG-----GGGGA---A-----AAG--AG----- 1345
Db 1827 CTA-AAT---TTTGAAGTCAAGTACCAAAAGGGGAGGAGCATTTTGAAGATAGAACCT 1883
Qy 1346 ---TTTTAAAA-AGAAATTT-----GAAA-----ATTG---CCTTGCGA--TATTTAG 1385
Db 1884 CTAATTTAAAGAGAAGTCTCACTCATPAACGTCATTTGATAGGTGGCTGATTTATTAG 1943
Qy 1386 G-----TAA-C-----AATGG---AGTTTTC---TTTTCCAAA---CGGGA 1416
Db 1944 GTTTTGTCAAGCTATCTATCAAGTAATGTGACAGTTACCCATCTACTCAAAATATCTG-- 2001
Qy 1417 A-GAACACAGCA-----CACCGGCTTGACC-----C-----A 1444
Db 2002 ATTTATCTACCAATCAATTAATCTACCCACCTGCTT---CCTCTAGCAATCTATTTA 2058
Qy 1445 CTG-----CAAGCTGCATC---G-----TG-C-AAC-CT-CTTTGGTGC----- 1476
Db 2059 CTGTTTATCAATCT-ATCAATGTAATGTCTAACACTCCCTT---CTATTCTCCCT 2112
Qy 1477 -----GAGTGTGGCAGGGCTAGCC-----TCTGCGCCACAGAGT---GCC 1518
Db 2113 ACTACTCACTAT---CAA---TTCATCCCATATGAATCTCTAAACATATTTGTATCTC 2166
Qy 1519 CCACGTGGA-----ACA---TTCTGGAG-C---TGGCCATC---CCAAA---TTCA 1556
Db 2167 CCAC-TGATTTATTTATACCATCAGCAGACATTTGG-CATCTTCAAAATTAATCTTCA 2224
Qy 1557 A-TCAGT-----CAATAGACGA-----ACAG-----AAT-----G-----A 1583
Db 2225 ACTTCTGTGAAGCCA-----ACGATCTCACAGGTTAAACAAATACAAAGCATACCT 2279
Qy 1584 -----GAC-CT-----TCCGG-----CCGAG----- 1599
Db 2280 GTGTTGTGAGCTCTTTAAATCTTGGTATCTCTATCCACCCCAAGGGAGACACTAACAGATAG 2339
Qy 1600 ---C-----GTGGC---GC---TG---CGGGCACT---TT---GGTAGA---CTGTG---C-- 1631
Db 2340 GCCAAGTAGCAAGCTAATGATCACTCACTACTATTTCCGGAAAGGCTGTGTTTCTA 2399
Qy 1632 ---CAC-----CA-----CGGC-----G-----TGTTG----- 1645
Db 2400 AAACACTTTCTTGGGAAGCAGATCAGCCTAGAAAAGTTTGTAGTACTGTGTTTTC 2459
Qy 1646 ---TTG---TGAA--AC---GT-----GAAA-T 1661
Db 2460 TTTTGCACCTTGAAGGACAAAGTGCCAGCCTTTATGCTTCTCTCAACCCCTTCAAGAAAGT 2519
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Qy 1662 A-----AA-----A-----AG-AGCAA-AA-----AAAA 1679
Db 2520 ACATGTCAAGAACCTATGTGCTGCTTTCTTTAGCAGCAAGAACTTGAGAGAAAA 2574

RESULT 23
LOCUS RATCALMA 3069 bp mRNA linear ROD 08-MAY-1993
DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete CDS.
ACCESSION M88709
VERSION M88709.1 GI:203245
KEYWORDS cell adhesion-like molecule; opiod binding protein.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 3069)
AUTHORS Lippman, D.A., Lee, N.M. and Loh, H.H.
TITLE Opioid-binding cell adhesion molecule (OBAM)-related clones from a rat brain cDNA library
JOURNAL Gene 117 (2), 249-254 (1992)
MEDLINE 92347701
PUBMED 1339369
COMMENT Original source text: Rattus norvegicus (strain Simonsen ICR) (library: UZ) brain cDNA to mRNA.
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        location/Qualifiers
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ISKAKNTGVSVGGKILSCSAVPMAPFQWFKEDTDLATGLDGVRIENKRISTLTF
FNVSEKDYGNITCVATNKLGNWTASITLYGPGAVIDGVNSASRALACLWLSGTFPAHF
FIKP"

Query Match 50.8%; Score 853; DB 10; Length 3069;
Best Local Similarity 49.2%; Pred. No. 0.014;
Matches 1329; Conservative 0; Mismatches 240; Indels 1130; Gaps 219;

Qy 2 TTGTG-----TCCVTC-----AGCAAAACAGTGGATTAAATCTCTTGCAAGCTT--G 50
Db 474 TTCTGCTCTCTCCCTCCCTTGC-AAACATGGATTTAAACCTGCT--CAGAA--TTGAG 528

Qy 51 ---AGAGCAA-CA--CAATC-----TATCAGGA--AGAA--AGAA--AGAAAAACCGA 94
Db 529 TACAGAGGAAGCAGCC--TCGGTGGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 579

Qy 95 ACCTGACAAAAAAGAAAAAG-A--AGAAGAA-----AAAAAT 132
Db 580 ACC-----ACGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 630

Qy 133 CAT-GAAA---ACCATCCAGCAAAATGCACAT--TCTATCTCTTTGGGCAATCTTCAAC 186
Db 631 CCTCGAGATGTACATCCGCC--TACTG---GATGCTCT-TCTC---GGCCA-C--CA- 677

Qy 187 GGGGCTG-GCTGCTCTGTCTTCTTCCAGAGAGTSCCGTSCCGCAGGAGATGCCACCT 245
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Db 678 ----CTGCCCTGCTCT-----TCATCCAGAGTGCCTGGCGAGATGCCACT 728
QY 246 TCCCAAAGCTATGGACAACGTGACGGTCCGGAGGGGAGAGCGCCACCTTCAGGTGCA 305
Db 729 TTTCCCAAAGCTATGGACAACGTGACGGTCCGGAGGGGAGAGCGCCACCTCAGGTGTA 788
QY 306 CTATTGACAACGGGTACCGGGTGGCTGGCTGAACCGCAGCACCATTCTCTATGCTG 365
Db 789 CCATAGATGACCGGGTACACAGATGAGCTGGCTGAACCGCAGCACAATCTCTAGCTG 848
QY 366 GGAATGACAAGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 423
Db 849 GGAATGACAAGTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 906
QY 424 GTACAGATCGAGATCCGAAGCTGATGTGTATGACGAGGGCCCTTACCTGCTGCTG 483
Db 907 GTACAGATCATGATCCGAAGTGTGATGTGTATGACGAGGGTCCGTACACCTGCTCTG 966
QY 484 GCAGACAGAACACCCAAAGACCTCTAGGGTCCACCTCATGTGCAAGTATCTCCCAA 543
Db 967 GCAGACAGAACATCACCCAAAGACCTCCCGGGTCCACCTCATGTGCAAGTATCTCCCAA 1026
QY 544 AAT--TGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGC---CTC 598
Db 1027 GATAATG-A-ACATCTCTTCAGA-----CATTTACT--GTGAATGAGATAGCAGTGTG 1075
QY 599 ACC-----TGATAGCACTGTAGACAGAGCTTACGGTCTTACTTTGGAGACATCTCTC- 651
Db 1076 ACCTTGTTATGTCTGCAATTTGGCAGACCCAGACCAACAGTGCATCTGGGACACCTGTCA 1135
QY 652 -TCCCA--AAG--CGGTTGGCTTTGTGAGTGAAGACGAATCTCTGGAAT--TCAGGGCA 704
Db 1136 GT--CAAGAGAGGCCAG--GGCTTTGTGAGTGAAGATGAATACCTGGAATCTCA--GACA 1190
QY 705 TCACCCGGAGCAGTCCAGGGACTACGAGTGCAGTGCCTTCAATGACGTGGCGGCCCGCG 764
Db 1191 TCAACGGCACCACATCTGGAGAGTATGAGTGCAGCGCTTGAATGATGTGCTGTGCACC-- 1248
QY 765 TG--GTACGGAGATTAAGTTCACCTGACCTGACATCTCACCATACATTTTCAGAGCCAGGG 822
Db 1249 TGATGTTCGGAAGTAAAAATCACTGTAACCTATCTCCCTATATCTCAAAAGCGAA--G 1306
QY 823 TACA--GGTGTCCCGTGGGACAAAAGGGGACA--CTGCAG-TGTGAAGCTTCAGCAGTTC 877
Db 1307 AACCTGGCGTTTCAGTAGGCCAGAGGG--CATCTTG-AGCTGTGAGCCCTCTGTCTGTC 1363
QY 878 CCCTCA--GCAGAAATCCAGTGTGTAACAAGGATGACAAAAG-----ACTG--ATTGAAG 926
Db 1364 CC--CATGGCTGAATTCAGTGGTTTCAAGGAAGATACAGGTTAGCCACTGGGCT----G 1417
QY 927 GAAAGAAAGGGTGA--AAGTG-GAABACAGACC--TTTCTCTCAAAACTCATCTCTTT 981
Db 1418 G-----ATGGCGTGAGAAATTTGAAACAAAGGCCGCATATCCACT--TTGACT-----TTCTT 1467
QY 982 CAATGTCTTGAACATGACTATGGGAACACTACCTGGTGGCCCTCAACAAAGCTGGGCGCA 1041
Db 1468 CAATGTCTCAGAGAGGAATATGGGAATATATCTGTGTGGCCACAAACAGCTTGGGAA 1527
QY 1042 CACCAATGCCAGCATCATGATTTTGGTCCAGCGCGCGTCCAGCGA--GGTG-AGCAA--CG 1097
Db 1528 CACCAATGCCAGCATCACCTGTATGGGCTTGAGCGAGTCAATGATGGTGTGA--AACTCG 1585
QY 1098 GCACGTCCGAGGGGCA--GGC-TGGCTGTGGCT-----G-----C--TGCC---TCT 1137
Db 1586 GC-C-CTA-GA--GCACTGGCTGTCTCTGGCTCTCAGGAGCCTTCTTTGGCCACTTCT 1640
QY 1138 TC-----T-GGTCTT---GCA---CCTGCTTCT----- 1158
Db 1641 TCATCAAGTTTGTATGAAGAAACCTTAGTCTCTCTGAGCATCGGCTGCTTCTCCATATCAC 1700
QY 1159 -----CAAA-----TTTTG--A----- 1168

Db 1701 AGACTTTAATCTACACTGCGGAGGGGCAACACGAGTTTGGGCTTCTCTTTGGTTATTTTTT 1760
QY 1169 TG-----TGAGTG-----C-----CA----- 1179
Db 1761 TGTCTCTCTGACTCTTTAGTTTGGTTTGGTTTGAATTTCTGGGATTTTCAATTTGATTTGT 1820
QY 1180 ---CTT-----CC-----CC-----CCACC-GG 1191
Db 1821 TTTCTTTTTCGTTGAATGGACCGGGTGGGGTGGGATGGGAGGGTCTTACACG 1880
QY 1192 ---GGA-AA-----GG-----CTG--CC--GCC- 1206
Db 1881 AGTAGGATAATCAGGTATTGGTGGGCCCCCAAAATGGAATATATTTCTCTGCTACCTTGGCT 1940
QY 1207 ---ACACC-----ACACC-----AC-CACCAACACA--ACA----- 1227
Db 1941 TCTTTTCTTCTACTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2000
QY 1228 ---GC-----AATG-----GGA-----ACA-----CCGACA-- 1245
Db 2001 AAGATGGCTTAAATAATGTCCCATGACACGACCCCTGAAGGTACAACTTGGCCACACT 2060
QY 1246 GCA--AC-CAATCAGA--T--ATATACA-----AA 1268
Db 2061 GCAGTACACATAAGAGTTGCATCTACATTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2120
QY 1269 T-----GA-----GG-----A-----ATTA-- 1276
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QY 1277 --G-----AAGAAAC-----ACAGCTC-ATGGG--ACA-G----- 1301
Db 2181 CTGCACACCTTCTTAAGAACTTTCTTACTATACCTTCAATGTCACACATGATACATTC 2240
QY 1302 ---AATTTGA-----GG----- 1311
Db 2241 TCATAAAATTTTACCATCTCTCTGGCAATCTGCTTAATCTGCAATTTTCCACTAGCAG 2300
QY 1312 ---G-----AG--G-GAA-----CAAGAATAC--TTT--G----- 1333
Db 2301 TAAGACTTACAGCTTGTATGAATATACATGATCCAAAG-CTACAAATTTAGAATCAC 2359
QY 1334 GGGGGAA--A--AG-----AG--TT--TTAAAA-----AAGAAAT 1360
Db 2360 GAGGGAAGTCTATCAGGGGTAGTACTTCCCTTAAATGCTAATGCACTCATAAAAG 2419
QY 1361 TGA-AAATTCG--CT-----T--GC-----AG-----ATATT-----T--AGGTA- 1388
Db 2420 TGATCAATAGCTAGCTTAATATATCAAGCTATCAAGCAATCATATTTATTTATCCAGTTAC 2479
QY 1389 -CAATGGAGTTT--TCT--TTTCC-----CAAGCGGA-----AGAA----- 1420
Db 2480 TCAATTGA--TTTCTCTCCATCTCTCTTCTCATATAC-CTATCTTCTTATATCTATTG 2537
QY 1421 --CA--CAGC--AC-ACCC-----GGCTTGGACCCACTGCA--AGC--TGCACTGTGC- 1462
Db 2538 TTTCAATTTATCACTACTCTTTTCTCTT-----CCCACTGCATCTCCATTCATC-T-CA 2592
QY 1463 ---AACCTCT-----TTG-----GTGCC-----AGTGTG-----G-----GCAA 1488
Db 2593 TTTAAATCTTAATCATATTTGTGACTGTGGCTTATATTTGTCTCTGCACTACCAACAA 2652
QY 1489 G---GGCTCAGCTCTC-----TGCC--CA-----CAG--A-GT-- 1514
Db 2653 GACATTGC-CA-CCT-TCAAAATTTGCTAGCACTTCTTATGTGAAGCCAGTAATGCT 2709
QY 1515 ---GC---C--CCCAGCTGGAACA--TTC-----TGAGC--TGG----- 1542
Db 2710 CGGGCTAATCACTACCA-GRAGAACAATTTCTTATACCATGGATCTTTGGGAATGCACTAAC 2768
QY 1543 CCAAT---CCCAATT-----CA-----ATCAGT 1562
Db 2769 CCATCCACCCAAATTAGGCTTTGTGAACAGATGGACCAAAAGTAGCAATCTATGGATCAGT 2828


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QY 1563 C---CATAGAGA-----CGAACAGATG-----AG--ACCTTC-----CG 1592
Db 2829 CACTCAT---GATTTTCG-AGAGACTGTTCCCTTAGCCACCTTCTCAGAGGCGAGTCA 2884
QY 1593 GCCC-----AAG-CGTG-----GC-G-----CT-----CGGGCACTTT--GGTA- 1623
Db 2885 GCCCCGAGAAGCCTTGATTATGCTGAATTCTCTTTAACAGCTGGAATAATTAAAGGTAC 2944
QY 1624 -GA--CTGTGC-----CA-CC-----AC--GG-----AC--GG----- 1639
Db 2945 CAACCTGTGCTTCTCTCAGCCTTTCAAGAAAGTACATGTCAGGAACCTTGGAGAAACTT 3004
QY 1640 ---CGTG--TG-----TTGT-----GA-----AACGTGA--AATAAAAGAGCAAAAAAAA 1679
Db 3005 CTTTCATGCTGGCTTTATTATAGCAGAAAGAACCTGACCAAAAAAACCACAAAAAAA 3063

RESULT 24
AF271233      1638 bp DNA linear SYN 21-MAY-2001
LOCUS         Synthetic construct secretory IgCEPUS-GFP fusion protein
DEFINITION   (IgCEPUS-GFP) gene, complete cds.
ACCESSION   AF271233
VERSION     AF271233.1 GI:14161268
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1 (bases 1 to 1638)
AUTHORS    Kim,D.-S. and Moss,D.J.
TITLE      Secretory IgCEPUS-GFP fusion protein expressions in transfected
           cell lines
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 1638)
AUTHORS    Kim,D.-S. and Moss,D.J.
TITLE      Direct Submission
JOURNAL     Submitted (24-MAY-2000) College of Natural Resources and Life
           Science, Division of Biological Resources R-6517, Dong-A
           University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of
           Korea

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ORIGIN
Query Match      50.1%; Score 842; DB 12; Length 1638;
Best Local Similarity 65.2%; Pred. No. 0.0069;
Matches 1154; Conservative 0; Mismatches 245; Indels 370; Gaps 128;

QY 134 ATGAAACCATCCAGCCAAATGACAAATCTATCTCTTGGGCNACTTTCACGGGGCTG 193

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Db 1 ATGG-----C--CCAGCGAAATGACGACCCCGTCTCATGGGTGATCTTCGCGGGATG 54
QY 194 GCTGCTCTGTGTCTCTTCCAGAGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCAA 253
Db 55 GCAGCACTCTCTCTTCCAGAGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCAA 114
QY 254 GCTATGGAACAACGTGACGGTCCGCGAGGGGAGAGCGCACCTTCAGGTGCACTATTGAC 313
Db 115 GCTATGGAACAACGTGACGGTCCGCGAGGGGAGAGTGCACCGCTCAGTGTCCGTGGAC 174
QY 314 AACCGGGTCAACCGGGTGGCTGGCTTAAACCGCAGACCACTCTCTATGTGGGAATGAC 373
Db 175 AACCGGGTCAACCGGGTGGCTGGCTTAAACCGCAGACCACTCTCTATGTGGGAATGAC 234
QY 374 AAGTGGTGGCTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAAGCGAGTACAGATC 433
Db 235 AAGTGGTGGCTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAAGCGAGTACAGATC 294
QY 434 GAGATCCAGAAACGTGGATGTGTATGACG-AGGGCCCTTACACCTGTCTCGGTGACAGAGA 492
Db 295 CAGATCCAGAAACGTGGATGTGTATGACG-AGGGCCCTTACACCTGTCTCGGTGACAGAGA 353
QY 493 CAACCAACCAAGACCTCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTA-- 550
Db 354 CAATCAACCAAGACCTCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTA-- 411
QY 551 GAGATTTCTTCAGATATCTCCATTATTAAG--GGAACAATATTAGCTCACCTGCATAG 608
Db 412 GAGATTTCTTCAGATATCTCCATTATTAAG--GGAACAATATTAGCTCACCTGCATAG 469
QY 609 CAATCTGTAGACACGAGACCTTACCGTTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCT 668
Db 470 CCACGGGCGAGCCAGACCCCAACATCACTTGGAGACACATCTCTCCAAAGCGGTGGCT 529
QY 669 TTGTGAGTGAAGACGAATCTTGGAAATTCAGAGCAACCGCGGAGAGTACAGGGAC 727
Db 530 TCATACGCGAGGACGAGTACCTGGAGA--TCACAGGATCATCAGAGGAGAGTACAGGGAC 588
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QY 788 GTGAATATCCACATACATTTTCAAGACCAAGGTTACAGGTGTCCCGTGGGACAAAAG 847
Db 649 GTCAACTTACCCACGTTACATCTCGGATGCGAAGAGCACCGGTGTGCGCGTGGGCGAAG 708
QY 848 GGGACA--CTGCAGTGTGAAGCCTCAGACGTCCCTCAGCAGAAATTCAGTGTGTACAGG 905
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Db 827 CCGGACTGACTTCTTCAAGCTCTCCGAGCAGGACTACGGCAACTACACCTGCGTGGCT 886
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Db 887 CCAACCCAG--GGGATCCACCGCGGTGCGCCACCATGTTGAGCAAGGCGAGGAGCTGTT 944
QY 1066 -----TGGT--CCAGGGCGCC--GTC-AGC--GA--GGTGAGC--AAACGG-CAC--GT 1103
Db 945 CACCGGGGTGTGCCCA---TCCTGTGTGAGTGTGAGCGGCA-CGTAACAGCCCAAGT 1000
QY 1104 ----CGAG-----GAGGGC-AGGCTGGC-T-----CT--GGC-TGCTG--CC-----T 1135
Db 1001 TCAGCGTGTCCGGCGAGGGGCGAGG--GCGATGCGCACCTACGCGAAGCTCCCTGGAAGTT 1058
QY 1136 CTTCTGTCTTGGACCTGCTTCTCAAAATTTTGTGAGTGTGCACTTCCCAAC--CGGG 1193

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Db 1059 CATCTGCAC-CAACGGC-AAA-GCTGCCGCTGCC-CTGGCCCAACCCCTCGTG 1104
QY 1194 A-----A-GCT---GCCGCCCAACCCAC-CAACA-1222
Db 1105 ACCACCTGACCTACGGCGTGCAGTGTCTACGCGCTACCCGACACATGAAGCAGCAC 1164
QY 1223 -----CAA-CAGCAATGGC-AA-C-AC-CGACAGCA-ACCAATCAGATAT 1261
Db 1165 GACTTCTTCAAGTCCGCAATGCCGAGGCTAGTC-CAGAGCGCAC-ATC-T-T 1217
QY 1262 ATACAA-ATGA-AAAATGAAGAAACACAGCTCATG-GGACAGAAATTTAGGG-1312
Db 1218 CTTCAAGGACGCGCACTACAGACCCGC-GCC-----GAGG--TGAAGTTCGAGGGG 1270
QY 1313 --A-----GGGACAAAGAT-A-CTTTGGGGGAAGAGTTTAAABAGAA-ATT 1361
Db 1271 ACACCTGTGTGAAC-CGATCGAGC-TGAAGGGCATCGACTT-----CAGGAGGAGC 1321
QY 1362 G-AAAATTGCCCTTGCAGATATTAGGTACAA-TGGAGTTTCTTTTCCCAACGGGAAG 1418
Db 1322 GCAACAT-CCTGG-----GGCACAAGCTGGAT-----AC---AAC 1353
QY 1419 AAC-ACAGACAC-CCGGT-----TGAACCCAC-TGC--AAG--CTGCATC---GTGC 1462
Db 1354 TACAACAGC-CACAACGCTATATCATGG-CGACAAAGCAGAGAACGCGCATCAAGGTG- 1410
QY 1463 AACCTCTTT---GGT-GCCA-----GTGTG--GGCAAGGC-T-CAGCCTCTCTGCC 1506
Db 1411 AAC-TTCAAGATCCGCAACAAATCGAG-GACGGCA---CGGTGAG-CTCGCCGAC 1461
QY 1507 CA-----CAGAGTCCGCCA-CGTGGA-----ACAATCTGAGCTGGCC-ATCCCAA- 1551
Db 1462 CACTACCAGCAGACACCCCATCGCGACGGCCCGTGTCT--GCTGCCGA---CAAC 1515
QY 1552 -ATT-----CAATCAGT---CCAT-AG--AGA-CGAAC-AGA-----ATG 1582
Db 1516 CACTACTGAGCACCACCGCTCGCCCTGAGCAAGAGACCCCAACGAGAAGCGCGATCATG 1575
QY 1583 AGACCTTCGGGCCAAG--CGTG-GCGCTG-CGGG--CACT-TTGTGAGTGTGCGCAC 1635
Db 1576 -GTCTGTCTGG---ASTTGTGACCGCCCGGGATCACTTCGGCA--TG-G-----1621
QY 1636 AG-GCGTGTGTGTGAACGTAATAA 1663
Db 1622 ACAGGC-----TGT--AC--AAGTAA 1638

RESULT 25
AC110642.2/c
WPCOMMENT
Sequence split into 5 fragments LOCUS AC110642 Accession AC110642
Fragment Name Begin End
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AC110642_1 100001 210000
AC110642_2 200001 310000
AC110642_3 300001 410000
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Continuation (3 of 5) of AC110642 from base 200001 (AC110642 Rattus norvegicus clone CH2)

Query Match 49.7%; Score 834.5; DB 2; Length 110000;
Best Local Similarity 45.7%; Pred. No. 17;
Matches 1388; Conservative 0; Mismatches 206; Indels 1440; Gaps 286;

QY 2 TTGTGTCC-TTC-AGCA-----AA-A-CAG-TGGAT---TTA-----AATC---34
Db 63038 TTG-----CAATTCTGATATTATTAATAGCAATGATACGTTACTGCAGAAATCGAG 62983
QY 35 --TCCTTG-----CAC---AAGCTTGAG-AGCA-----ACACAAT---CTA-----66
Db 62982 GAGCAATTGTCTATACCACTGGATCTCTGAGTAGAGTTGAACAAATGAATTAATGAAGT 62923
QY 67 -----TC-----AGGA--A-AGAA-----AG-----AAAGAAAA-AA-----90

Db 62922 GTGTTTCCAGAAAGGACTAGAGATGTGAGCTTATGAAGAAAAAAGATATGTCTGTGG 62863
QY 91 -----CC-----GA-----94
Db 62862 AGTGCAGTTTCTCTGCGTGTGCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 62803
QY 95 -----ACCTG---ACA--A-AAA--AG-----AAGAAA-----AAG 117
Db 62802 GGGGGGTACATGTGCGCCACATGCTAGTACTGAGAAATATTTAAGAAAGCATTTGGAGGAAG 62743
QY 118 A-AG--AA-----GAAAA-----AATCA-----TGA-----AA-----ACCATC 145
Db 62742 ACAGTCTAAGGTGCGAAATAGTAGGACATCAATTTGTGTGTGTGTGTGTGTGTGTGTGT 62683
QY 146 CAGCCAAA-----AA--TG-----CA-----CAATTC-----T-----166
Db 62682 GAGCCAGACGTTCTTGTGTAAAGCTGTAGGGTCTAGCTGGAGCAGTCCGGAGGTGTGAA 62623
QY 167 -AT--CTCT-----TG-----GGCAATCTTTCAG--187
Db 62622 CATTACTCTGGAATTAGTGTAAAGGATAAATGTGAGATGTCCAGGCAAGC--CATGGCAG 62565
QY 188 -GG--GCTGGCTG--CTCTGTGTCTTCCAGAGGAGTCCCGTGC-----G-----CA 230
Db 62564 TGGTAGCT-GCTGAACCTCTGTG--ACTTGAAGAGGTGAG--CCATGCAAGTGTCTTCTTTTCA 62509
QY 231 GC-----GGAGA-----TG--CCACC--TTCC--CCAA--AGCT-----256
Db 62508 GUAGGTGTGGGAGACCTTCTCCCTTGGCCCGCTTATTTCTGTCTAATTCAGCTTTCCCC 62449
QY 257 ATGGAACAG--TGACG-GTCCGGCAGG-GGAG--AGGCCCAACCTCA-----GG 301
Db 62448 ATAGA--GGCTGAAGAGACAGGAGGAGGAGAGAGAG-----T-ATTGTATGGGG 62400
QY 302 T---GCA-----CT--AT-TGACACCGGGTCAACC-----GGGT 330
Db 62399 TGAGCAGTGGTAGGTGAGTATGATAAC-----TCAGCCTTGAATGAATGAACAGCAGGAA 62344
QY 331 GGCCTGGGTAA-----ACCGCAGCACCATCC-TCT-----ATGTCTGGGAATG-----AC 373
Db 62343 GGCCTTGTGAATTTACCG-AG-ACAATCTTCTTTTAAAGAAAGGTG---AAGTATTCAC 62289
QY 374 AAG-----TG--GTGC-----CTGG-----ATCCTGCG-----GTG 397
Db 62288 AGGCCCTGTCTCTTTCTGTGTGTGACCTCACTGGCTTAGGAGCTATCC--CTACAGAT 62232
QY 398 GTCC---TTC-----TGAGCA--ACACC-CAA-----AC-GCA-----GT- 425
Db 62231 GTCCGTGTTTCCCAACAT-AGCATTAACCAACCAAGTCTGAGGACTGCACCAATGTAGTTA 62173
QY 426 -AC--AGCATC--GAG-ATCCAGAA--CG-TG--GATGT-----GTATG--AC 460
Db 62172 AACAGAGCATCAGGGAGCACCAGCAGAGCCGTTGSCACAGAGTTTTCAGGT-TGGACAC 62114
QY 461 GAGG-G--C--CCTTA-----CA-----C-CTGC---478
Db 62113 AAGGTGTTTCATCTATATATGTCATTTTGTGGCAGGCTGGCAGGGCCTCTCTGT 62054
QY 479 --TC-----GG-----TG-----CAG--AC-----AGAC 493
Db 62053 ATTCTGTTGGCTTATGACTTCTACCCCTCAGTTACGTAAAGAGGAATGAAGAA 61994
QY 494 A-----ACCA-----CCCAAGA-----CCTCTAGGGTCC-----518
Db 61993 AAGAGAGCACCAGTGTGTCTCAGAGAACTAGCATTTCTCT-GGG-CCATGSCAGGTAG 61936
QY 519 ---AC-----C-----TCATTG-----TG--C-----AAGT---AATC 537
Db 61935 CTAGACAGAGAGGGTGAAGTGTGAGTGTCAATGAGGAATGCACTTTAAAGTTGAATC 61876
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Db 61875 CTTGATATTTCAGACAGCAAAAGAGATAGAGAAATAATATAGGAGCCCTGTGTACAGTT 61816

QY	557	T	-----CT-----TCAG-----A-TA-----TCTCCATT-----	574
Db	61815	TGTGCCCTGATGACTCAGCGGCTTAAGTACACAGACACATTTTCAATTGTTGGACA	61756	
QY	575	-----AA---TCRAGGGRACA---ATATTA-----	594	-----G
Db	61755	AGGTACATGAGAAAGATTGAATGGACCACTCATTTTACCAGGGAAGAAATGGAACTGG	61696	
QY	595	C-CTCAC---CTGCATA-----	615	-----GC---AACTGG---
Db	61695	CTCTCAGAGCTGCATATATGGTCTCATTTGACAAATCAGGACAAATGGCCAAAGTGGAAA	61636	
QY	616	---TAGACGAG---AGCCT-AC---GGT-TA-C-TTGAGACACACATCTCTCC---	654	
Db	61635	GAATAGAACAGTCCGACTCACTCAAAGTATAGCAATGTA---ACCTCTTCCAGGGGCC	61579	
QY	655	---CAAAAGCGTTGGC---TT-TCGTGA-----GTGAA---GAC---GA	684	
Db	61578	TGTCAGAGAG---TGGCTCTCTTCTGGGAAAAGAGAGAAAGTGGGTGAAGGTGACGTGGA	61521	
QY	685	---ATACTTGGAA-----ATTC---AG---GGCA-----TC---ACCCGG---	712	
Db	61520	GTGGCTAC-AGGAAGGGCGCTTAGTCGAAAAGCTAGCAGTTTAGATTCTAGAA---GGTG	61465	
QY	713	GAGCAGTCAGGGGACTACG---AGTG---CA-----GT---G-CCTC---	744	
Db	61464	TGAGCAGT-AGGTGACTAAGCCTAAGTGAACAACCAATTGAAAAGTAAAGTCTCTCAGGGTTT	61406	
QY	745	CA---ATG-----AC---GTGGCCGC---GC---CCGTG---GT---	768	
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QY	769	---AC-----GG---AGATGA---AAGTCAAC---GTGAACATATC-CACCAT	803	
Db	61345	GGATCACTCCCTGCCGGGCAGACAGACAGAAAGGTTCCCTGGGG---CT-TCTCAGCAT	61289	
QY	804	---ACATTTTC---AGAGCCRAGGTA-----CAGGTGTCCC-----C---	835	
Db	61288	GATGCCCTTAACATGCCAAGAGC---TGTATGATCTTGTGACCCCAAGCTAATATAA	61233	
QY	836	GTGGGACA-----AAAGGG---GACACTG---CA---GTGT-GAAGC---	867	
Db	61232	GTTGACAGCTGTGACTTCAAGGGCCAGA-AATGGAATCACATGGGTAGTAGCTAGA	61174	
QY	868	-----CT---CAG---CAGTCCCC-----TC-----AGCA-----GAAT	890	
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QY	891	TCCAGTGGT-----ACAAGA-TGACA-AAAGACTGA-T-TGA-AGG-----	927	
Db	61114	---GTGGTGTGATTTAACAGAGAGTGCACCAATCTAGCTCTCTAGTAGGGCGATCG	61059	
QY	928	-----A---AAGAAAGGG-GTGAAGTGGA-----AAAACAGAC	956	
Db	61058	GGTTTTGGCAGTGTTCAGGTGAGGACAGGAGGGGAATATGGACACCACTTCTAATATGCC	60999	
QY	957	CT-----TTTCCT-----C---TCAAA-A---CTCAT-----CTT---C---	979	
Db	60998	CTGAAAATTCATTGTACAGACAGATCAGAGCGAGTCTAATCAGAGGCCCTTATCCCTG	60939	
QY	980	TTCA---ATGTCTCTGAA--CA-----TGAC---TATGGGAAC---TA---C	1012	
Db	60938	TTCAATTATTTCT-ATGTCATCTGATTTCTGACTTTAT-GTACATCAATATATCACC	60882	
QY	1013	A-----CTTGCGTGG---CCT-----CCAA-----C-----	1030	
Db	60881	ACTTCTCTTTTCATGGAAAGTCTTAGACCMAAAAGCAATATAGCCAGAGTTTGTATG	60822	
QY	1031	---AAGC-TG-----G---GCCACACCAA---TG-----CC-----	1051	
Db	60821	AGAAACGCTGAGCAGCAGTAACGACAGACCAAGTACTGGCAGAGAGCTTTTCTGTGT	60762	

Qy	1052	-----AGCAT-----CA-----TGCATTT-----GCTCCAGCGCGCGTCAGCG	1085
Db	60761	TGAGCTGCGAGTAGCTTACCGGACATGTGTGTTCTTTCCACAGCGCCAGTGCTGTGCAGCG	60702
Qy	1086	AGGTGAGCAACGCGACGTCGAGGAGGCGAGGCTGGCTGCTGGCTGCTGCTCTCTCTGGTCT	1145
Db	60701	AGGTCAACAATGGGACGTCAGGAGGGGCGGCTGATTTGGCTCTCTCTCTCTCTCTGGTCT	60642
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Db	60641	TACACCTGCTCTCTCAAAATTTGATGTGAGTGCCTTCCTCCCGGGGAGA-GGTGTGTCG	60583
Qy	1206	CACACCCACCCACACAAACAGCAATGCGCAACCGCAGCAGCAACCAATCAGATATATAC	1265
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Qy	1266	AAATGAATAATTAGAGAAAACAGAGCTCATGGACAGAAATTTGGGAGGGGAGCAAAAGA	1325
Db	60531	AAATGAATAATTCGAGAATCACAGCC-AATGACACAGAAATTCGAGGAGGGGAGCAAAAGC	60473
Qy	1326	ATACTTTGG-----GGGG--AAAGAGATTTTAAAAA-GAAA-TTGAAAAATTGCCCTTGCGAG	1377
Db	60472	ATACTGTGTAAAGGGGAAAAAAAGCTTAAAAAAAGAAATTTGAAAAATTTGCCCTTGCGAG	60413
Qy	1378	ATATTTAGGTACAAATGGAGT-----TTTCTTTTCCAAACGGGAGAAACACAGCACACCCG	1433
Db	60412	ACATTTCCGTTACCACTGAGTTTCTTTCTTTTCCCAATGGGAGAA---GGCGCACCTA	60356
Qy	1434	GCITTTGACCCA-CTGCAAGCTGCATGTCACACCTTTTGTGCCAGTGTGGGCAAGGGC	1492
Db	60355	GCITTTGACCCACCAACAGCTGCATGTGTGACCTCTCTTTGCCAGGGTGGGCAAGGGC	60296
Qy	1493	TCAGCTCTCTGCCCCAC-AGAGTGCCC--CCAGTGGAAACATTCGAGCTGGGCATCCC	1549
Db	60295	TCAGCCACTCTGCCACTAAAGTGCCCCACCA--TGAACATTCCTGAGTGGGCATCCC	60238
Qy	1550	AAATTCAAATCAGTCCATAGAGAC--GAACAGAAATCAGACCTTCC---GGCCC--AAGCGT	1602
Db	60237	AAATTTTCATCGTCCATAGACAAAGCAGAGTGAAGA---AACAGGGGCCACAGAA--GT	60183
Qy	1603	GGCGCTGCGGGCACTTTGGTAGACTGTGCCACCACCGCGGTGTGT-----TGTGAAA--	1653
Db	60182	GCCACGGAGGGCCCTTTGTTGGCTGCGCATGATGGCGTGTGTCTATCAAGTGTGAATC	60123
Qy	1654	C---GT-GAAATAAA---AAGAGCAAAAAA-AA	1679
Db	60122	CGAAGTAGAAAAAANAACAGAAATAAAAAAGA	60089
RESULT	26		
LOCUS	AF271618	2935 bp	DNA
DEFINITION	Synthetic construct secretory IgGEPUS-GFP fusion protein	linear	SYN 21-MAY-2001
ACCESSION	AF271618	(IgTCEPUS-GFP) gene, complete cds.	
VERSION	AF271618.1	GI:14161270	

RESULT 26	
AF271618	linear SYN 21-MAY-2001
LOCUS	
DEFINITION	2935 bp DNA
	Synthetic construct secretory IgGCEPUS-GFP fusion protein
	(IgTCEPUS-GFP) gene, complete cds.
ACCESSION	
AF271618	GI:14161270
VERSION	
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
	artificial sequences.
REFERENCE	1 (bases 1 to 2935)
AUTHORS	Kim,D.-S. and Moss,D.J.
TITLE	Neuronal-specific secretory IgGCEPUS-GFP fusion protein expression
	in transfected cells
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2935)
AUTHORS	Kim,D.-S. and Moss,D.J.
TITLE	Direct Submission
JOURNAL	Submitted (24-MAY-2000) College of Natural Resources and Life
	Science, Division of Biological Resources R-6517, Dong-A
	University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of
FEATURES	Korea
	Location/Qualifiers

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ORIGIN
Query Match 49.3%; Score 828.5; DB 12; Length 2935;
Best Local Similarity 47.3%; Pred. No. 0.033;
Matches 1283; Conservative 0; Mismatches 249; Indels 1181; Gaps 187;

QY 1 GTTG---T---GTCT---TC-----A-GCAAAA-----C----- 20
DB 354 GTTGCTTTTCGAGGCGCTTTGTCTGAAGGATGCAAAATCTACGGATGCTAGCGAGGGGG 413
QY 21 --AGTG-----GATT-----TA-AATCTC-CTTGACAAAGCTTGAGAGCAACACATC 64
DB 414 GAAGGGGGAGAGATTACCTCATACATGTCGTTGCACCA-----ATCACAC--TC 464
QY 65 -----TATCGAGGAAGA--AAG-----AA-AGAAAAAACC---G--- 93
DB 465 CTGTCGGCGGCTTCTCTGGGAGACGAGGGGCTCTGGACCAACACAGGAAAGGCGCTTGCGCC 524
QY 94 AACC-----TGAC-----AAAAAGAG--A-----AA-----A-AGA 118
DB 525 ATCCCATGTGACCGAGCTGTATATAAGAGGCGCATCCGCCAAGTCCGCTACCGGA 584
QY 119 ---AGA---AGAAAA---AAAT-----AAAT-----CA- 134
DB 585 CTCAGATCTCGAGCTCAGCTTCGAATCTTGCAATCTGCAATCGGATACCGGGCCCTGGCAG 644
QY 135 TGA-----AA-----AC-CA--TC--A---G--CCA-----AAATGCACA 161
DB 645 TGAGTGGGGAGAGAGGGGAGGACGACGAGCTCCGAATATGCGCCAGGCGGAAAAATGCAGC 704
QY 162 ATTCTATCTCTGGCAATCTTCACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 221
DB 705 ACCCGGTCTCATGGGTGATCTTCGCGGGATGGCCGCACCTCTCTCTTCCAGAGGATGC 764
QY 222 CCGTGCAGCGGAGATGCCACCTTCCCAAGCTATGGACAACTGACGGTCCGGCAGG 281
DB 765 CCGTGCAGCGGAGATGCCACCTTCCCAAGCTATGGACAACTGACGGTCCGGCAG 824
QY 282 GGGAGAGCGGACCTCAGGTGCATATTGACAAACGGGTGACCCGGGTGGCTTGGCTAA 341
DB 825 GGGAGAGTGGACGCTCAGGTGCTCCGTGGACAAACCGGTCACCCGGCTGGCTGCTGA 884
QY 342 ACCGACACCATCTCTATCTGGGAATGACAGTGGTGGCTGGATCTCGGTGGTCC 401
DB 885 ACCGACACCATCTCTATCTGGGAATGACAGTGGTGGCTGGATCTCGGTGGTCC 944

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QY 402 TTCTGAGCAACACCCAAACGCGAGTACAGCATCGAGATCCAGACGCTGGATGTCTATCAACG 461
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QY 462 -AGGGCCCTTACACCTGCTCGGTGCGAGACAGCAACACCCAAAGACCTCTAGGGTCCAC 520
DB 1005 AAGGGCCC-TACACCTGCTCGGTGCGAGACAGCAACATCACCCCAAGACATCTCGCGTGAC 1063
QY 521 CTCATTGTGCAAGTATCTCCAAAATTGTA--GAGATTTCTTCAGATATCTCATTAATG 578
DB 1064 CTCATTGTGCAAGTGTGCGGAAAT--TACCGAGATCTCTTGTGACATCTCCATCAATG 1121
QY 579 AAG--CGAAACATATTAGCTCACCTGACATAGCACTGTAGTACACGAGAGCTACGGTTAC 636
DB 1122 AAGGTGG--CAAGCTCAGCTCACCTGATAGCCAGGGCAGGACCCCAATCAATC 1179
QY 637 TTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGACGAATATCTTGGAAAT 696
DB 1180 CTGGAGACACATCTGCCCAAGCTGTGGCTTCATCAGCGAGGACGAGTACCTGGAGA- 1238
QY 697 TCA--GGGCATCACCGGGAGCAGTACGGGAGCTACGAGTGCAGTGCCTCCAAATGAGTGG 755
DB 1239 TCACAGGCATCAGAGGGAGCAGTCCGGGCGAGTACGAGTGCAGTGCCTCCACGACGTGG 1298
QY 756 CCGCGCC--CGT-----G-----GT--ACGGAGAGTA-----TCACC----- 787
DB 1299 CCGCGCTCTGTCAGCGAGTCAAGTCAACGTCACCTCACTGTGAGTACGTGGGGTGG 1358
QY 779 -----A-----AGG-----TCACC----- 787
DB 1359 GGACAGCCAGGGCCACATTTGTCACCCCGAGGGATGACCGTTCACTGCTTGTGGT 1418
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DB 1419 CCACACCCAGCTGCGGAGCAGAGTTCCAAGCAGTGGTGTGCTTGTGCTTTTATTC 1478
QY 791 -----AA-----CTATC 797
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QY 798 CACC-----ATA----- 804
DB 1539 AACCTCAGTTTCTGCTGTGTGAGATGTGTCTGATAAACCCTCAGGGAGAGAGGGA 1598
QY 805 -----CATTT----- 809
DB 1599 AGTGAGCAGTAAACAGGCATTTCTTCTGTTTGAATAAAAGGAGAGAGAGAGGA 1658
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DB 1659 AAGCAGACTGTTTGTGCTCATAGACAGAGTGAAGACCTCCACACCCCGGAGCTCC 1718
QY 814 -----AGCCAAG-----GGT----- 823
DB 1719 ACTCTGGCCACCCCTGGAGCTTCGGGCGATCAGGGAGAGCAAGGAGTGTGCTTGG 1778
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DB 1779 AGGATCAGGGATGTGGTTGGTGGTCCCATCTGCTCAGCCCTTCGACAGCAGACAA 1838
QY 843 ----- 842
DB 1839 GAGCTCAGGAGCTGGGCAATAGCTCGGAGATGATTTTCTCTCTCTTGTGAGTGGGAA 1898
QY 843 ---AAAG-----GGGA-----CAC 854
DB 1899 AGAAAAAGGAGAGAGAGTGGGAGGACCAACCCCGAGCTCGCTCTCCCGACAGACCCAC 1958
QY 855 -----TGC-----AG-----T 860
DB 1959 CGTACATCTCGGATGCAAGACACCGGTGTGCGGGGAGAGGGGATCTCTGATGT 2018

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 2179)

Lipman,D.A., Lee,N.M. and Loh,H.H.
Opicoid-binding cell adhesion molecule (ORCAM)-related clones from a rat brain cDNA library (1992)

Gene 117 (2), 249-254 (1992)

92347701

1339369

Original source text: Rattus norvegicus (strain Simonsen ICR) brain cDNA to mRNA.

Location/Qualifiers

1. .2179

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ORIGIN

Query Match 48.8%; Score 819.5; DB 10; Length 2179;

Best Local Similarity 53.6%; Pred. No. 0.028;

Matches 1242; Conservative 0; Mismatches 260; Indels 815; Gaps 185;

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QY	45	A-GCT-----TGAGAGCA-----ACAC--AATCTAT-----CAGGAA---AG-AA-- 77
DB	62	ATGTTAAACAGTGGAGCAGGGCTGTCTGACTCTGTGTCCTGCGCGCAGTGAGCAATG 121
QY	78	-----AGAAGA--A-AAAAACCG--AACCTG-----A----- 100
DB	122	GTCTTAG-AAGACTTATTAGCTCCGAGAGCGCTGGACTCAGCCTTGCCCTTCTCCCGCTC 180
QY	101	-CA-----CA-----TATCT-----CT-----TGGGCAA-T-CTTCACG 187
DB	181	CCAGCTCTCGGTTTGTCTCTGTGTGCTTTCGTTCCTCTCAATCTCCGGCTATTCTGAGAG 240
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DB	241	G-----GCAGGGA-----CA--AGGACCGTGCAGCTGCAAGAGTTCTAGGAAGTTG 285
QY	157	--GC-----ACAAAT-----TC-----TATCT-----CT-----TGGGCAA-T-CTTCACG 187
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QY	188	GGG-----CT--GGCTCTCTGTGTCTCTT-----CCA-AGGAGTGCCCGTGGCGAGC 232
DB	341	TGTCGTGTCTCTGAGGCTG--CTGT-TC-CTTGATCCACAGAGGTGCGCGTGGCGAGC 396
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QY	589	TATTAGC---CTCACC-----TGATAGCAACTGGTAGACAGAGCCCTACGGTTACTTG 639
DB	744	GATAAGCAGTGTGACCTTGTATGTCTGCAATTTGGCAGACCAACCAAGTGCATG 803
QY	640	GAGACATCTCTC---CCA--AAG--CGTTGGCTTTGTGAGTGAAGACGATATCTTGG 592
DB	804	GCGCAC--CTGTAGTCAAGGAAGGCCAG--GGCTTTGTGAGTGAAGATGAATACCTGG 859
QY	693	AAAT--TCAGGGCATCACCCGGGAGCAGTCAAGGGGACTACAGTGCAGTGCCTCCCAATGAC 751
DB	860	AAATCTCA-GACATCAAGCGACCAATCTGAGAGTATGAGTGCAGCGCTTGAATGAT 918
QY	752	GTGGCGCGCCCGTG--GTACGAGAGTAAAGGTCACTGAGTAACTATCCACCATACATTT 809
DB	919	GTGCTGTCACC--TGATGTTCCGAAAGTAAAAAATCACTGTAATACTATCTCCTATATCT 976
QY	810	CAGAGCCCAAGGTACA--GGTGTCCCGTGGGACAAAGGGGACA--CTGCAG-TGTCA 864
DB	977	CAAAAACGAA--GAACACTGGCGTTTCAGTAGCCAGAGAGGG--CATCTG-AGCTGTGA 1031
QY	865	AGCCTCAGCAGTCCCTCA--GCAGAAATCCAGTGTGTACAAGGATGACAAAAG----- 915
DB	1032	AGCCTGTGTGTCCC--CATGCTGATTCAGTGTGTTCAAGGAAGATACCAAGTTAGCC 1089
QY	916	ACTG--ATTGAAGGAAGAAAGGGTGA-AGTG-GAAACAGACC---TTTCTCTCAA 968
DB	1090	ACTGGCCT---GG-----ATGGCGTGAGATTGAGAACAAAGCGCGCATATCACT-TT 1139
QY	969	AACTCATCTTCTCAATGTCTCTGAACTGACTATGGGAACACTACCTCTGGCGCTCCA 1028
DB	1140	GACT-----TCTTCAATGTCTCAGAGAGGATTTAGGAACTATATCTGTGGGCCACAA 1195
QY	1029	ACAAGCTGGGCCACCAATGCCATCATGCTATTTGGTCCAGGCGCGTCAGCGA-G 1087
DB	1196	ACAAGCTTGGGAACCAATGCCAGCATCACCTGTATGGCGCTGGAGCAGTCATTGATG 1255
QY	1088	GTG-AGCAA--CGGACAGTGGAGGAGGCA--GGC-TGGCTCTGGCTGT---GCCTCT 1137
DB	1256	GTGTA-AACTCGGC-C-TCTA-GA-GCAGTGGCTTGTCTCTGGCT-CTCAGGAGC-CT 1306
QY	1138	TCTGTCTTGCAC-CTGCTTC-TCAAATTTTGTATGTAGTGCCA--CTTCCCCACCCGGG 1193
DB	1307	TCT---TTGCCACTTCTTCATCAAGTTTGTGAAAGA-----AACCTT----- 1346
QY	1194	AAAGG---CTG--C--CGCCACCAACCAACCAACACA-ACAGCAATGGCAACAC--C- 1241
DB	1347	--AGGTCTCTGAGCATGCGCTTCTCCA-TATCAGAGACTTTAAT--CTACACTGG 1401
QY	1242	GA---CAGCAACCA-----ATC-----AGATATAT-----ACAAATG 1270
DB	1402	GAGGGCA--AACCAAGTTTGGGCTTCTTTTGTGTTATTTTGTCTCTTGTAC---TG 1456
QY	1271	AAATTAG-----AAGAAACACAGCCTCATGGGA---CAGAAATTTGA----- 1309
DB	1457	--TTTGTGTTTGGTTGA-----TTTC-TGGGATTTTC---AATTGATTTGTTTT 1503
QY	1310	-----G-----GGA--GGGGAACAAAGATACTTTGGG-----GGA--AAAGA 1344

	Db	1504	TCCTTTTTCGTTGAATGGACCGGG-----TTGGGGGTGGGAATGGGCAGG	1550
	Qy	1345	GTTTATA-----AAAA--AGAAATTG-----AAAATTCCTTCACGATAT	1381
	Db	1551	GTCTCACCAGTAGGATAAATCAGGTATTGGTGGGCCCCCAA--TG---GAATATAT	1604
	Qy	1382	T--TAGTACAATGGAGTT-----TTCTTTTTTC-----	1407
	Db	1605	TCCT-GCTACTTGGCCTTCCTTTCTCFACCTCTCTCTCTACCAACATAACACAAA	1663
	Qy	1408	----CAA--ACG-----GG--AAGAA--CACA-G-CA--CACCC---GG	1434
	Db	1664	CACACRACACACGCCCTAAAGATGGCTAAAAAATGTCCCATGACACGCACTGAAGG	1723
	Qy	1435	----CTTGACCCAC--TGCA-----AGCTGATCGTGA--ACC---TC	1468
	Db	1724	TACAACTTGG-CCACAGTGGGTACACAATAGAGATTGCATC-TACATTTCTGTTTC	1781
	Qy	1469	TTTG-----GT-----GCCAGTGTGGCA--AGGGCTCAGCCT-----	1499
	Db	1782	TTTGTCCTTTAAAGTTTTCAATTAAGACAGTTT-----AAAAAGACACATCCTTATCCCTAT	1837
	Qy	1500	-----CT-----CTGCCAC-----AGA-----	1512
	Db	1838	GTTTGTATACCTTATCCATTAACTGTGCACCTTTCTTAAGAAACCTTCTTACTACATC	1897
	Qy	1513	-----GTGCCCCACGTGGAAACATTCGTGAGC-----TGGCCATC-----CC	1549
	Db	1898	CTCAATGTGCACACATGT--ACATTC-----CATAAAAATTTTACCATCTTCTCTGGCC	1950
	Qy	1550	AATTC-----AATCAG-----TCCA-TAG--AGACGAACAG-----AATGAG	1584
	Db	1951	--ATTCTGTTAATCTGCATTTTCCACTAGCAATGACACTTACAGGCTTGATGAAT-AT	2007
	Qy	1585	ACCTTCGG--CCCAGC-----GTGGCGCTGCGGACA-CTTT-----GG	1621
	Db	2008	ACAT-----GTATCCAAAGCTACAAATTTAGAAGT--CAC-GAGGGAAGTCTATCTAGGGG	2060
	Qy	1622	TAG-AC-----TG-----TGCCAC-CACGCGTGTTGT-GAAGCTGA--AAT	1661
	Db	2061	TAGTACTTCCTTAAATAGCTAATGCAACTCA-----TAAAAAGTGATCAAT	2108
	Qy	1662	A-----AA-----AAG--AGCAAA--AA--AAA	1678
	Db	2109	AGCTAGCTAATATATCAAGCTATCAAGGAATCATTA	2145

Search completed: May 28, 2004, 18:56:48
Job time : 6950.01 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 13:09:09 ; Search time 743.61 Seconds
(without alignments)
9592.021 Million cell updates/sec

Title: US-10-017-084a-522

Perfect score: 1679

Sequence: 1 gttgtcttcagcaaac.....ataaaagagcaaaaaaaa 1679

Scoring table: IDENTITY NUC

Gapop 1.0 , Gapext 0.1

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N Geneseq_29Jan04:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001bs:*

5: geneseqn2001bs:*

6: geneseqn2002s:*

7: geneseqn2003as:*

8: geneseqn2003bs:*

9: geneseqn2003cs:*

10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1679	100.0	1679	2	Aaz34324 Human PRO
2	1679	100.0	1679	3	Aac78590 Human PRO
3	1679	100.0	1679	4	Aac87037 Nucleotid
4	1679	100.0	1679	4	Aas21431 Human CDN
5	1679	100.0	1679	6	Abk33598 cDNA enco
6	1679	100.0	1679	6	Abk33598 Human PRO
7	1679	100.0	1679	6	Abk33598 Human PRO
8	1679	100.0	1679	6	Abk33598 Human PRO
9	1679	100.0	1679	7	Abk33598 Human PRO
10	1679	100.0	1679	7	Abk33598 Human PRO
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25	1679	100.0	1679	7	ACA04211	Human CDN
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27	1679	100.0	1679	8	ADA45894	Novel hum
28	1679	100.0	1679	8	ADA76325	Human PRO
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30	1679	100.0	1679	8	ADA18975	Human PRO
31	1679	100.0	1679	8	ADA61598	Homo sapi
32	1679	100.0	1679	8	ADB19383	Novel hum
33	1679	100.0	1679	8	ADB27924	cDNA enco
34	1679	100.0	1679	8	ADA86403	Novel hum
35	1679	100.0	1679	8	ADB15967	Human PRO
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37	1679	100.0	1679	8	ADA67548	Human PRO
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39	1679	100.0	1679	8	ADA85851	Novel hum
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58	1679	100.0	1679	8	ADA75221	Human PRO
59	1679	100.0	1679	8	ADA85299	Novel hum
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61	1679	100.0	1679	8	ADB30003	cDNA enco
62	1679	100.0	1679	8	ADA80531	Human PRO
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69	1679	100.0	1679	8	ABT44571	Human PRO
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73	1679	100.0	1679	8	ADA81083	Human PRO
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86	1679	100.0	1679	8	ADA76980	Human PRO
87	1679	100.0	1679	8	ADA88610	Novel hum
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92	1679	100.0	1679	8	ABT43944	Human mem
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94	1679	100.0	1679	8	ADB22857	Human PRO
95	1679	100.0	1679	8	ADB23630	Human PRO
96	1679	100.0	1679	8	ADA92352	Novel hum

97 1679 100.0 1679 8 ADB15415 Human PRO
98 1679 100.0 1679 8 ADB83615 Novel hum
99 1679 100.0 1679 8 ADB80721 Novel hum
100 1679 100.0 1679 8 ADB73262 Novel hum

ALIGNMENTS

RESULT 1
AAZ34324
ID AAZ34324 standard; cDNA; 1679 BP.
XX
AC AAZ34324;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO337 nucleotide sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.
XX
OS Homo sapiens.
XX
PN WO946281-A2.
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99W0-US005028.
XX
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
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PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-0040202P.
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PR 08-APR-1998; 98US-0081049P.
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PR 15-APR-1998; 98US-0081817P.
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PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.

PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
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PR 07-MAY-1998; 98US-0084627P.
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PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
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PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
XX
PA (GETH) GENENTECH INC.
XX
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI, 1999-551358/46.
XX P-PSDB; AAY41773.
XX
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders.
XX
XX Claim 2; Fig 221; 530pp; English.
XX
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as sources
XX of probes, primers, for chromosome mapping, and for generation of
XX antisense sequences. They can also be used to create transgenic animals.
XX The proteins can be used to treat a variety of diseases and disorders,
XX depending on their function. Diseases that may be treated include blood
XX coagulation disorders, cancers and cellular adhesion disorders. They may
XX also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
XX AAY41774 represent polynucleotide and polypeptide sequence given in the
XX exemplification of the present invention

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1679;	DB 2;	Length 1679;	
Best Local Similarity	100.0%;	Pred. No. 1.5e-15;			
Matches 1679;	Conservative	0;	Mismatches	0;	Gaps
QY	1	GTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTTCCTTGACAAAGCTTTGAGACCAAC	60		
DB	1	GTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTTCCTTGACAAAGCTTTGAGACCAAC	60		
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DB	61	AATCTATCAGGAAGAAAGAAAGAAAGAAACCGAAACCTTGACAAAGAAAGAAAGAAAG	120		
QY	121	AAGAAAGAAATCATGAAAGCAATCCAGCCAAAATATGCAAAATCTCTCTTGGGCAAT	180		
DB	121	AAGAAAGAAATCATGAAAGCAATCCAGCCAAAATATGCAAAATCTCTCTTGGGCAAT	180		
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DB	181	CTTCACGGGCTGGCTGTCTGTGTCTCTTCAAGAGTGGCCGTGCGCAGCGAGATGC	240		
QY	241	CACCTTCCCAGAGCTATCGACAACGTGACCGTCCGCGAGGGGAGCGCCACCTCTAG	300		
DB	241	CACCTTCCCAGAGCTATCGACAACGTGACCGTCCGCGAGGGGAGCGCCACCTCTAG	300		
QY	301	GTGCACATTTGCAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTTA	360		
DB	301	GTGCACATTTGCAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTTA	360		
QY	361	TGCTGGGAATGACAGTGTGCTGTGATCTCTCGTGTCTCTCTTGAGCAACCCAAAC	420		
DB	361	TGCTGGGAATGACAGTGTGCTGTGATCTCTCGTGTCTCTCTTGAGCAACCCAAAC	420		
QY	421	GCAGTACAGATCGAGATCCAGAAAGTGTGATGACAGAGGGCCCTTACACCTGCTC	480		
DB	421	GCAGTACAGATCGAGATCCAGAAAGTGTGATGACAGAGGGCCCTTACACCTGCTC	480		
QY	481	GGTGAGACAGACACCCAAAGACCTTTAGGTGCCACCTCAATTTGCAAGTATCTCC	540		
DB	481	GGTGAGACAGACACCCAAAGACCTTTAGGTGCCACCTCAATTTGCAAGTATCTCC	540		
QY	541	CAAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGACAAATATAGCTTAC	600		
DB	541	CAAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGACAAATATAGCTTAC	600		
QY	601	CTGCATAGCAACTGGTAGACAGACCTACGGTTACTTTGGAGACACATCTCTCCAAAGC	660		
DB	601	CTGCATAGCAACTGGTAGACAGACCTACGGTTACTTTGGAGACACATCTCTCCAAAGC	660		
QY	661	GGTTGGCTTTGTGAGTGAGAGCAATCTTGGAAATTCAGGGCATCCCGGGAGCAGTC	720		
DB	661	GGTTGGCTTTGTGAGTGAGAGCAATCTTGGAAATTCAGGGCATCCCGGGAGCAGTC	720		
QY	721	AGGGGACTACGAGTGCAGTGCCTCAATGACGTGGCGCGCCGTGGTACGGAGAGTAA	780		
DB	721	AGGGGACTACGAGTGCAGTGCCTCAATGACGTGGCGCGCCGTGGTACGGAGAGTAA	780		
QY	781	GGTCACCGTGAATATCCACATACATTTCAAGACGAAAGGTACAGGTGTCCCGTGG	840		
DB	781	GGTCACCGTGAATATCCACATACATTTCAAGACGAAAGGTACAGGTGTCCCGTGG	840		
QY	841	ACAAAGGGGACACTGACGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGA	900		
DB	841	ACAAAGGGGACACTGACGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGA	900		
QY	901	CAAGGATGACAAAGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT	960		
DB	901	CAAGGATGACAAAGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT	960		
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DB	1021	GGCTCTCAAAAGCTGGGGCCACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGGT	1080		

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PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 05-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
XX Kijavini IU, Kuo SS, Napier MA, Pan J, Paoi NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2000-611443/58.
XX
XX P-PSDB; AAB44329.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
XX target bioactive molecules to specific cells, and to modulate cellular
XX activities.
XX
XX Claim 2; Fig 221; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
XX tag) sequences which encode secreted or transmembrane PRO polypeptides.
XX The PRO polynucleotides and polypeptides have cytosolic activity. The
XX polynucleotides and polypeptides can be used for detecting the presence
XX of PRO polypeptides in samples, for linking bioactive molecules to cells
XX and for modulating biological activities of cells, using the polypeptides
XX for specific targeting. The polypeptide targeting can be used to kill the
XX target cells, e.g. for the treatment of cancers. The polypeptide pairs
XX provide specific targeting of bioactive molecules to cells. AAC78600 to
XX AAC78987 represent PCR primers and probes used in the isolation of the
XX PRO polynucleotide sequences
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1679; DB 3; Length 1679;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-15;
XX Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GTTGTGCTCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACAAAGCTTGAGAGCAAC 60
XX
XX 1 GTTGTGCTCTTCAGCAAAACAGTGGATTTAAATCTCCTTGACAAAGCTTGAGAGCAAC 60
XX
XX 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
XX
XX 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
XX
XX 121 AAGAAAAAATCATGAAACCATCCAGCAGCAAAATGCAAAATCTATCTCTTGGGCAAT 180
XX
XX 121 AAGAAAAAATCATGAAACCATCCAGCAGCAAAATGCAAAATCTATCTCTTGGGCAAT 180
XX
XX 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCCAGAGTGTCCGTCGCGAGGAGATGC 240
XX
XX 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCCAGAGTGTCCGTCGCGAGGAGATGC 240
XX
XX 241 CACCTTCCCAAGCTATGGAACAGTGCAGTCCGCGAGGGGAGAGCCACCTCAG 300
XX
XX 241 CACCTTCCCAAGCTATGGAACAGTGCAGTCCGCGAGGGGAGAGCCACCTCAG 300
XX
XX 301 GTGCACTATGCAACACCGGGTCAACCGGGTGGCTGTGGCTTAAACCGCAGCAATCCTCTA 360
XX
XX 301 GTGCACTATGCAACACCGGGTCAACCGGGTGGCTGTGGCTTAAACCGCAGCAATCCTCTA 360
XX
XX 361 TGCTGGGATGCAAGTGGTGGCTGGATCCCTGCTGCTCTTCTGAGCAACACCCAAAC 420
XX
XX 361 TGCTGGGATGCAAGTGGTGGCTGGATCCCTGCTGCTCTTCTGAGCAACACCCAAAC 420
QY 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
QY 481 GGTGACAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
DB 481 GGTGACAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
QY 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
DB 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
QY 601 CTGCATAGCACTGGTATAGACAGAGCCTTACGGTTACTTGGAGACACATCTCTCCAAAGC 660
DB 601 CTGCATAGCACTGGTATAGACAGAGCCTTACGGTTACTTGGAGACACATCTCTCCAAAGC 660
QY 661 GGTGGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
DB 661 GGTGGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCTGTGTAAGAGTAA 780
DB 721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCCGCGCCCTGTGTAAGAGTAA 780
QY 781 GGTCAACGCTGAATCTCCACATATCTTCAGAACCAAGGTACAGGTGTCGCCGCTGG 840
DB 781 GGTCAACGCTGAATCTCCACATATCTTCAGAACCAAGGTACAGGTGTCGCCGCTGG 840
QY 841 ACAAAGGGGACACTGCGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGA 900
DB 841 ACAAAGGGGACACTGCGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGA 900
QY 901 CAAGATGACAAAGACTGATTGAAGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 960
DB 901 CAAGATGACAAAGACTGATTGAAGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 960
QY 961 CCTCTCAAACTCATCTTCTCAATGCTCTGAAATGACATGATGGAAGTACATCTGCT 1020
DB 961 CCTCTCAAACTCATCTTCTCAATGCTCTGAAATGACATGATGGAAGTACATCTGCT 1020
QY 1021 GGCTTCCAAAGCTGGGCGCACCAATGCGAGCATCATGCTATTTGGTCAGGCGCGCT 1080
DB 1021 GGCTTCCAAAGCTGGGCGCACCAATGCGAGCATCATGCTATTTGGTCAGGCGCGCT 1080
QY 1081 CAGCGAGTGAACAGCGCAGCTGAGAGGGAGGCTGGTCTGGCTGCTGCTCTTCT 1140
DB 1081 CAGCGAGTGAACAGCGCAGCTGAGAGGGAGGCTGGTCTGGCTGCTGCTCTTCT 1140
QY 1141 GGTCTTGCACTGCTCTCAAAATTTGATGTAGTGCCACTTCCCGCCCGGGAAGGCT 1200
DB 1141 GGTCTTGCACTGCTCTCAAAATTTGATGTAGTGCCACTTCCCGCCCGGGAAGGCT 1200
QY 1201 GCGGCCACCAACCAACCAAGCAATGCAACCGCAGCAACCAACCAACCAATCAGATA 1260
DB 1201 GCGGCCACCAACCAACCAAGCAATGCAACCGCAGCAACCAACCAATCAGATA 1260
QY 1261 TATCAATGAAATGAAAGAAACAGACCTCATGGGACAGAAATTTGAGGGGGGGAAC 1320
DB 1261 TATCAATGAAATGAAAGAAACAGACCTCATGGGACAGAAATTTGAGGGGGGGAAC 1320
QY 1321 AAGAATACCTTGGGGGGAAGAGATTTTAAAGAAATTTGAAATTTGCTTGCAGATA 1380
DB 1321 AAGAATACCTTGGGGGGAAGAGATTTTAAAGAAATTTGAAATTTGCTTGCAGATA 1380
QY 1381 TTTAGGTACAAATGAGATTTCTTTTCCAAACCGGGAAGAAACAGACACACCCGGCTTGA 1440
DB 1381 TTTAGGTACAAATGAGATTTCTTTTCCAAACCGGGAAGAAACAGACACACCCGGCTTGA 1440
QY 1441 CCGACTGCAAGCTGCATCGTCAACCTCTTTTGGTGGCAGTGTGGGCAAGGGCTCAGCCTC 1500
DB 1441 CCGACTGCAAGCTGCATCGTCAACCTCTTTTGGTGGCAGTGTGGGCAAGGGCTCAGCCTC 1500
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QY 1501 TCTGCCACAGAGTGGCCCAAGTGGACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
Db 1501 TCTGCCACAGAGTGGCCCAAGTGGACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
QY 1561 GTCCATAGAGACGAACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTGGCGCACTTTG 1620
Db 1561 GTCCATAGAGACGAACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTGGCGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCAAGCGGTGTGTGTAACCGTGAATATAAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAAGCGGTGTGTGTAACCGTGAATATAAAGAGCAAAAAA 1679

RESULT 3

AC87037
ID AAC87037 standard; cDNA; 1679 BP.

XX
AC AAC87037;

XX
DT 20-APR-2001 (first entry)

DE Nucleotide sequence of human polypeptide PRO337.

XX Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
XX ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH CDS 134..1168
FT /*tag= a
FT 134..216
FT /*tag= b

XX sig_peptide

XX WO200077037-A2.

PN 21-DEC-2000.

XX 22-MAY-2000; 2000WO-US014042.

XX 15-JUN-1999; 99US-0139695P.

XX 20-JUL-1999; 99US-0145070P.

XX 26-JUL-1999; 99US-0145698P.

XX 17-AUG-1999; 99US-0149396P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1999; 99WO-US028501.

XX 02-DEC-1999; 99WO-US028565.

XX 07-DEC-1999; 99US-0169495P.

XX 05-JAN-2000; 2000WO-US000219.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 20-MAR-2000; 2000WO-US007377.

XX 30-MAR-2000; 2000WO-US008439.

XX 15-MAY-2000; 2000WO-US013358.

XX 17-MAY-2000; 2000WO-US013705.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,

XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,

XX Godowski PJ, Gurney AJ, Kljavin LJ, Mather JP, Napier MA, Pan J;

PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2001-050091/06.
XX P-PSDB; AAB31204.
PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
XX of related polypeptides.
XX Claim 2; Fig 51; 244pp; English.
XX
CC The present sequence encodes a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 4; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTCTCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAACTTGAGAGCAAC 60
Db 1 GTTGTCTCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAACTTGAGAGCAAC 60
QY 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTGACAAAAGAAAGAAAGAG 120
Db 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTGACAAAAGAAAGAAAGAG 120
QY 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAAAATCTCTCTTTGGCAAT 180
Db 121 AAGAAAAAATCATGAAACCATCCAGCAAAATGCAAAATCTCTCTTTGGCAAT 180
QY 181 CTTACGGGGCTGGCTGCTCTGTGTCTCTTCCAGGAGTGCCCGTGGCAGCGAGATGC 240
Db 181 CTTACGGGGCTGGCTGCTCTGTGTCTCTTCCAGGAGTGCCCGTGGCAGCGAGATGC 240
QY 241 CACCTTCCCAAGCTATGACACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
Db 241 CACCTTCCCAAGCTATGACACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
QY 301 GTGCACTATTGACAAACGGGTCAACCGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 360
Db 301 GTGCACTATTGACAAACGGGTCAACCGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 360
QY 361 TGTGGGAATGACAACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
Db 361 TGTGGGAATGACAACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
QY 421 GCAGTACAGCTCAGATCAGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 480
Db 421 GCAGTACAGCTCAGATCAGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
QY 481 GGTGCAGACAGCAACACCGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
Db 481 GGTGCAGACAGCAACACCGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
QY 541 CAAAATTGTAGAGATTCTTCAGATATCTCCATTAAATGAAGGAAACAATATTAGCCTC 600
Db 541 CAAAATTGTAGAGATTCTTCAGATATCTCCATTAAATGAAGGAAACAATATTAGCCTC 600

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Db 541 CAAAATTGTAGATTTCCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
QY 601 CTGCATAGCACTGCTAGACGAGCCCTACGGTACTTGGAGACACATCTCTCCCAAGC 660
Db 601 CTGCATAGCACTGCTAGACGAGCCCTACGGTACTTGGAGACACATCTCTCCCAAGC 660
QY 661 GGTTCGCTTTGTGAGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Db 661 GGTTCGCTTTGTGAGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGACTACAGTGCAGTGCCTCAATGACGTGGCGCGCCGCTGGTACGAGAGTAAA 780
Db 721 AGGGACTACAGTGCAGTGCCTCAATGACGTGGCGCGCCGCTGGTACGAGAGTAAA 780
QY 781 GGTCAACGCTGAATATCAACCATACATCTTCAAGAGCAAGGGTACAGTCTCCCGTGGG 840
Db 781 GGTCAACGCTGAATATCAACCATACATCTTCAAGAGCAAGGGTACAGTCTCCCGTGGG 840
QY 841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAATTCAGTGGTA 900
Db 841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAATTCAGTGGTA 900
QY 901 CAAGGATGACAAAAGACTGATTGAAGAAAGGGGTGAAGTGAAGAAACGACCTTT 960
Db 901 CAAGGATGACAAAAGACTGATTGAAGAAAGGGGTGAAGTGAAGAAACGACCTTT 960
QY 961 CCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGCCT 1020
Db 961 CCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGCCT 1020
QY 1021 GGCTCTCAAAGCTGGGCGCACCAATGCAGCATCATGCTATTTGGTCCAGCGCGCT 1080
Db 1021 GGCTCTCAAAGCTGGGCGCACCAATGCAGCATCATGCTATTTGGTCCAGCGCGCT 1080
QY 1081 CAGCGAGTGCAGCAACGGCAGCTCGAGGAGCGAGGCTGCTGGTGTGCTCTTCT 1140
Db 1081 CAGCGAGTGCAGCAACGGCAGCTCGAGGAGCGAGGCTGCTGGTGTGCTCTTCT 1140
QY 1141 GGTCTTGACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCAACCGGGAAGGCT 1200
Db 1141 GGTCTTGACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCAACCGGGAAGGCT 1200
QY 1201 GCGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260
Db 1201 GCGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260
QY 1261 TATACAAATGAAATTAGAGAAACACAGCCTCATGGACAGAAATTTGAGGGAGGGGAAC 1320
Db 1261 TATACAAATGAAATTAGAGAAACACAGCCTCATGGACAGAAATTTGAGGGAGGGGAAC 1320
QY 1321 AAAGAAATACCTTTGGGGGAAAAGAGTTTAAAAAGAAATTTGAAATTTGCCTTGCAGATA 1380
Db 1321 AAAGAAATACCTTTGGGGGAAAAGAGTTTAAAAAGAAATTTGAAATTTGCCTTGCAGATA 1380
QY 1381 TTTAGGTACAAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGCAACCCCGCTTGGGA 1440
Db 1381 TTTAGGTACAAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGCAACCCCGCTTGGGA 1440
QY 1441 CCACACTGCAAGTGCATCGTGCACCTCTTTTGGTCCAGTGTGGCAAGGGCTCAGCCTC 1500
Db 1441 CCACACTGCAAGTGCATCGTGCACCTCTTTTGGTCCAGTGTGGCAAGGGCTCAGCCTC 1500
QY 1501 TCTGCCACAGAGTGGCCCCCAGCTGGAACATTTCTGAGCTGGCCATCCCAATTCATCA 1560
Db 1501 TCTGCCACAGAGTGGCCCCCAGCTGGAACATTTCTGAGCTGGCCATCCCAATTCATCA 1560
QY 1561 GTCCATAGACGACGACGAGATGACACCTTCGGGCCCAAGCGTGGCGCTGGCGGCACTTTG 1620
Db 1561 GTCCATAGACGACGACGAGATGACACCTTCGGGCCCAAGCGTGGCGCTGGCGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCGCGTGTGTGTAACGCTGAATTAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACCGCGTGTGTGTAACGCTGAATTAAGAGCAAAAAA 1679
```

RESULT 4

AAS21431
ID AAS21431 standard; cDNA; 1679 BP.

XX AAS21431,

XX AC

XX DT 24-OCT-2001 (first entry)

XX DE Human cDNA sequence encoding for PRO337 polypeptide.

XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;

XX KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;

XX KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;

XX KW A-peptide; factor VIIa; gene therapy; ss.

OS Homo sapiens.

XX PN WO2001.40466-A2.

XX PD 07-JUN-2001.

XX PF 01-DEC-2000; 2000WO-US032678.

XX PR 01-DEC-1999; 99WO-US028301.

XX PR 01-DEC-1999; 99WO-US028634.

XX PR 02-DEC-1999; 99WO-US028551.

XX PR 02-DEC-1999; 99WO-US028564.

XX PR 02-DEC-1999; 99US-0170262P.

XX PR 16-DEC-1999; 99WO-US030095.

XX PR 20-DEC-1999; 99WO-US030911.

XX PR 20-DEC-1999; 99WO-US030999.

XX PR 30-DEC-1999; 99WO-US031243.

XX PR 30-DEC-1999; 99WO-US031274.

XX PR 05-JAN-2000; 2000WO-US000219.

XX PR 06-JAN-2000; 2000WO-US000277.

XX PR 06-JAN-2000; 2000WO-US000376.

XX PR 11-FEB-2000; 2000WO-US003565.

XX PR 18-FEB-2000; 2000WO-US004341.

XX PR 22-FEB-2000; 2000WO-US004342.

XX PR 24-FEB-2000; 2000WO-US004914.

XX PR 24-FEB-2000; 2000WO-US005004.

XX PR 01-MAR-2000; 2000WO-US005601.

XX PR 02-MAR-2000; 2000WO-US005841.

XX PR 03-MAR-2000; 2000US-0187202P.

XX PR 10-MAR-2000; 2000WO-US006319.

XX PR 15-MAR-2000; 2000WO-US006884.

XX PR 20-MAR-2000; 2000WO-US007377.

XX PR 30-MAR-2000; 2000WO-US007532.

XX PR 17-MAY-2000; 2000WO-US013705.

XX PR 22-MAY-2000; 2000WO-US014042.

XX PR 30-MAY-2000; 2000WO-US014941.

XX PR 02-JUN-2000; 2000WO-US015264.

XX PR 05-JUN-2000; 2000US-0209832P.

XX PR 28-JUL-2000; 2000WO-US020710.

XX PR 11-AUG-2000; 2000WO-US022031.

XX PR 23-AUG-2000; 2000WO-US023522.

XX PR 24-AUG-2000; 2000WO-US023328.

XX PR 08-NOV-2000; 2000WO-US030952.

XX PR 10-NOV-2000; 2000WO-US030873.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

XX PI Gerritsen MB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

XX PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX DR WPI; 2001-408281/43.

XX DR P-PSDB; AAU12359.

XX	Isolated , secretory and transmembrane PRO polypeptide used to detect	Db	541	CAAAATTGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	600
PT	other PRO polypeptides, link bioactive molecules to cells expressing PRO	QY	601	CTGCAATAGCAACTGTGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC	660
PT	polypeptides, and detect the presence of mammalian tumors e.g. lung,	Db	601	CTGCAATAGCAACTGTGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC	660
XX	breast, prostate, cervical.	QY	661	GCTTGGCTTTGTAGTGAAGACGAATATCTTGAAATTCAGGGCATCACCCGGGAGCAGTC	720
XX	Claim 3; Fig 375; 813pp; English.	Db	661	GCTTGGCTTTGTAGTGAAGACGAATATCTTGAAATTCAGGGCATCACCCGGGAGCAGTC	720
CC	AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO	QY	721	AGGGACTACGAGTGCAGTGCTCCATGACGTGCGCGCGCCCGTGGTACGAGAGTAAA	780
CC	polypeptides, to link bioactive molecules to cells expressing PRO	Db	721	AGGGACTACGAGTGCAGTGCTCCATGACGTGCGCGCGCCCGTGGTACGAGAGTAAA	780
CC	polypeptides, and to detect the presence of mammalian lung, colon,	QY	781	GGTCAACCGTGAACCTATCCACCATATCATTTTCAAGAACCCAAAGGTACAGGTGTCCCGGTGGG	840
CC	breast, prostate, rectal, cervical or liver tumours by comparing PRO	Db	781	GGTCAACCGTGAACCTATCCACCATATCATTTTCAAGAACCCAAAGGTACAGGTGTCCCGGTGGG	840
CC	polypeptide expression in a cell sample to that in a control sample. Some	QY	841	ACAAAAGGGGACACTGCAAGCTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTGA	900
CC	of the 275 sequences are also useful to stimulate the release of tumour	Db	841	ACAAAAGGGGACACTGCAAGCTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTGA	900
CC	necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or	QY	901	CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAACAGACCTTT	960
CC	differentiation of chondrocytes, the proliferation or gene expression in	Db	901	CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAACAGACCTTT	960
CC	pericyte cells, the release of proteoglycans from cartilage, the	QY	961	CCTCTCAAACTCATCTTCTCAATGTCTCTGAAATGATGGAATGGAATGGAATGGAATGGA	1020
CC	proliferation of inner ear utricular supporting cells or of T-	Db	961	CCTCTCAAACTCATCTTCTCAATGTCTCTGAAATGATGGAATGGAATGGAATGGAATGGA	1020
CC	lymphocytes, the release of a cytokine from peripheral blood monocytes	QY	1021	GGCTCTCAACCAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTTGGTCCAGGCGCGCT	1080
CC	(PBMCs), or the proliferation of endothelial cells. Some of the PRO	Db	1021	GGCTCTCAACCAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTTGGTCCAGGCGCGCT	1080
CC	polypeptides may modulate glucose or free fatty acid uptake by skeletal	QY	1081	CAGCAGGTGAGCAACGGCACTGAGGAGGCGGCGGTGCGTCTGCGCTGCTGCGCTCTTCT	1140
CC	muscle cells or by adipocytes; or inhibit binding of A-peptide to factor	Db	1081	CAGCAGGTGAGCAACGGCACTGAGGAGGCGGCGGTGCGTCTGCGCTGCTGCGCTCTTCT	1140
CC	VIIA. The PRO polypeptides can be used in assays to identify molecules	QY	1141	GCTCTTGGACCTGCTTCTCAAAATTTTGTATGTGAGTGCCACTTCCCAACCCCGGGAAGGCT	1200
CC	involved in binding interactions. The polynucleotides encoding PRO	Db	1141	GCTCTTGGACCTGCTTCTCAAAATTTTGTATGTGAGTGCCACTTCCCAACCCCGGGAAGGCT	1200
CC	polypeptides can be used to generate probes, antisense RNA/DNA,	QY	1201	GGCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	1260
CC	transgenic or knock out animals and can be used in gene therapy	Db	1201	GGCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	1260
XX	Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;	QY	1261	TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGAGGAAAC	1320
QY	Query Match 100.0%; Score 1679; DB 4; Length 1679;	Db	1261	TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGAGGAAAC	1320
Best Local Similarity 100.0%; Pred. No. 1.5e-15;	QY	1321	AAAGAAATCTTTGGGGGAAAGAGTGTAAAGAAAGAAATTTGAAATTTGCTTTCACAGATA	1380	
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1321	AAAGAAATCTTTGGGGGAAAGAGTGTAAAGAAAGAAATTTGAAATTTGCTTTCACAGATA	1380	
1 GTTGTGCTTTCAGCAAAACAGTGGATTAAATCTCTTTCGCAAGCTTGAGAGCAACAC	QY	1381	TTTAGGTAACAATGAGATTTTCTTTTCCCAACCGGGAAGAAACACAGCACACCCCGGCTTGGGA	1440	
1 GTTGTGCTTTCAGCAAAACAGTGGATTAAATCTCTTTCGCAAGCTTGAGAGCAACAC	Db	1381	TTTAGGTAACAATGAGATTTTCTTTTCCCAACCGGGAAGAAACACAGCACACCCCGGCTTGGGA	1440	
61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	QY	1441	CCCACTGCAAGCTGCATCGTGCACCTCTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTC	1500	
61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	Db	1441	CCCACTGCAAGCTGCATCGTGCACCTCTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTC	1500	
121 AAGAAAAAATCATGAAAAACCATCAGCCAAAAATTCATCTCTTGGGCAAT	QY	1501	TCCTGCCACAGAGTGCCTCCCACTTCTGGAGCTGGCCATCCCAAAATTCATATCA	1560	
121 AAGAAAAAATCATGAAAAACCATCAGCCAAAAATTCATCTCTTGGGCAAT	Db	1501	TCCTGCCACAGAGTGCCTCCCACTTCTGGAGCTGGCCATCCCAAAATTCATATCA	1560	
181 CTTTCAAGGGGCTGGTGTCTGTGTCTCTTCAAGGAGTGCCGTCGCGAGGAGATGC	QY	1561	GTCCATAGAGACGAAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTCGCGGCACTTTG	1620	
181 CTTTCAAGGGGCTGGTGTCTGTGTCTCTTCAAGGAGTGCCGTCGCGAGGAGATGC	Db	1561	GTCCATAGAGACGAAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTCGCGGCACTTTG	1620	
241 CACCTTCCCAAGCTATGGAACAACGTGAGTGGTGGGAGGAGGAGGAGGAGGAGGAG	QY	1621	GTAGACTGTGCCACCAACCGGCTGTGTGTGAAACGTGAAATTAAGAGAGCAAAAAA	1679	
241 CACCTTCCCAAGCTATGGAACAACGTGAGTGGTGGGAGGAGGAGGAGGAGGAGGAG	Db	1621	GTAGACTGTGCCACCAACCGGCTGTGTGTGAAACGTGAAATTAAGAGAGCAAAAAA	1679	

CC	proliferation of, or gene expression, in pericyte cells, for stimulating
CC	the proliferation or differentiation of chondrocyte cells, for
CC	stimulating the release of tumour necrosis factor- α from human blood,
CC	for stimulating or inhibiting the proliferation of normal human dermal
CC	fibroblast cells. The PRO polypeptide may also be used as molecular
CC	weight markers and for tissue typing. The PRO nucleic acids have
CC	applications in molecular biology, including use as hybridisation probes,
CC	and in chromosome and gene mapping. ABK3356-ABK3365 represent human PRO
XX	protein coding sequences of the invention
SQ	Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
	Query Match 100.0%; Score 1679; DB 6; Length 1679;
	Best Local Similarity 100.0%; Pred. No. 1.5e-15;
	Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTCTGCACAAAGCTTCAGAGCAACAC 60
Db	1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTCTGCACAAAGCTTCAGAGCAACAC 60
Qy	61 AATCTATCAGGAAGAAAGAAAGAAAGAAACCGAACCTGTGCAAAAAGAAAGAAAGAAAG 120
Db	61 AATCTATCAGGAAGAAAGAAAGAAAGAAACCGAACCTGTGCAAAAAGAAAGAAAGAAAG 120
Qy	121 AAGAAAAAATCATGAAAAACCATCCAGGCCAAAAATGCAAATTTCTATCTCTTGGGCAAT 180
Db	121 AAGAAAAAATCATGAAAAACCATCCAGGCCAAAAATGCAAATTTCTATCTTCTGGGCAAT 180
Qy	181 CTTTCAGGGGCTGGCTGCTCTGTGTCTCTTCAGAGAGTGCCGTGGCGAGCGGAGATGC 240
Db	181 CTTTCAGGGGCTGGCTGCTCTGTGTCTCTTCAGAGAGTGCCGTGGCGAGCGGAGATGC 240
Qy	241 CACCTTCCCCAAAGCTATGCAACACGTGACGGTCCGGCAGGGGAGAGCGCCACCCCTCAG 300
Db	241 CACCTTCCCCAAAGCTATGCAACAGTGTGACGGTCCGGCAGGGGAGAGCGCCACCCCTCAG 300
Qy	301 GTGCACATTTTGA CAACCGGGTCAACCGGGTGGGCTGGCTTAAACCGCAGCACCAATCTCTTA 360
Db	301 GTGCACATTTTGA CAACCGGGTCAACCGGGTGGGCTGGCTTAAACCGCAGCACCAATCTCTTA 360
Qy	361 TGTCTGGGAATGCAAGTGGTGCTCGATCCTCGGTGGTCTCTCTGAGCAACACCCAAAC 420
Db	361 TGTCTGGGAATGCAAGTGGTGCTCGATCCTCGGTGGTCTCTCTGAGCAACACCCAAAC 420
Qy	421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGGCCCTTACACCTGCTC 480
Db	421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGGCCCTTACACCTGCTC 480
Qy	481 GGTGCGACAGACAACACCCAAAGACCTCTAGGTTCCACCTCATTTGTGCAAGTATCTCC 540
Db	481 GGTGCGACAGACAACACCCAAAGACCTCTAGGTTCCACCTCATTTGTGCAAGTATCTCC 540
Qy	541 CAAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCAC 600
Db	541 CAAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCAC 600
Qy	601 CTGCATAGCAACTGTGTAGACAGAGCCTACGGTTACTTGTGAGACACATCTCTCCAAAGC 660
Db	601 CTGCATAGCAACTGTGTAGACAGAGCCTACGGTTACTTGTGAGACACATCTCTCCAAAGC 660
Qy	661 GGTGTGGCTTTTGTGAGTGAAGACCAATACTTTGGAAATTCAGGGCATACCCGGGAGCAGTC 720
Db	661 GGTGTGGCTTTTGTGAGTGAAGACCAATACTTTGGAAATTCAGGGCATACCCGGGAGCAGTC 720
Qy	721 AGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCGCGCCCGTGGTACGGAGAGTAA 780
Db	721 AGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCGCGCCCGTGGTACGGAGAGTAA 780
Qy	781 GGTCAACCGTGAACTATCCCAACATACATTTTCAGAAAGCCAGGGTACAGGGTGTCCCGTGG 840
Db	781 GGTCAACCGTGAACTATCCCAACATACATTTTCAGAAAGCCAGGGTACAGGGTGTCCCGTGG 840
Qy	841 ACAAAGGGGACACTGCAGTGTGAAGCCTTCAGCAGTCCCTTCAGAGCAAAATTCAGGTGGTA 900


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25-JUL-2000; 2000US-0220624P.
25-JUL-2000; 2000US-0220664P.
28-JUL-2000; 2000WO-US020710.
02-AUG-2000; 2000US-0222595P.
17-AUG-2000; 2000US-00643657.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
07-SEP-2000; 2000US-0230978P.
18-SEP-2000; 2000US-00664610.
18-SEP-2000; 2000US-00665350.
24-OCT-2000; 2000US-0242922P.
08-NOV-2000; 2000US-00709238.
08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
22-JAN-2001; 2001US-00767609.
28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
05-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00828366.
10-MAY-2001; 2001US-00854208.
25-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
30-MAY-2001; 2001WO-US017092.
30-MAY-2001; 2001US-00870574.
01-JUN-2001; 2001WO-US017443.
20-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.

(GETH ) GENENTECH INC.
(BAKE/) BAKER K P.
(FERR/) FERRARA N.
(GERB/) GERBER H.
(GERR/) GERITSEN M E.
(GODD/) GODDARD A.
(GODO/) GODOWSKI P J.
(GURN/) GURNEY A L.
(HILL/) HILLAN K J.
(MARS/) MARSTERS S A.
(PANJ/) PAN J.
(PAON/) PAONI N F.
(STEP/) STEPHAN J F.
(WATA/) WATANABE C K.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
WPI; 2002-171999/22.
P-PSDB; ABB95450.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal.

Claim 1; Fig 55; 567pp; English.

The present invention provides the protein and coding sequences of human
PRO proteins. These are useful for treating or diagnosing a
cardiovascular, endothelial or angiogenic disorder, including cardiac
hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The present sequence is a coding sequence of the invention

```

```

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1679; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGCTCTTCAGCAAAACAGTGGATTTAAATCTCTTGCACAAAGCTTGAGAGCAAC 60
DB 1 GTTGTGCTCTTCAGCAAAACAGTGGATTTAAATCTCTTGCACAAAGCTTGAGAGCAAC 60

QY 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

QY 121 AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180
DB 121 AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180

QY 181 CTTACGGGGCTGGCTGCTCTGTCTCTTCCAAAGAGTGCCCGTGGCAGCGGAGATGC 240
DB 181 CTTACGGGGCTGGCTGCTCTGTCTCTTCCAAAGAGTGCCCGTGGCAGCGGAGATGC 240

QY 241 CACCTTCCCAAGCTATGGAACAACGTGACGGTCCCGCAGGGGAGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAGCTATGGAACAACGTGACGGTCCCGCAGGGGAGAGCGCCACCTCAG 300

QY 301 GTGCACATTTGACAACCCGGGTACCCGGGTGGCTGGCTAAACCCGAGACCATCTCTA 360
DB 301 GTGCACATTTGACAACCCGGGTACCCGGGTGGCTGGCTAAACCCGAGACCATCTCTA 360

QY 361 TGCTGGGAATGACAAGTGTGCTGATCTCTCGCGTGGTCTTCTCAGCAACACCCAAAC 420
DB 361 TGCTGGGAATGACAAGTGTGCTGATCTCTCGCGTGGTCTTCTCAGCAACACCCAAAC 420

QY 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTC 480

QY 481 GGTGCAGACAGACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
DB 481 GGTGCAGACAGACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540

QY 541 CAAATTGTAGAGATTTCTTTCAGATATCTCCATATGAGGAAAGCAATATAGCCCTAC 600
DB 541 CAAATTGTAGAGATTTCTTTCAGATATCTCCATATGAGGAAAGCAATATAGCCCTAC 600

QY 601 CTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
DB 601 CTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660

QY 661 GGTGGCTTTGTAGTGAAGAGCAATCTTGGAAATTCAGGGCATCCCGGGAGCAGTC 720
DB 661 GGTGGCTTTGTAGTGAAGAGCAATCTTGGAAATTCAGGGCATCCCGGGAGCAGTC 720

QY 721 AGGGGACTACGAGTGCAGTCCCTCCAAATGACGTGGCGCGCCCGTGGTACGAGAGTAA 780
DB 721 AGGGGACTACGAGTGCAGTCCCTCCAAATGACGTGGCGCGCCCGTGGTACGAGAGTAA 780

QY 781 GGTCAACGTTGAATPCCACCATATCTTTCAGAGCAAGGGGTACAGGTGTCCCGTGGG 840
DB 781 GGTCAACGTTGAATPCCACCATATCTTTCAGAGCAAGGGGTACAGGTGTCCCGTGGG 840

QY 841 ACAGAGGGGACATGTCAGTGTGAAGCCTCAGAGTCCCTCAGCAGATTCAGAGTGA 900
DB 841 ACAGAGGGGACATGTCAGTGTGAAGCCTCAGAGTCCCTCAGCAGATTCAGAGTGA 900

QY 901 CAAGGATGCAAGAGACTGATTTGAAGAGAAAGAAAGGGGTGAAGTGAAGAAAGAGACCTTT 960
DB 901 CAAGGATGCAAGAGACTGATTTGAAGAGAAAGAAAGGGGTGAAGTGAAGAAAGAGACCTTT 960

QY 961 CCTCTCAAACATCATCTTCTTCAATGTCTCTGAAACATGATCTATGGAACTACATCTGCGT 1020
DB 961 CCTCTCAAACATCATCTTCTTCAATGTCTCTGAAACATGATCTATGGAACTACATCTGCGT 1020

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		Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
PR	20-DEC-2000; 2000WO-US034956.	QY	1	GTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAAC	60
PR	28-FEB-2001; 2001US-00796498.	DB	1		60
PR	01-MAR-2001; 2001WO-US006520.	QY	61		120
PR	09-MAR-2001; 2001US-00802706.	DB	61		120
PR	14-MAR-2001; 2001US-00808689.	QY	121		180
PR	22-MAR-2001; 2001US-00816744.	DB	121		180
PR	05-APR-2001; 2001US-00828366.	QY	181		240
PR	10-MAY-2001; 2001US-00854208.	DB	181		240
PR	18-MAY-2001; 2001US-00860216.	QY	241		300
PR	25-MAY-2001; 2001US-00866028.	DB	241		300
PR	25-MAY-2001; 2001US-00866034.	QY	301		360
PR	25-MAY-2001; 2001WO-US017092.	DB	301		360
PR	01-JUN-2001; 2001US-00872035.	QY	361		420
PR	01-JUN-2001; 2001WO-US017800.	DB	361		420
PR	05-JUN-2001; 2001US-00874503.	QY	421		480
PR	14-JUN-2001; 2001US-00882636.	DB	421		480
PR	19-JUN-2001; 2001US-00886342.	QY	481		540
PR	20-JUN-2001; 2001WO-US019692.	DB	481		540
PR	21-JUN-2001; 2001US-00887879.	QY	541		600
PR	22-JUN-2001; 2001WO-US020116.	DB	541		600
PR	29-JUN-2001; 2001WO-US021066.	QY	601		660
PR	09-JUL-2001; 2001WO-US021735.	DB	601		660
PR	18-JUL-2001; 2001US-00908827.	QY	661		720
PR	06-AUG-2001; 2001US-00924419.	DB	661		720
PR	09-AUG-2001; 2001US-00927796.	QY	721		780
PR	16-AUG-2001; 2001US-00931836.	DB	721		780
PR	19-DEC-2001; 2001US-00028072.	QY	781		840
XX		DB	781		840
PA	(GETH) GENENTECH INC.	QY	841		900
XX		DB	841		900
PI	Baker KP, Betesini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;	QY	901		960
PI	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;	DB	901		960
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	QY	961		1020
XX		DB	961		1020
DR	WPI; 2003-341980/32.	QY	1021		1080
DR	P-PSDB; ABO17803.	DB	1021		1080
XX		QY			
PT	New secreted and transmembrane PRO nucleic acids, for treating				
PT	inflammation, organ failure, atherosclerosis, cardiac injury,				
PT	infertility, birth defects, premature aging, acquired immunodeficiency				
PT	syndrome (AIDS), or cancer.				
XX					
XX	Claim 2; Fig 375; 660pp; English.				
CC	The invention describes an isolated nucleic acid (I) comprising, or which				
CC	has 80 % sequence identity to, or the full-length coding sequence of, one				
CC	of 275 nucleotide sequences, and which encodes a corresponding				
CC	polypeptide selected from 275 amino acid sequences, where all sequences				
CC	are given in the specification. The polypeptide encoded by (I) is used to				
CC	detect PRO polypeptides, link a bioactive molecule to a cell expressing a				
CC	PRO polypeptide, modulate a biological activity of a cell, stimulate the				
CC	release of tumour necrosis factor (TNF)-alpha from human blood, modulate				
CC	the uptake of glucose or free fatty acid by cells, stimulate or inhibit				
CC	the proliferation or differentiation of cells or gene expression,				
CC	stimulate the release of proteoglycans, stimulate the release of cytokine				
CC	from peripheral blood mononuclear cells, inhibit the binding of A-peptide				
CC	to factor VIIA, or detect the presence of tumour in a mammal. The nucleic				
CC	acid and polypeptide encoded by it, are useful for treating inflammatory				
CC	diseases, organ failure, atherosclerosis, cardiac injury, infertility,				
CC	birth defects, premature aging, acquired immunodeficiency syndrome				
CC	(AIDS), cancer, or diabetic complications. The nucleic acid is useful as				
CC	hybridisation probes, in chromosome and gene mapping, and in generating				
CC	antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,				
CC	diagnostics, biosensors or bioreactors. Both are useful in tissue typing.				
CC	This sequence encodes a novel human secreted and transmembrane PRO				
XX	polypeptide				
XX					
SQ	Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;				
	Query Match 100.0%; Score 1679; DB 7; Length 1679;				
	Best Local Similarity 100.0%; Pred. No. 1.5e-15;				

QY 661 GGTTCGCTTGTGAGTGAAGAGCAATCTTGAAATTCAGGSCATCACCCGGGAGCAGTC 720
Db |||||
QY 661 GGTTCGCTTGTGAGTGAAGAGCAATCTTGAAATTCAGGSCATCACCCGGGAGCAGTC 720
Db |||||
QY 721 AGGGGACTACGAGTGCAGTCCCAATGACGTGCGCCCGTGGTACGGAGAGTAAA 780
Db |||||
QY 781 GGTCCACGTGAATCTACCACTATCTCAGAACGCAAGGTACAGGTGTCCTCCGTGGG 840
Db |||||
QY 781 GGTCCACGTGAATCTACCACTATCTCAGAACGCAAGGTACAGGTGTCCTCCGTGGG 840
Db |||||
QY 841 ACAAAGGGGACACTGCAGTGTGAAGCTTCAGAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db |||||
QY 841 ACAAAGGGGACACTGCAGTGTGAAGCTTCAGAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db |||||
QY 901 CAAGGATGACAAAGACTGATTTGAAGGAAAGAGGGGTGAAAGTGGAAAAAGACCTTT 960
Db |||||
QY 901 CAAGGATGACAAAGACTGATTTGAAGGAAAGAGGGGTGAAAGTGGAAAAAGACCTTT 960
Db |||||
QY 961 CCTCTCAAACTCATCTTCTCAATGTCTCTGAAATGACTATGGAACTACACTTGGT 1020
Db |||||
QY 961 CCTCTCAAACTCATCTTCTCAATGTCTCTGAAATGACTATGGAACTACACTTGGT 1020
Db |||||
QY 1021 GGCCTCCAAAGCTGGGCGCACACCAATGCCAGCATCATGCTATTGGTCCAGGCGCGT 1080
Db |||||
QY 1021 GGCCTCCAAAGCTGGGCGCACACCAATGCCAGCATCATGCTATTGGTCCAGGCGCGT 1080
Db |||||
QY 1081 CAGCAGGTGAGCAACGCGCACTCGAGAGGGGAGGCTGCTGCTGCTCTCTTCT 1140
Db |||||
QY 1081 CAGCAGGTGAGCAACGCGCACTCGAGAGGGGAGGCTGCTGCTGCTCTCTTCT 1140
Db |||||
QY 1141 GGTCTTGACCTGCTCTCAATTTTGATGTCAGTGCACCTTCCCAACCCGGGAAGGCT 1200
Db |||||
QY 1141 GGTCTTGACCTGCTCTCAATTTTGATGTCAGTGCACCTTCCCAACCCGGGAAGGCT 1200
Db |||||
QY 1201 GCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1260
Db |||||
QY 1261 TATACAAATGAAATAGAGAAACACAGCCTCATGGGACAGAAATTTAGGAGGGGGAAC 1320
Db |||||
QY 1261 TATACAAATGAAATAGAGAAACACAGCCTCATGGGACAGAAATTTAGGAGGGGGAAC 1320
Db |||||
QY 1321 AAAGAAATCTTGGGGGAAAGAGTTTAAAGAAATTCGAAATTCGCTTGCAGATA 1380
Db |||||
QY 1321 AAAGAAATCTTGGGGGAAAGAGTTTAAAGAAATTCGAAATTCGCTTGCAGATA 1380
Db |||||
QY 1381 TTAGGTACAAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCCGGCTTGA 1440
Db |||||
QY 1441 CCCACTGCAAGTGCATCTGTGCAACCTCTTTGGTGCAGTGTGGCAAGGGCTCAGCCTC 1500
Db |||||
QY 1441 CCCACTGCAAGTGCATCTGTGCAACCTCTTTGGTGCAGTGTGGCAAGGGCTCAGCCTC 1500
Db |||||
QY 1501 TCTGCCACAGAGTGCCTCCACAGTGAACATTTCTGGAGTGGCCATCCCAAAATTCATCA 1560
Db |||||
QY 1501 TCTGCCACAGAGTGCCTCCACAGTGAACATTTCTGGAGTGGCCATCCCAAAATTCATCA 1560
Db |||||
QY 1561 GTCCATAGAGACGAAACAGAGATGAGACTTCCGCGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
Db |||||
QY 1561 GTCCATAGAGACGAAACAGAGATGAGACTTCCGCGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
Db |||||
QY 1621 GTAGACTGTGCCACAGCGGCTGTGTTGAAACGTGAAATTAAGAGCAAAAAA 1679
Db |||||
QY 1621 GTAGACTGTGCCACAGCGGCTGTGTTGAAACGTGAAATTAAGAGCAAAAAA 1679
Db |||||

RESULT 10

ACD42387

ID ACD42387 standard; cDNA; 1679 BP.

XX

AC ACD42387;
XX 05-SEP-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO337 cDNA.
XX Human; secreted and transmembrane protein; PRO; antidiabetic;
XX ophthalmological; cytotatic; immunostimulant; gene therapy;
XX vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
XX protein secretion disorder; pancreas disorder; diabetes;
XX vascular permeability; retinal neuron cell survival; retinal disorder;
XX immune response; inflammation; mononuclear cell infiltration;
XX eosinophil infiltration; apoptosis; neoplastic growth; gene; ss.
OS Homo sapiens.
XX US2003040014-A1.
PN 27-FEB-2003.
XX 01-FEB-2002; 2002US-00066269.
XX 26-AUG-1997; 97US-0056974P.
XX 17-SEP-1997; 97US-0059115P.
XX 18-SEP-1997; 97US-0059263P.
XX 19-SEP-1997; 97US-0059588P.
XX 17-OCT-1997; 97US-0062285P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063082P.
XX 27-OCT-1997; 97US-0063329P.
XX 29-OCT-1997; 97US-0063733P.
XX 21-NOV-1997; 97US-0066364P.
XX 25-NOV-1997; 97US-0066840P.
XX 16-DEC-1997; 97US-0069694P.
XX 09-FEB-1998; 98US-0074086P.
XX 09-FEB-1998; 98US-0074092P.
XX 23-MAR-1998; 98US-0079294P.
XX 08-APR-1998; 98US-0081049P.
XX 14-JUL-1998; 98WO-US014552.
XX 10-AUG-1998; 98US-0095998P.
XX 18-AUG-1998; 98US-0097000P.
XX 09-SEP-1998; 98US-0099601P.
XX 10-SEP-1998; 98US-0099803P.
XX 10-SEP-1998; 98US-0099811P.
XX 10-SEP-1998; 98US-0099812P.
XX 14-SEP-1998; 98WO-US018824.
XX 16-SEP-1998; 98WO-US019093.
XX 17-SEP-1998; 98WO-US019330.
XX 24-SEP-1998; 98WO-US019437.
XX 24-SEP-1998; 98US-0101922P.
XX 28-OCT-1998; 98US-0106032P.
XX 20-NOV-1998; 98US-0109304P.
XX 20-NOV-1998; 98WO-US024855.
XX 25-NOV-1998; 98WO-US025190.
XX 01-DEC-1998; 98WO-US025108.
XX 08-MAR-1999; 99WO-US005028.
XX 23-MAR-1999; 99US-0125778P.
XX 02-JUN-1999; 99WO-US012252.
XX 15-JUN-1999; 99US-0139695P.
XX 20-JUL-1999; 99US-0145070P.
XX 26-JUL-1999; 99US-0145698P.
XX 17-AUG-1999; 99US-0149366P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028565.
XX 07-DEC-1999; 99US-0169495P.
XX 20-DEC-1999; 99WO-US030999.
XX 05-JAN-2000; 2000WO-US000219.


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PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2001WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Deenoyers L, Eaton DL,
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AJ, Kljavin IJ, Mather JP, Napier MA, Pan J,
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
PI Wood WI, Zhang Z;
XX
XX MPI; 2003-503396/47.
XX P-PSDB; ABO25175.
XX
XX New secreted and transmembrane PRO polypeptides, useful for treating
XX diabetes, retinal disorders and stimulating an immune response.
XX
XX Claim 2; Fig 51; 254pp; English.
XX
XX The invention describes an isolated polypeptide (I) having at least 80 %
XX amino acid sequence identity to 30 secreted and transmembrane
XX polypeptides. PRO polypeptides are also useful for stimulating
XX hypertrophy of adult heart, for inhibiting vascular endothelial growth
XX factor stimulated proliferation of endothelial cells, stimulating
XX proliferation of stimulated T-lymphocytes and for inducing proliferation
XX of PDB12 pancreatic ductal cells and are thus useful in the treatment of
XX disorders which involve protein secretion by the pancreas, including
XX diabetes. PRO polypeptides are useful for inducing vascular permeability
XX and in enhancing survival of retinal neurons cells and are thus useful
XX for the treatment of retinal disorders. PRO polypeptides are also useful
XX for stimulating an immune response and inducing inflammation by inducing
XX mononuclear cell and eosinophil infiltration at the site of infection of
XX an animal. The PRO polypeptides are further useful for inducing apoptosis
XX in endothelial cells for inhibiting neoplastic growth. This sequence
XX encodes a novel human secreted and transmembrane PRO polypeptide
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1679; DB 7; Length 1679;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-15;
XX Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCCTTGACAGCTTGAGACCAAC 60
XX
XX 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCCTTGACAGCTTGAGACCAAC 60
XX
XX 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
XX
XX 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
XX
XX 121 AAGAAAAAATATGAAAAACCATCCAGCCAAAAATGCAAAATTCATCTCTTGGGCAAT 180

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Db 1201 GCGGCCACACACACACCAACAGCAATGTCACACCGACAGCAACCAATCAGATA 1260
QY 1261 TATACAAATGAAATAGAAAGAAACACAGCTCATGGGACAGAAATTTGAGGAGGGGAAC 1320
Db 1261 TATACAAATGAAATAGAAAGAAACACAGCTCATGGGACAGAAATTTGAGGAGGGGAAC 1320
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Db 1321 AAAGAATACTTTGGGGGGAAGAAGAGTTTAAAAAGAAATTCGAAATTCGCTTGAGATA 1380
QY 1381 TTTAGGTCAATGGAGTTTCTTTTCCCAACGGGAAGAACACACACACCCCGGCTTGGGA 1440
Db 1381 TTTAGGTCAATGGAGTTTCTTTTCCCAACGGGAAGAACACACACACCCCGGCTTGGGA 1440
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QY 1561 GTCCATAGAGACGAACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTGGCGGCACTTTG 1620
Db 1561 GTCCATAGAGACGAACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTGGCGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACACGCGCTGTGTGTGAACCTGAAATGAAATGAAATGAAATGAA 1679
Db 1621 GTAGACTGTGCCACACGCGCTGTGTGTGAACCTGAAATGAAATGAAATGAAATGAA 1679

RESULT 11
ACD42857
ID ACD42857 standard; cDNA; 1679 BP.
XX AC ACD42857;
XX DT 09-SEP-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX KW Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
XX KW cell death; growth induction cascade; blood coagulation cascade;
XX KW viral infection; gene; ss.
XX OS Homo sapiens.
XX PN US2003050239-A1.
XX PD 13-MAR-2003.
XX PF 15-OCT-2001; 2001US-00978191.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 03-NOV-1997; 97US-0064249P.
XX PR 13-NOV-1997; 97US-0065311P.
XX PR 21-NOV-1997; 97US-0066364P.
XX PR 10-MAR-1998; 98US-0077450P.
XX PR 11-MAR-1998; 98US-0077632P.
XX PR 11-MAR-1998; 98US-0077641P.
XX PR 11-MAR-1998; 98US-0077649P.
XX PR 12-MAR-1998; 98US-0077791P.
XX PR 13-MAR-1998; 98US-0078004P.
XX PR 17-MAR-1998; 98US-00040220.
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PR 01-APR-1998; 98US-0080333P.
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PR 08-APR-1998; 98US-0081049P.
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PR 27-APR-1998; 98US-0083336P.
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PR 15-MAY-1998; 98US-0085582P.
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PR 28-MAY-1998; 98US-0087098P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090863P.
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PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
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PR 07-OCT-1998; 98US-00168978.
PR 02-NOV-1998; 98US-00211141.
PR 06-NOV-1998; 98US-00184216.
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PR 20-NOV-1998; 98US-0109304P.
PR 07-DEC-1998; 98US-00204855.
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PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 98US-0000106.
PR 05-MAR-1999; 98US-00254465.
PR 08-MAR-1999; 98US-0005028.
PR 10-MAR-1999; 98US-00265686.
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PR 12-MAR-1999; 98US-00267213.
PR 12-MAR-1999; 98US-0123957P.
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PR 26-APR-1999; 98US-0131022P.
PR 28-APR-1999; 98US-0131445P.
PR 14-MAY-1999; 98US-00311832.
PR 14-MAY-1999; 98US-0134287P.
PR 02-JUN-1999; 98US-00107933.
PR 16-JUN-1999; 98US-0012252.
PR 23-JUN-1999; 98US-0141037P.
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PR 26-JUL-1999; 98US-0145698P.
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PR 25-AUG-1999; 98US-00380137.
PR 25-AUG-1999; 98US-00380138.
PR 25-AUG-1999; 98US-00380142.
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PR 30-NOV-1999; 98US-00283113.
PR 02-DEC-1999; 98US-0028551.
PR 02-DEC-1999; 98US-0028565.
PR 30-DEC-1999; 98US-0031243.
PR 30-DEC-1999; 98US-0031274.
PR 05-JAN-2000; 2000US-0000219.
PR 06-JAN-2000; 2000US-0000277.
PR 11-FEB-2000; 2000US-0000376.
PR 18-FEB-2000; 2000US-0003565.
PR 24-FEB-2000; 2000US-0004341.
PR 02-MAR-2000; 2000US-0005004.
PR 10-MAR-2000; 2000US-0005841.
PR 21-MAR-2000; 2000US-0006319.
PR 30-MAR-2000; 2000US-0007532.
PR 17-MAY-2000; 2000US-0008439.
PR 22-MAY-2000; 2000US-0013705.
PR 30-MAY-2000; 2000US-0014042.
PR 02-JUN-2000; 2000US-0014941.
PR 28-JUL-2000; 2000US-0015264.
PR 24-AUG-2000; 2000US-0020710.
PR 08-NOV-2000; 2000US-0023328.
PR 27-NOV-2000; 2000US-00709238.
PR 01-DEC-2000; 2000US-00723749.
PR 20-DEC-2000; 2000US-0032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2000US-0034956.
PR 22-MAR-2001; 2001US-0006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-0017092.

PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-00886342.
PR 29-JUN-2001; 2001US-00886342.
PR 09-JUL-2001; 2001US-00886342.
PR 30-JUL-2001; 2001US-00918585.
XX (GETH ) GENENTECH INC.
XX
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB;

Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTCGCAAAAGCTTGAGAGCAAC 60
DB 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTCGCAAAAGCTTGAGAGCAAC 60
QY 61 AATCTATCAGAAAGAAAGAAAGAAACCGAACCTGACAAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGAAAGAAAGAAAGAAACCGAACCTGACAAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAGAAATCATGAAACCATCCAGCCAAATGCAATCTCTCTTTGGGCAAT 180
DB 121 AAGAAAGAAATCATGAAACCATCCAGCCAAATGCAATCTCTCTTTGGGCAAT 180
QY 181 CTTACGGGGCTGGCTCTGTGTCTCTTCCAAAGAGTCCCGTGCAGCGGAGATGC 240
DB 181 CTTACGGGGCTGGCTCTGTGTCTCTTCCAAAGAGTCCCGTGCAGCGGAGATGC 240
QY 241 CACCTTCCCAAAGCTATGGAACAAAGTACGGTCCGGAGGGGAGAGCGCCCTCAG 300
DB 241 CACCTTCCCAAAGCTATGGAACAAAGTACGGTCCGGAGGGGAGAGCGCCCTCAG 300
QY 301 GTGCACATTTGACAAACCGGTCCCGGGTGGCTGCTTAAACCGCAGACCACTCTTA 360
DB 301 GTGCACATTTGACAAACCGGTCCCGGGTGGCTGCTTAAACCGCAGACCACTCTTA 360
QY 361 TGTGGGAATGACAAAGTGGTGCCTGGATCTCGCGTGGTCTTCTTGAGCAACCCAAAC 420
DB 361 TGTGGGAATGACAAAGTGGTGCCTGGATCTCGCGTGGTCTTCTTGAGCAACCCAAAC 420
QY 421 GCAGTACAGCATCGAGATCCAGAACGTTGATGATGAGAGGGCCCTTACAGCTGCTC 480
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QY 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTACTTTGAGAGACACATCTCTCCAAAGC 660
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QY 661 GGTGGCTTTGTAGTGAAGACGAATATTTGGAATTCAGGGCATCACCCGGGAGCAGTC 720
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Qy 841 ACAAAGGGGACACTGCGAGTGTGAAGCTTCACAGCTCCCTCAGCAGATTTCCAGTGTGA 900
Db 841 ACAAAGGGGACACTGCGAGTGTGAAGCTTCACAGCTCCCTCAGCAGATTTCCAGTGTGA 900
Qy 901 CAAGGATGACAAAAGACTGATTTCAAGGAAAGAAAGGGGTGAAGTGGAAAAAGACACCTTT 960
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Qy 961 CCTCTCAAAACTCATCTTCTCAATGTCTCTCAATGTCTCTCAATGTCTCTCAATGTCTCT 1020
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Db 1081 CAGCAGGTGAGCAACGGCAGCTCGAGGAGGGCAGGCTCGCTGTGGCTCTGCTCTCTCTCT 1140
Qy 1141 GGTCTTGACCTGCTTCTCAATTTTGTATGTGATGTGATGTGATGTGATGTGATGTGATGT 1200
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Qy 1261 TATACAAATGAATTAGAAGAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGGAAAC 1320
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Db 1321 AAAGATATCTTTGGGGGAAAGAGTTTAAAGAAAGAAATTTGAAATTTGAAATTTGAAATTT 1380
Qy 1381 TTTAGTACATGGAGTCTTTCTTTTCCCAACGGGAAAGAACACAGCACACCCCGCTTGA 1440
Db 1381 TTTAGTACATGGAGTCTTTCTTTTCCCAACGGGAAAGAACACAGCACACCCCGCTTGA 1440
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Db 1441 CCCACTGCAAGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 1500
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Db 1501 TCTGCCACAGAGTGCCTCCACAGTGAACATTTCTGAGCTGGCCATCCCAATTCATCA 1560
Qy 1561 GTCCATAGAGACGAAGATGAGACTTTCCGGCCCAAGCGTGGCGCTGGGGCACTTTG 1620
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Qy 1621 GTAGACTGTGCCACCAACGGCGTGTGTGAAACGTGAAATTAATAAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAACGGCGTGTGTGAAACGTGAAATTAATAAAGAGCAAAAAA 1679

RESULT 12

ACD68655
ID ACD68655 standard; cDNA; 1679 BP.

XX ACD68655;

DT 17-SEP-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO337 cDNA.

XX Human; secreted and transmembrane protein; PRO; cytosolic;

XX antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;

XX chondrocyte stimulator; pericyte stimulator; fibroblast modulator;

XX pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;

KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
XX arthritis; wound; gene; ss.

OS Homo sapiens.

XX US2003045687-A1.

XX 06-MAR-2003.

XX 12-AUG-2002; 2002US-00218631.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-512315/48.

DR P-PSDB; ABO33767.

XX New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.

PS Claim 2; Fig 125; 314pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTTGTGCAAGCTTGAGCAACAC 60

Db 1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTTGTGCAAGCTTGAGCAACAC 60

Qy 61 AATCTATCAGGAAAGAGAAAGAAAAACCGAACCTTGACAAAAAGAGAAAAAGAG 120

Db 61 AATCTATCAGGAAAGAGAGAAAGAAAAACCGAACCTTGACAAAAAGAGAAAAAGAG 120

Qy 121 AAGAAAAAATCATGAAACCATCCAGCCAAAAATGCAATTTCTTCTTGGCAAT 180

121	DB	AAGNAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAAAATCTTAATCTCTTTGGGGCAAT	180
181	QY	CTTCACGGGGTGGCTGCTCTGTGTCTCTCTTCCAAGAGAGTCCCGTGCGCAGCGGAGATGC	240
181	DB	CTTCACGGGGTGGCTGCTCTGTGTCTCTCTTCCAAGAGAGTCCCGTGCGCAGCGGAGATGC	240
241	QY	CACCTTCCCAAAGCTATGCAACAGCTGACGGTCCGCGAGGGGGAGAGCGCACCCTCAG	300
241	DB	CACCTTCCCAAAGCTATGCAACAGCTGACGGTCCGCGAGGGGGAGAGCGCACCCTCAG	300
301	QY	GTGCACATATTGACAAACCGGGTCAACCCGGGTGGCTGTGGCTAAACCGCAGCACCATCTCTTA	360
301	DB	GTGCACATATTGACAAACCGGGTCAACCCGGGTGGCTGTGGCTAAACCGCAGCACCATCTCTTA	360
361	QY	TGCTGGGAATGACAAGTGGTGCTTGGATCCTCGGTGGTCTCTTCTGAGCAACACCAAAAC	420
361	DB	TGCTGGGAATGACAAGTGGTGCTTGGATCCTCGGTGGTCTCTTCTGAGCAACACCCAAAC	420
421	QY	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTC	480
421	DB	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTC	480
481	QY	GGTGCAGACAGAAACCAACCCAAAGACCTCTAGGGTCCACTCATNTGTGCAAGTATCTCC	540
481	DB	GGTGCAGACAGAAACCAACCCAAAGACCTCTAGGGTCCACTCATNTGTGCAAGTATCTCC	540
541	QY	CAAAATTTGACAGATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCAC	600
541	DB	CAAAATTTGACAGATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCAC	600
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601	DB	CTGCATAGCAACTGGTAGACACAGAGCCTTAGGTTACTTTGGAGACACATCTCTCCCAAAGC	660
661	QY	GTTTGGCTTTGTGAGTGAAGACGAATACTTTGGAAATTCAGGGCATCACCGGAGCAGTC	720
661	DB	GTTTGGCTTTGTGAGTGAAGACGAATACTTTGGAAATTCAGGGCATCACCGGAGCAGTC	720
721	QY	AGGGGACTACGAGTGCAGTGCTCCAAATGACGTGGCCGCGCCCTGGTGTAGGAGAGTAAA	780
721	DB	AGGGGACTACGAGTGCAGTGCTCCAAATGACGTGGCCGCGCCCTGGTGTAGGAGAGTAAA	780
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781	DB	GGTCACCGTGAACATATCACCATATCATTTTCHAGAGCCAGGGTACAGGTGTCCCCGTGGG	840
841	QY	ACAAAAGGGGACATGCAAGTGTGAAGCCTCAGCAGTCCCTTCAGCAGAAATTCAGATGGTA	900
841	DB	ACAAAAGGGGACATGCAAGTGTGAAGCCTCAGCAGTCCCTTCAGCAGAAATTCAGATGGTA	900
901	QY	CAAGGATGACAAAAGACATGATGTAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTT	960
901	DB	CAAGGATGACAAAAGACATGATGTAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTT	960
961	QY	CCTCTCAAAACTCATCTTTCTTCAATGTCTCTGAAACATGACTATCGGAACTACACTTCGCT	1020
961	DB	CCTCTCAAAACTCATCTTTCTTCAATGTCTCTGAAACATGACTATCGGAACTACACTTCGCT	1020
1021	QY	GGCTTCCAAAGCTGGGCCACCAATTCAGCATCATGCTATTTGGTCCAGCGCCGT	1080
1021	DB	GGCTTCCAAAGCTGGGCCACCAATTCAGCATCATGCTATTTGGTCCAGCGCCGT	1080
1081	QY	CAGCGAGGTGACCAACGGCAGTGCAGAGAGGCGAGGTGCGCTCTGGCTGTGCTCTTCT	1140
1081	DB	CAGCGAGGTGACCAACGGCAGTGCAGAGAGGCGAGGTGCGCTCTGGCTGTGCTCTTCT	1140
1141	QY	GGTCTTGCACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTTCGCCACCCGGGAAAGCT	1200
1141	DB	GGTCTTGCACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTTCGCCACCCGGGAAAGCT	1200
1201	QY	GCCGCCACACCAACCAACAGCAATGGCAACACGACAGCAACCAATCAGATA	1260
1201	DB	GCCGCCACACCAACCAACAGCAATGGCAACACGACAGCAACCAATCAGATA	1260

Qy	1261	TATACAAATGAATTTAGAGAAACACAGCCTCATGGACAGAAATTTGAGGGAGGGAAC	1321
Db	1261	TATACAAATGAATTTAGAGAAACACAGCCTCATGGACAGAAATTTGAGGGAGGGAAC	1321
Qy	1321	AAAGATACATTTTGGGGGAAAGAGTTTTTAAAAAGAAATTTGAAAAATTTGCTTGCAGATA	1380
Db	1321	AAAGATACATTTTGGGGGAAAGAGTTTTTAAAAAGAAATTTGAAAAATTTGCTTGCAGATA	1380
Qy	1381	TTTAGGTACAAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCCCGCTTTGGA	1440
Db	1381	TTTAGGTACAAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCCCGCTTTGGA	1440
Qy	1441	CCCACTGCAGCTGCATCGTGCAACCTCTTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC	1500
Db	1441	CCCACTGCAGCTGCATCGTGCAACCTCTTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC	1500
Qy	1501	TCGTGCCACAGAGTGCCTCCCAACGCTGGAAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA	1560
Db	1501	TCGTGCCACAGAGTGCCTCCCAACGCTGGAAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA	1560
Qy	1561	GTCATATAGACAGAAACAGAAATGAGACCTTCGGGCCCAAGCGTGGCGCTCGGGCACCTTTG	1620
Db	1561	GTCATATAGACAGAAACAGAAATGAGACCTTCGGGCCCAAGCGTGGCGCTCGGGCACCTTTG	1620
Qy	1621	GTAGACTGTGCCACCGCCGCTGTGTGTGTAACCGTGAATATAAGAGACAAAAA	1679
Db	1621	GTAGACTGTGCCACCGCCGCTGTGTGTGTAACCGTGAATATAAGAGACAAAAA	1679
RESULT 13			
ACA67181			
ID	ACA67181 standard; cDNA; 1679 BP.		
XX	ACA67181;		
AC			
XX			
DT	23-JUN-2003 (first entry)		
XX			
DE	cDNA encoding human PRO polypeptide #188.		
XX	Human; PRO polypeptide; secreted and transmembrane protein;		
KW	anti-PRO antibody; diagnostic assay; gene expression; diabetes;		
KW	bone disorder; cartilage disorder; rheumatoid arthritis; obesity;		
KW	sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;		
KW	hearing loss; coagulation disorder; stroke; heart attack; cardiac;		
KW	antidiabetic; anorectic; vulnerable; auditory; cerebrotective; angiogenic; gene; ss.		
XX	Homo sapiens.		
OS			
XX	US2003004311-Al.		
PN			
XX			
PD	02-JAN-2003.		
XX			
PF	19-DEC-2001; 2001US-00028072.		
XX			
PR	18-JUN-1997; 97US-0049911P.		
ER	26-AUG-1997; 97US-0056974P.		
PR	17-SEP-1997; 97US-0059113P.		
PR	17-SEP-1997; 97US-0059115P.		
PR	17-SEP-1997; 97US-0059117P.		
PR	17-SEP-1997; 97US-0059122P.		
PR	17-SEP-1997; 97US-0059184P.		
PR	18-SEP-1997; 97US-0059263P.		
PR	19-SEP-1997; 97US-0059352P.		
PR	19-SEP-1997; 97US-0059588P.		
PR	24-SEP-1997; 97US-0059836P.		
PR	17-OCT-1997; 97US-0062250P.		
PR	17-OCT-1997; 97US-0062285P.		
PR	17-OCT-1997; 97US-0062287P.		
PR	17-OCT-1997; 97US-0063755P.		
PR	24-OCT-1997; 97US-0062814P.		
PR	24-OCT-1997; 97US-0062816P.		

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PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 28-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063550P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079728P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WQ-US012456.
PR 14-JUL-1998; 98WQ-US014552.
PR 28-AUG-1998; 98WQ-US017888.
PR 10-SEP-1998; 98WQ-US018824.
PR 14-SEP-1998; 98WQ-US019093.
PR 14-SEP-1998; 98WQ-US019094.
PR 14-SEP-1998; 98WQ-US019177.
PR 16-SEP-1998; 98WQ-US019330.
PR 17-SEP-1998; 98WQ-US019437.
PR 27-OCT-1998; 98WQ-US021141.
PR 29-OCT-1998; 98WQ-US022991.
PR 29-OCT-1998; 98WQ-US022992.
PR 20-NOV-1998; 98WQ-US024855.
PR 01-DEC-1998; 98WQ-US025108.
PR 05-JAN-1999; 99WQ-US000106.
PR 08-MAR-1999; 99WQ-US005028.
PR 10-MAR-1999; 99WQ-US005190.
PR 20-APR-1999; 99WQ-US008615.
PR 14-MAY-1999; 99WQ-US010733.
PR 02-JUN-1999; 99WQ-US012252.
PR 01-SEP-1999; 99WQ-US020111.
PR 08-SEP-1999; 99WQ-US020594.
PR 13-SEP-1999; 99WQ-US020944.
PR 15-SEP-1999; 99WQ-US021090.
PR 15-SEP-1999; 99WQ-US021547.
PR 05-OCT-1999; 99WQ-US023089.
PR 29-NOV-1999; 99WQ-US028214.
PR 30-NOV-1999; 99WQ-US028313.
PR 30-NOV-1999; 99WQ-US028409.
PR 01-DEC-1999; 99WQ-US028301.
PR 01-DEC-1999; 99WQ-US028634.
PR 02-DEC-1999; 99WQ-US028551.
PR 02-DEC-1999; 99WQ-US028564.
PR 02-DEC-1999; 99WQ-US028565.
PR 16-DEC-1999; 99WQ-US030095.
PR 20-DEC-1999; 99WQ-US030911.
PR 20-DEC-1999; 99WQ-US030999.
PR 30-DEC-1999; 99WQ-US031243.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX
XX WPI; 2003-352836/33.
XX P-PSDB; ABU81057.
XX
XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
XX Claim 2; Fig 375; 643pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ACA66994-ACA67268 represent cDNA sequences encoding
CC the human PRO polypeptides of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from the USPTO web
CC site at seqdata.uspto.gov/paidsIDEntry.html
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTTGAGAGCAAC 60
DB 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTTGAGAGCAAC 60
QY 61 AATCTATCAGGAAGAAGAAAGAAAGAAACCGAACCTTCAAAAGAGAAAGAAAGAG 120
DB 61 AATCTATCAGGAAGAAGAAAGAAAGAAAGAAACCGAACCTTCAAAAGAGAAAGAAAGAG 120
QY 121 AAGAAAAAAATCATGAAAAACCATCCAGCAAAAATTCACAATTTCTTTGGGCAAT 180
DB 121 AAGAAAAAAATCATGAAAAACCATCCAGCAAAAATTCACAATTTCTTTGGGCAAT 180
QY 181 CTTACGGGGCTGGGTGCTCTGTGTCTCTTCAAGAGTGCCTGCGCAGCGGAGATGC 240
DB 181 CTTACGGGGCTGGGTGCTCTGTGTCTCTTCAAGAGTGCCTGCGCAGCGGAGATGC 240
QY 241 CACCTTCCCAAGCTATGGACAAGCTGCGTCCGCGAGGGGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAGCTATGGACAAGCTGCGTCCGCGAGGGGAGCGCCACCTCAG 300
QY 301 GTGCACCTATTGACAAACCGGGTCAACCGGGTGCCTTAAACCGCAGCACCCTCTA 360
DB 301 GTGCACCTATTGACAAACCGGGTCAACCGGGTGCCTTAAACCGCAGCACCCTCTA 360
QY 361 TGCTGGGAATGCAAGTGGTGCCTGGATCTCTCGCTGGTCTTCTTGTAGCAACCCAAAC 420
DB 361 TGCTGGGAATGCAAGTGGTGCCTGGATCTCTCGCTGGTCTTCTTGTAGCAACCCAAAC 420
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Db 361 TCTGGGAATGACAAGTGGTGGTGGATCCTCGGTGGTGGTCTCTGAGCAACACCCAAAC 420
Qy 421 GCAGTACAGCATCGAGATCCAGACGTCGATGATGACAGAGGCGCTTACACTGCTC 480
Db 421 GAGGTACAGCATCGAGATCCAGACGTCGATGATGACAGAGGCGCTTACACTGCTC 480
Qy 481 GGTGAGACAGACACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
Db 481 GGTGAGACAGACACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
Qy 541 CAAATTTGAGAGATTTCTTCCAGATATCTCCATTAATGAAGGGAACATATGAGCTCAC 600
Db 541 CAAATTTGAGAGATTTCTTCCAGATATCTCCATTAATGAAGGGAACATATGAGCTCAC 600
Qy 601 CTGATAGCAACTGTGAGACAGAGCTTACGTTTACTTTGGAGACACATCTCTCCCAAGC 660
Db 601 CTGATAGCAACTGTGAGACAGAGCTTACGTTTACTTTGGAGACACATCTCTCCCAAGC 660
Qy 661 GGTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Db 661 GGTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Qy 721 AGGGACTACAGTGCAGTGCCTCAATGACGTGGCGCGCCCGTGGTACGGAGAGTAA 780
Db 721 AGGGACTACAGTGCAGTGCCTCAATGACGTGGCGCGCCCGTGGTACGGAGAGTAA 780
Qy 781 GGTCAACGTGAATATCCACCATATCTTCAAGAGCCAAAGGTACAGTGTCCCGGTGG 840
Db 781 GGTCAACGTGAATATCCACCATATCTTCAAGAGCCAAAGGTACAGTGTCCCGGTGG 840
Qy 841 ACAAAGGGGACATGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db 841 ACAAAGGGGACATGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Qy 901 CAAGGATGACAAAGACTGATTTGAGGAGAAAGAGGGGTGAAGTGGAAACAGACCTTT 960
Db 901 CAAGGATGACAAAGACTGATTTGAGGAGAAAGAGGGGTGAAGTGGAAACAGACCTTT 960
Qy 961 CCTCTCAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAACACTCTTGGT 1020
Db 961 CCTCTCAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAACACTCTTGGT 1020
Qy 1021 GGCTTCAACAGCTGGGCCACACAAATGCGAGCATCATGTATTTGGTCCAGGCGCGT 1080
Db 1021 GGCTTCAACAGCTGGGCCACACAAATGCGAGCATCATGTATTTGGTCCAGGCGCGT 1080
Qy 1081 CAGCGAGTGAACAGCAGTCTGAGGAGGCGAGTGGTCTGGTCTGCTGCTCTTCT 1140
Db 1081 CAGCGAGTGAACAGCAGTCTGAGGAGGCGAGTGGTCTGGTCTGCTGCTCTTCT 1140
Qy 1141 GGTCTTGACCTGCTTCTCAATTTTGTATGTAGTGGCCACTTCCCCACCCGGGAAAGCT 1200
Db 1141 GGTCTTGACCTGCTTCTCAATTTTGTATGTAGTGGCCACTTCCCCACCCGGGAAAGCT 1200
Qy 1201 GCGGCCACCCACACCAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
Db 1201 GCGGCCACCCACACCAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
Qy 1261 TATCAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGGGGAAAC 1320
Db 1261 TATCAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGGGGAAAC 1320
Qy 1321 AAAGAATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCCCTTCAGATA 1380
Db 1321 AAAGAATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCCCTTCAGATA 1380
Qy 1381 TTTAGTACATGAGTTTCTTTTCCCAACGGGAGAAACACAGCACACCCGGCTTGA 1440
Db 1381 TTTAGTACATGAGTTTCTTTTCCCAACGGGAGAAACACAGCACACCCGGCTTGA 1440
Qy 1441 CCCACTGCAAGCTGATCGTCAACCTCTTTGGTGGCAGTGTGGGCAAGGGCTCAGCCTC 1500
Db 1441 CCCACTGCAAGCTGATCGTCAACCTCTTTGGTGGCAGTGTGGGCAAGGGCTCAGCCTC 1500

Qy 1501 TCTGCCACAGAGTGGCCCAACGTCGGAGACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
Db 1501 TCTGCCACAGAGTGGCCCAACGTCGGAGACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
Qy 1561 GTCCATAGAGACCAACACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGTGGGGCACTTTG 1620
Db 1561 GTCCATAGAGACCAACACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGTGGGGCACTTTG 1620
Qy 1621 GTAGACTGTGCCACCAACGCGGTGTGTGTGAAACGTGAAATATAAAGAGCAAAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAACGCGGTGTGTGTGAAACGTGAAATATAAAGAGCAAAAAAAA 1679

RESULT 14
ACA63892
ID ACA63892 standard; cDNA; 1679 BP.
XX
AC ACA63892;
AC
DT 16-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; inflammatory disease; organ failure;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
KW gene mapping; pharmaceutical; diagnostic; biosensor; bio reactor;
KW tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192706-A1.
XX
PD 19-DEC-2002.
XX
PF 24-OCT-2001; 2001US-00999832.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-0004020.
PR 20-MAR-1998; 98US-0078886P.
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PR 20-MAR-1998; 98US-0078936P.
PR 25-MAR-1998; 98US-0078939P.
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PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 30-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
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PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
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PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.

PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
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PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
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PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98WO-US024855.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI: 2003-328860/31.
DR P-PSDB; ABU72281.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 2; Fig 221; 453pp; English.

XX The invention describes an isolated nucleic acid (1) comprising, or which
CC is at least 80 % sequence identity to, or the full-length coding sequence
CC of, any of 118 300-2100 nucleotide sequences, which encodes its
CC corresponding PRO polypeptide selected from 118 100-700 amino acid
CC sequences, all given in the specification. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS, cancer, or diabetic complications. The nucleic
CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTGAGAGCAAC 60
DB |||||
QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTGAGAGCAAC 60
DB |||||
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGCTGACAAAGAAAGAAAGAAAG 120
DB |||||
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGCTGACAAAGAAAGAAAGAAAG 120
DB |||||
QY 121 AAGAAAAAATCATGAAACCATCCAGCCAAAAATGCAATTCCTCTTGGGCAAT 180
DB |||||
QY 121 AAGAAAAAATCATGAAACCATCCAGCCAAAAATGCAATTCCTCTTGGGCAAT 180
DB |||||
QY 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGAGTGCCTGCGGAGGAGATGC 240
DB |||||
QY 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGAGTGCCTGCGGAGGAGATGC 240
DB |||||
QY 241 CACCTTCCCAAGCTATGGAACAAGTACGGTCCGGAGGGGGAGAGCGCCCTCAG 300
DB |||||
QY 241 CACCTTCCCAAGCTATGGAACAAGTACGGTCCGGAGGGGGAGAGCGCCCTCAG 300
DB |||||
QY 301 GTGCATATTTGCAACCCGGGTCAACCGGGTGGCTTAAACCGCAGCACCATCTCTA 360
DB |||||
QY 301 GTGCATATTTGCAACCCGGGTCAACCGGGTGGCTTAAACCGCAGCACCATCTCTA 360
DB |||||
QY 361 TCGTGGGATGACAGTGGTGGCTGCTGATCCTCGGTGGTCTCTTCTGAGCAAGTATCC 420
DB |||||
QY 361 TCGTGGGATGACAGTGGTGGCTGCTGATCCTCGGTGGTCTCTTCTGAGCAAGTATCC 420
DB |||||
QY 421 GCAGTACAGCATCGAGATCCAGAACTGGATGTATGACGAGGGGCCCTTACACCTGCTC 480
DB |||||
QY 421 GCAGTACAGCATCGAGATCCAGAACTGGATGTATGACGAGGGGCCCTTACACCTGCTC 480
DB |||||
QY 481 GGTGAGACAGCAACCCAGGCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
DB |||||
QY 481 GGTGAGACAGCAACCCAGGCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
DB |||||
QY 541 CAAATGTTAGAGATTTCTTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTC 600
DB |||||
QY 541 CAAATGTTAGAGATTTCTTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTC 600
DB |||||
QY 601 CTGCATAGCAACTGGTGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660
DB |||||
QY 601 CTGCATAGCAACTGGTGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGC 660
DB |||||
QY 661 GGTGGCTTTGTGAGTGAAGCAATATCTTGAATTCAGGGCATCACCCGGGAGCAGTC 720
DB |||||
QY 721 AGGGACTACGATGAGTGCCTCCAAATGACCTGCGCGCGCGTGGTACGAGAGTAA 780
DB |||||
QY 721 AGGGACTACGATGAGTGCCTCCAAATGACCTGCGCGCGCGTGGTACGAGAGTAA 780
DB |||||

QY 781 GGTCAACCGTGAAGTACTTCCACCATATATTTCAAGCCCAAGGTACAGGTGTCCTCCGCTGGG 840
Db |||||
781 GGTCAACCGTGAAGTACTTCCACCATATATTTCAAGCCCAAGGTACAGGTGTCCTCCGCTGGG 840
QY 841 ACAAAAGGGGACACTGCGAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db |||||
841 ACAAAAGGGGACACTGCGAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
QY 901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 960
Db |||||
901 CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTT 960
QY 961 CTTCTCAAAACTCACTTTCTTCAATGTCTCTGAACATGACTATGGAAGTCACTTTGGT 1020
Db |||||
961 CTTCTCAAAACTCACTTTCTTCAATGTCTCTGAACATGACTATGGAAGTCACTTTGGT 1020
QY 1021 GGCCTCCCAAGCTGGGCCACCAATGCCAGCATCATGCTATTTGTCAGGGCCGCT 1080
Db |||||
1021 GGCCTCCCAAGCTGGGCCACCAATGCCAGCATCATGCTATTTGTCAGGGCCGCT 1080
QY 1081 CAGCAGGTGAGCAACGGCAGCTCGAGGAGGCGAGCTGCGTCTGCTGCTGCTCTTCT 1140
Db |||||
1081 CAGCAGGTGAGCAACGGCAGCTCGAGGAGGCGAGCTGCGTCTGCTGCTGCTCTTCT 1140
QY 1141 GGTCTTGACCTGCTTCTCAATTTTGAATGAGTGCCACTTCCCAACCCGGGAAAGGCT 1200
Db |||||
1141 GGTCTTGACCTGCTTCTCAATTTTGAATGAGTGCCACTTCCCAACCCGGGAAAGGCT 1200
QY 1201 GCCGCCATCAGATA 1260
Db |||||
1201 GCCGCCATCAGATA 1260
QY 1261 TATACAAATGAATTTAGAGAAACACACGCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
Db |||||
1261 TATACAAATGAATTTAGAGAAACACACGCTCATGGGACAGAAATTTGAGGGAGGGGAAC 1320
QY 1321 AAGAATGACTTTGGGGGAAAGAGTTTTTAAAGAAATTTGAAATTTGCTTGCAGATA 1380
Db |||||
1321 AAGAATGACTTTGGGGGAAAGAGTTTTTAAAGAAATTTGAAATTTGCTTGCAGATA 1380
QY 1381 TTTAGTACATGAGTGTCTTTTCCCAACGGGAGGAACACACACACACACACCGGCTTGA 1440
Db |||||
1381 TTTAGTACATGAGTGTCTTTTCCCAACGGGAGGAACACACACACACACCGGCTTGA 1440
QY 1441 CCCACTGCAAGTGCATGTCGCAACCTCTTTGGTCCAGTGTGGGCAAGGCTCAGCCTC 1500
Db |||||
1441 CCCACTGCAAGTGCATGTCGCAACCTCTTTGGTCCAGTGTGGGCAAGGCTCAGCCTC 1500
QY 1501 TCTGCCACAGAGTCCCGCCAGTGGACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
Db |||||
1501 TCTGCCACAGAGTCCCGCCAGTGGACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
QY 1561 GTCCATAGACGACAGAAATGAGACCTTTCGGGCCCAAGCTGGCGCTGGCGGCACTTTG 1620
Db |||||
1561 GTCCATAGACGACAGAAATGAGACCTTTCGGGCCCAAGCTGGCGCTGGCGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCAACCGGCTGTGTGGAACCTGGAATTAAGAGAGCAAAAAA 1679
Db |||||
1621 GTAGACTGTGCCACCAACCGGCTGTGTGGAACCTGGAATTAAGAGAGCAAAAAA 1679

RESULT 15

ACR03790

ID ACR03790 standard; cDNA; 1679 BP.

XX AC

XX ACR03790;

XX AC

DT 23-MAY-2003 (first entry)

DE cDNA encoding human PRO polypeptide #188.

XX DE

XX Human; PRO polypeptide; secreted and transmembrane protein;

XX tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;

KW KW

differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene; ss.

Homo sapiens.

US2003036180-A1.

20-FEB-2003.

09-MAY-2002; 2002US-00143114.

31-MAR-1997; 97WO-US005230.

12-JUN-1998; 98WO-US012456.

14-JUL-1998; 98WO-US014552.

28-AUG-1998; 98WO-US017888.

10-SEP-1998; 98WO-US018824.

14-SEP-1998; 98WO-US019093.

14-SEP-1998; 98WO-US019094.

16-SEP-1998; 98WO-US019177.

17-SEP-1998; 98WO-US019330.

07-OCT-1998; 98WO-US021141.

29-OCT-1998; 98WO-US022991.

29-OCT-1998; 98WO-US022992.

20-NOV-1998; 98WO-US024855.

01-DEC-1998; 98WO-US025108.

05-JAN-1999; 99WO-US000106.

08-MAR-1999; 99WO-US005028.

10-MAR-1999; 99WO-US005190.

20-APR-1999; 99WO-US008615.

14-MAY-1999; 99WO-US010733.

02-JUN-1999; 99WO-US012252.

01-SEP-1999; 99WO-US020111.

08-SEP-1999; 99WO-US020594.

13-SEP-1999; 99WO-US020344.

15-SEP-1999; 99WO-US021090.

15-SEP-1999; 99WO-US021547.

05-OCT-1999; 99WO-US023089.

29-NOV-1999; 99WO-US028214.

30-NOV-1999; 99WO-US028313.

30-NOV-1999; 99WO-US028409.

01-DEC-1999; 99WO-US028301.

01-DEC-1999; 99WO-US028634.

02-DEC-1999; 99WO-US028551.

02-DEC-1999; 99WO-US028564.

02-DEC-1999; 99WO-US028565.

16-DEC-1999; 99WO-US030095.

20-DEC-1999; 99WO-US030911.

20-DEC-1999; 99WO-US030999.

22-DEC-1999; 99WO-US030720.

30-DEC-1999; 99WO-US031243.

30-DEC-1999; 99WO-US031274.

05-JAN-2000; 2000WO-US000219.

06-JAN-2000; 2000WO-US000277.

06-JAN-2000; 2000WO-US000376.

11-FEB-2000; 2000WO-US003565.

18-FEB-2000; 2000WO-US004341.

18-FEB-2000; 2000WO-US004342.

22-FEB-2000; 2000WO-US004414.

24-FEB-2000; 2000WO-US004914.

24-FEB-2000; 2000WO-US005004.

01-MAR-2000; 2000WO-US005601.

02-MAR-2000; 2000WO-US005746.

02-MAR-2000; 2000WO-US005841.

15-MAR-2000; 2000WO-US006319.

20-MAR-2000; 2000WO-US006884.

21-MAR-2000; 2000WO-US007377.

30-MAR-2000; 2000WO-US007532.

17-MAY-2000; 2000WO-US013705.

22-MAY-2000; 2000WO-US014042.

30-MAY-2000; 2000WO-US014941.

02-JUN-2000; 2000WO-US015264.

XX	Claim 2; SEQ ID NO 522; 55pp; English.	
PS	The invention relates to an isolated secreted and transmembrane	
CC	polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful	
CC	in PRO polypeptide detection methods. The PRO polypeptide is useful for	
CC	linking a bioactive molecule to a cell. The PRO polypeptide or an	
CC	antibody against it is useful for modulating a biological activity of a	
CC	cell. The PRO polypeptide is useful in industrial applications including	
CC	pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO	
CC	polypeptide is also useful as a thrombolytic agent, interferon,	
CC	interleukin, erythropoietin, colony stimulating factor and other	
CC	cytokines. The PRO polypeptide is useful for treating disease such as	
CC	cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,	
CC	amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,	
CC	atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,	
CC	Parkinson's disease; cardiovascular disease e.g. hypertension and	
CC	myocardial ischaemia; kidney disease e.g. renal failure and	
CC	glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial	
CC	asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory	
CC	bowel disease; reproductive disorders e.g. premature labour and	
CC	pre-eclampsia; carcinogenesis. The present sequence represents a cDNA	
CC	encoding a PRO polypeptide of the invention. Note: The sequence data for	
CC	this patent did not form part of the printed specification but was	
CC	obtained in electronic format directly from USPTO at	
CC	seqdata.uspto.gov/sequence.html?DocID=20020177553	
XX		
SQL	Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 1679; DB 7; Length 1679;	
	Best Local Similarity 100.0%; Pred. No. 1.5e-15;	
	Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GTTGTGCTTCAGCAAAACAGTGGATTTAAATCTCTTGCACAAGCTTGAGGCAAC	60
DB	1 GTTGTGCTTCAGCAAAACAGTGGATTTAAATCTCTTGCACAAGCTTGAGGCAAC	60
QY	61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTTGACAAAAGAAAGAAAG	120
DB	61 AATCTATCAGGAAGAAAGAAAGAAACCGAACCTTGACAAAAGAAAGAAAG	120
QY	121 AAGAAAAAATCATGAAACCATCCAGCCAAATATGCACAAATCTATCTCTGGCAAT	180
DB	121 AAGAAAAAATCATGAAACCATCCAGCCAAATATGCACAAATCTATCTCTGGCAAT	180
QY	181 CTTTCAGGGGCTGGCTGCTCTGTGTCTCTTCCAGAGTGCCTGCGCAGCGAGATGC	240
DB	181 CTTTCAGGGGCTGGCTGCTCTGTGTCTCTTCCAGAGTGCCTGCGCAGCGAGATGC	240
QY	241 CACCTTCCCAAGCTATGGACAACTGACGTTCGGCAGGGGAGAGGGCCACCTCAG	300
DB	241 CACCTTCCCAAGCTATGGACAACTGACGTTCGGCAGGGGAGAGGGCCACCTCAG	300
QY	301 GTGCATATTGACAAACCGGCTCACCGGGTGGCTGAGTAAACCGACCATCTCTTA	360
DB	301 GTGCATATTGACAAACCGGCTCACCGGGTGGCTGAGTAAACCGACCATCTCTTA	360
QY	361 TGCTGGGAATGACAAAGTGTGCTCGATCCTCGCGTGGTCTTCTGAGCAACCCCAAC	420
DB	361 TGCTGGGAATGACAAAGTGTGCTCGATCCTCGCGTGGTCTTCTGAGCAACCCCAAC	420
QY	421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGATGACAGGGGCCCTTACCTGCTC	480
DB	421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGATGACAGGGGCCCTTACCTGCTC	480
QY	481 GGTGCACACAGACAAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540
DB	481 GGTGCACACAGACAAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540
QY	541 CAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	600
DB	541 CAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	600

RESULT 18
ABX89328
ID ABX89328 standard; cDNA; 1679 BP.
XX
AC ABX89328;
XX
DT 13-MAY-2003 (first entry)
XX
DE DNA encoding novel secreted and transmembrane protein PRO337.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
XX US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-00140808.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 27-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008415.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00892636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-148238/14.
XX P-PSDB; ABUS9838.
XX
XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,
XX useful for treating pericyte-associated tumors, diabetes and various bone
XX and/or cartilage disorders, e.g. arthritis.
XX
XX Claim 2; Fig 375; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX CC

CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC encodes a novel human PRO protein
XX
SQ

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GTGTGTCTCTTACGAAACAGTGGATTAAATCTCTCTGCAACAGCTTGAGAGCAAC	60
DB	1	GTGTGTCTCTTACGAAACAGTGGATTAAATCTCTCTGCAACAGCTTGAGAGCAAC	60
QY	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120
DB	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120
QY	121	AAGAAAAAATCATGAAACCATCGAGCCAAAGAAATGCAATCTCTCTTTGGCAAT	180
DB	121	AAGAAAAAATCATGAAACCATCGAGCCAAAGAAATGCAATCTCTCTTTGGCAAT	180
QY	181	CTTCACGGGGCTGGCTGTCTGTCTCTTCCAGGAGTCCCGTGGCGAGCGAGATGC	240
DB	181	CTTCACGGGGCTGGCTGTCTGTCTCTTCCAGGAGTCCCGTGGCGAGCGAGATGC	240
QY	241	CACCTTCCCAAAGCTATGGAACAGTACCGTCCGCGAGGGGAGCGCCACCTCAG	300
DB	241	CACCTTCCCAAAGCTATGGAACAGTACCGTCCGCGAGGGGAGCGCCACCTCAG	300
QY	301	GTCACTATTGACACCGGTGACCCGGTGGCTGGCTTAACCGCAGACCATCTCTTA	360
DB	301	GTCACTATTGACACCGGTGACCCGGTGGCTGGCTTAACCGCAGACCATCTCTTA	360
QY	361	TGCTGGGAATGACAAAGTGTGCTGGATCCTCGCGTGGTCTCTTGAGAAACCCAAAC	420
DB	361	TGCTGGGAATGACAAAGTGTGCTGGATCCTCGCGTGGTCTCTTGAGAAACCCAAAC	420
QY	421	GCAGTACAGATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGTC	480
DB	421	GCAGTACAGATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGTC	480
QY	481	GGTGACAGACAGAAACACCCAAAGACCTTAGGGTCCACCTCATTTGTGCAGATCTCC	540
DB	481	GGTGACAGACAGAAACACCCAAAGACCTTAGGGTCCACCTCATTTGTGCAGATCTCC	540
QY	541	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTC	600
DB	541	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTC	600

QY	601	CTGCATAGCAACTGTGTAGACGAGCCTACGGTTACTTGAGACACATCTCTCCCAAGC	660
DB	601	CTGCATAGCAACTGTGTAGACGAGCCTACGGTTACTTGAGACACATCTCTCCCAAGC	660
QY	661	GGTTGGCTTTGTGAGTGAAGACGAATACATTGGAATTTCAAGGGCATCACCCGGGAGCAGTC	720
DB	661	GGTTGGCTTTGTGAGTGAAGACGAATACATTGGAATTTCAAGGGCATCACCCGGGAGCAGTC	720
QY	721	AGGGGACTAGAGTGCAGTGCCTCCAAATGAGTGGCGCGCGCTGTGAGAGAGTAA	780
DB	721	AGGGGACTAGAGTGCAGTGCCTCCAAATGAGTGGCGCGCGCTGTGAGAGAGTAA	780
QY	781	GGTCCCGTGAATCTATCCACCATACATTTTCAAGAACCAAGGGTACAGGTGTCTCCCGTGG	840
DB	781	GGTCCCGTGAATCTATCCACCATACATTTTCAAGAACCAAGGGTACAGGTGTCTCCCGTGG	840
QY	841	ACAAAAGGGGACATGTCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
DB	841	ACAAAAGGGGACATGTCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900
QY	901	CAAGGATGACAAAGACTGATTGAAGAAAGAAAGGGGTGAAAGTGGAAAAAGACCTTT	960
DB	901	CAAGGATGACAAAGACTGATTGAAGAAAGAAAGGGGTGAAAGTGGAAAAAGACCTTT	960
QY	961	CTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTTGCGT	1020
DB	961	CTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTTGCGT	1020
QY	1021	GGCTTCAAACAGCTGGGCGACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGT	1080
DB	1021	GGCTTCAAACAGCTGGGCGACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGT	1080
QY	1081	CAGCAGGTGAGCAACGCGACGCTCGAGGAGGCGAGCTGGCTGTGCTGTCTTCT	1140
DB	1081	CAGCAGGTGAGCAACGCGACGCTCGAGGAGGCGAGCTGGCTGTGCTGTCTTCT	1140
QY	1141	GGTCTTGACCTTCTCTCAAAATTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT	1200
DB	1141	GGTCTTGACCTTCTCTCAAAATTTGATGTGAGTGCCACTTCCCCACCCGGGAAAGGCT	1200
QY	1201	GGCGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	1260
DB	1201	GGCGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	1260
QY	1261	TATACAAATGAATTAGAAGAAACACAGCTCATGGACAGAAATTTGAGGGGAGGAAAC	1320
DB	1261	TATACAAATGAATTAGAAGAAACACAGCTCATGGACAGAAATTTGAGGGGAGGAAAC	1320
QY	1321	AAAGAAATCTTTGGGGGAAAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTGCAGATA	1380
DB	1321	AAAGAAATCTTTGGGGGAAAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTGCAGATA	1380
QY	1381	TTTAGGTACATGGAGTTTCTTTTCCAAACGGGAGAAACACAGACACCCGGCTTGA	1440
DB	1381	TTTAGGTACATGGAGTTTCTTTTCCAAACGGGAGAAACACAGACACCCGGCTTGA	1440
QY	1441	CCCACTGCAAGCTGCATCGTCAACCTTTTGTGCGAGTGGGCAAGGGCTCAGCCTC	1500
DB	1441	CCCACTGCAAGCTGCATCGTCAACCTTTTGTGCGAGTGGGCAAGGGCTCAGCCTC	1500
QY	1501	TTTGGCCACAGAGTGCCTCCACGTGGAACATTTCTGAGCTGGCCATTCCTCAATCA	1560
DB	1501	TTTGGCCACAGAGTGCCTCCACGTGGAACATTTCTGAGCTGGCCATTCCTCAATCA	1560
QY	1561	GTCCATAGAGAGCAACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGGCACTTTG	1620
DB	1561	GTCCATAGAGAGCAACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGGCACTTTG	1620
QY	1621	GTAGACTGTGCCACACCGCGGTGTGTGAAACCTGTGAATATAAAGAGCAAAAAA	1679
DB	1621	GTAGACTGTGCCACACCGCGGTGTGTGAAACCTGTGAATATAAAGAGCAAAAAA	1679

RESULT 19
 ABX92696
 ID ABX92696 standard; cdna; 1679 bp.
 XX
 XX
 ABX92696;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 XX
 DE cDNA encoding human PRO337 polypeptide.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
 KW cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 KW genetic disorder; cycostatic; antidiabetic; antiinflammatory;
 KW antarthritic; anti-tumour; vulnery; antianaemic; dermatological;
 KW cardiant; gene; ss.
 XX
 XX Homo sapiens.
 XX
 XX US2002169284-A1.
 XX
 XX
 PD 14-NOV-2002.
 XX
 XX 16-OCT-2001; 2001US-00978697.
 XX
 PR 26-MAY-1981; 81US-00267213.
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-0004020P.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 26-JUN-1998; 98US-00105413.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98US-0021141.
 PR 02-NOV-1998; 98US-00184216.
 PR 06-NOV-1998; 98US-00187368.
 PR 20-NOV-1998; 98US-0024855.
 PR 22-DEC-1998; 98US-00202054.
 PR 22-DEC-1998; 98US-00218517.
 PR 05-JAN-1999; 99US-0000106.
 PR 05-MAR-1999; 99US-00254465.
 PR 08-MAR-1999; 99US-00050028.
 PR 10-MAR-1999; 99US-00265686.
 PR 10-MAR-1999; 99US-00050190.
 PR 12-APR-1999; 99US-00284291.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99US-0010733.
 PR 02-JUN-1999; 99US-0012252.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380142.
 PR 30-NOV-1999; 99US-00283113.
 PR
 PR 02-DEC-1999; 99US-0028551.
 PR 02-DEC-1999; 99US-0028551.
 PR 16-DEC-1999; 99US-0030095.
 PR 30-DEC-1999; 99US-0031243.
 PR 30-DEC-1999; 99US-0031274.
 PR 05-JAN-2000; 2000US-0000219.
 PR 06-JAN-2000; 2000US-0000277.
 PR 11-FEB-2000; 2000US-0000376.
 PR 18-FEB-2000; 2000US-0004341.
 PR 24-FEB-2000; 2000US-0005004.
 PR 02-MAR-2000; 2000US-0005841.
 PR 10-MAR-2000; 2000US-0006319.
 PR 21-MAR-2000; 2000US-0007532.
 PR 30-MAR-2000; 2000US-0008439.
 PR 17-MAY-2000; 2000US-0013705.
 PR 22-MAY-2000; 2000US-0014042.
 PR 30-MAY-2000; 2000US-0014941.
 PR 02-JUN-2000; 2000US-0015264.
 PR 28-JUL-2000; 2000US-0020710.
 PR 24-AUG-2000; 2000US-0023328.
 PR 08-NOV-2000; 2000US-00709238.
 PR 27-NOV-2000; 2000US-00723749.
 PR 01-DEC-2000; 2000US-00832678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000US-00834956.
 PR 28-FEB-2001; 2001US-0006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 22-MAR-2001; 2001US-00816920.
 PR 22-MAR-2001; 2001US-00809552.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00854280.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001US-0019692.
 PR 29-JUN-2001; 2001US-0021066.
 PR 09-JUL-2001; 2001US-0021735.
 PR 30-JUL-2001; 2001US-00918585.
 XX
 XX (GETH) GENENTECH INC.
 PA Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2003-288163/28.
 DR P-PSDB; AB061159.
 XX
 XX Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies.
 XX
 XX Claim 2; Fig 221; 459pp; English.
 PS
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The bioactive molecule may be a
 CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
 CC The PRO polypeptides are useful for treating immune disorders, diabetes
 CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
 CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
 CC tumours, and wound healing. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and gene

CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. The present sequence encodes a human PRO polypeptide
CC of the invention. Note: The sequence data for this patent was obtained in
CC electronic format directly from the USPTO web site at
XX seqdata.uspto.gov/psipSIDEntry.html

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTTGTGCTCTTCAGCAACACAGTGGATTTAAATCTCTTGTGCAACAGCTTGAGAGCAAC 60
Db |||
QY |||
Db 1 GTTGTGCTCTTCAGCAACACAGTGGATTTAAATCTCTTGTGCAACAGCTTGAGAGCAAC 60
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Db |||
QY |||
Db 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAAAATATGAAAAACCATCCAGCCAAAAATGCAATTTCTATCTCTTGGGCAAT 180
Db |||
QY |||
Db 121 AAGAAAAAATATGAAAAACCATCCAGCCAAAAATGCAATTTCTATCTCTTGGGCAAT 180
QY 181 CTTTCAGGGGCTGGCTGCTCTGTGCTCTTCCAGAGTGGCCGTCGCGAGGGAGATGC 240
Db |||
QY |||
Db 181 CTTTCAGGGGCTGGCTGCTCTGTGCTCTTCCAGAGTGGCCGTCGCGAGGGAGATGC 240
QY 241 CACCTTCCCAAGCTATGGCAACAGTGAACGTCGCGAGGGGAGAGCGCCACCTCAG 300
Db |||
QY |||
Db 241 CACCTTCCCAAGCTATGGCAACAGTGAACGTCGCGAGGGGAGAGCGCCACCTCAG 300
QY 301 GTGCACATATTGACAAACCGGTGTCACCGGGTGGCTGGCTGAAACCGCAGCAACCTCTA 360
Db |||
QY |||
Db 301 GTGCACATATTGACAAACCGGTGTCACCGGGTGGCTGGCTGAAACCGCAGCAACCTCTA 360
QY 361 TGCTGGGAATGACAGTGTGCTGGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db |||
QY |||
Db 361 TGCTGGGAATGACAGTGTGCTGGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 GCAGTACAGCTACGAGATCCAGAAAGTGGATGTGTATGACAGAGGCGCTTACACCTGCTC 480
Db |||
QY |||
Db 421 GCAGTACAGCTACGAGATCCAGAAAGTGGATGTGTATGACAGAGGCGCTTACACCTGCTC 480
QY 481 GGTGACAGACACACACACACACACACACACACACACACACACACACACACACACACAC 540
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QY |||
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Db |||
QY |||
Db 601 CTGCATAGCAACTGGTAGACAGAGCTTACGTTTACTTTGGAGACACATCTCTCCCAAGC 660
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Db |||
QY |||
Db 661 GGTGGCTTTGTGAGTGAAGAGCAATATCTTGGAAATTCAGGGCATCACCGGGAGCAGTC 720
QY 721 AGGGGACTACGAGTGCAGTCTCCAAATGAGTGGCGCGCGCTGGTGAACGAGATGAA 780
Db |||
QY |||
Db 721 AGGGGACTACGAGTGCAGTCTCCAAATGAGTGGCGCGCGCTGGTGAACGAGATGAA 780
QY 781 GGTCACTGAACTATCCACCATACATTTTCAAGAGCCCAAGGGTACAGGTGTCCTCGTGG 840
Db |||
QY |||
Db 781 GGTCACTGAACTATCCACCATACATTTTCAAGAGCCCAAGGGTACAGGTGTCCTCGTGG 840
QY 841 ACMAAGGGGACATGAGTGTGAAGCTCAGAGTCCCTCAGCAGAAATTCAGATGTA 900
Db |||
QY |||
Db 841 ACMAAGGGGACATGAGTGTGAAGCTCAGAGTCCCTCAGCAGAAATTCAGATGTA 900
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QY 901 CAAGGATCACAAGACGTGATTGAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT 960
Db |||
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QY 961 CCTCTCAAACTCATCTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGGT 1020
Db |||
QY 961 CCTCTCAAACTCATCTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGGT 1020
QY 1021 GGCCTTCAAAAGCTGGGCCACACCAATTTGATGTGAGTCCAGCATCATGCTATTGGTCCAGGCGCGT 1080
Db |||
QY 1021 GGCCTTCAAAAGCTGGGCCACACCAATTTGATGTGAGTCCAGCATCATGCTATTGGTCCAGGCGCGT 1080
QY 1081 CAGGAGTGAAGCAACGGCAGCTGAGAGGAGGAGGCTGCGTCTGGCTGCTCTTCTTCT 1140
Db |||
QY 1081 CAGGAGTGAAGCAACGGCAGCTGAGAGGAGGAGGCTGCGTCTGGCTGCTCTTCTTCT 1140
QY 1141 GGTCTTGACCTGCTCTTCAAAATTTGATGTGAGTCCAGCTTCCACCCCGGAAAGCT 1200
Db |||
QY 1141 GGTCTTGACCTGCTCTTCAAAATTTGATGTGAGTCCAGCTTCCACCCCGGAAAGCT 1200
QY 1201 GCCGCCACACACACCAACCAACAGCAATGGCAACACCGACAGCAACCAATCAGATA 1260
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QY 1261 TATACAAATGAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC 1320
Db |||
QY 1261 TATACAAATGAATTAGAAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC 1320
QY 1321 AAAGAAATTTGGGGGAAAGAGTTTAAAGAAAGAAATTTGAAATTTGCCCTTCAGATA 1380
Db |||
QY 1321 AAAGAAATTTGGGGGAAAGAGTTTAAAGAAAGAAATTTGAAATTTGCCCTTCAGATA 1380
QY 1381 TTTAGGTACAAATGAGTTTCTTTTCCAAACCGGAAAGAAACACAGCACACCCGGCTTGG 1440
Db |||
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QY 1441 CCCACTGCAGCTGCATGTCGTCACCTTTGGTGGCCAGTGTGGGCAAGGCTCAGCCTC 1500
Db |||
QY 1441 CCCACTGCAGCTGCATGTCGTCACCTTTGGTGGCCAGTGTGGGCAAGGCTCAGCCTC 1500
QY 1501 TCTGCCACAGAGTGCCTCCACGTCGGAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
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QY 1501 TCTGCCACAGAGTGCCTCCACGTCGGAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
QY 1561 GTCCATAGAGACGAACAGAAATGAGACTTTCGGCCCAAGGCTGGCTGGGGCACTTTG 1620
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QY 1561 GTCCATAGAGACGAACAGAAATGAGACTTTCGGCCCAAGGCTGGCTGGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACACGCGGTGTGTGTGAACGTGAATATAAAGAGCAAAAAA 1679
Db |||
QY 1621 GTAGACTGTGCCACACGCGGTGTGTGTGAACGTGAATATAAAGAGCAAAAAA 1679
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RESULT 20

ACD41982

ID ACD41982 standard; cDNA; 1679 BP.

XX ACD41982;

XX ACD41982;

DT 05-SEP-2003 (first entry)

XX Human secreted/transmembrane protein (PRO) cDNA #188.

XX Human; ss; gene; PRO; secreted protein; transmembrane protein; tumour;
XX cystostatic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
XX proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
XX BMC; Glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
XX chondrocyte cell proliferation; chondrocyte cell differentiation;
XX pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
XX endothelial cell; A-peptide; factor VIIa.
OS Homo sapiens.

XX PN US2003036179-A1.
XX PD 20-FEB-2003.
XX PF 10-MAY-2002; 2002US-00142431.
XX PR 31-MAR-1997; 97WO-US005230.
XX PR 12-JUN-1998; 98WO-US012456.
XX PR 14-JUL-1998; 98WO-US014552.
XX PR 28-AUG-1998; 98WO-US017888.
XX PR 10-SEP-1998; 98WO-US018824.
XX PR 14-SEP-1998; 98WO-US019093.
XX PR 14-SEP-1998; 98WO-US019094.
XX PR 14-SEP-1998; 98WO-US019177.
XX PR 16-SEP-1998; 98WO-US019330.
XX PR 17-SEP-1998; 98WO-US019437.
XX PR 07-OCT-1998; 98WO-US021141.
XX PR 29-OCT-1998; 98WO-US022991.
XX PR 29-OCT-1998; 98WO-US022992.
XX PR 20-NOV-1998; 98WO-US024855.
XX PR 01-DEC-1998; 98WO-US025108.
XX PR 05-JAN-1999; 99WO-US000106.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 10-MAR-1999; 99WO-US005190.
XX PR 20-APR-1999; 99WO-US010733.
XX PR 14-MAY-1999; 99WO-US012252.
XX PR 02-JUN-1999; 99WO-US020111.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 13-SEP-1999; 99WO-US020944.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 05-OCT-1999; 99WO-US023089.
XX PR 29-NOV-1999; 99WO-US028214.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 30-NOV-1999; 99WO-US028409.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 01-DEC-1999; 99WO-US028634.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 02-DEC-1999; 99WO-US028564.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 16-DEC-1999; 99WO-US030095.
XX PR 20-DEC-1999; 99WO-US030911.
XX PR 22-DEC-1999; 99WO-US030999.
XX PR 22-DEC-1999; 99WO-US030720.
XX PR 30-DEC-1999; 99WO-US031243.
XX PR 30-DEC-1999; 99WO-US031274.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000277.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US003565.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 18-FEB-2000; 2000WO-US004342.
XX PR 22-FEB-2000; 2000WO-US004414.
XX PR 24-FEB-2000; 2000WO-US004914.
XX PR 24-FEB-2000; 2000WO-US005004.
XX PR 01-MAR-2000; 2000WO-US005501.
XX PR 02-MAR-2000; 2000WO-US005746.
XX PR 02-MAR-2000; 2000WO-US005941.
XX PR 10-MAR-2000; 2000WO-US006319.
XX PR 15-MAR-2000; 2000WO-US006884.
XX PR 20-MAR-2000; 2000WO-US007377.
XX PR 21-MAR-2000; 2000WO-US007532.
XX PR 30-MAR-2000; 2000WO-US008439.
XX PR 17-MAY-2000; 2000WO-US013705.
XX PR 22-MAY-2000; 2000WO-US014042.
XX PR 30-MAY-2000; 2000WO-US014941.
XX PR 02-JUN-2000; 2000WO-US015264.
XX PR 28-JUL-2000; 2000WO-US020710.
XX PR 11-AUG-2000; 2000WO-US022031.
XX PR 23-AUG-2000; 2000WO-US023522.
XX PR 24-AUG-2000; 2000WO-US023328.
XX PR 08-NOV-2000; 2000WO-US030952.
XX PR 10-NOV-2000; 2000WO-US030873.
XX PR 01-DEC-2000; 2000WO-US032678.
XX PR 20-DEC-2000; 2000US-00747259.
XX PR 20-DEC-2000; 2000WO-US034956.
XX PR 28-FEB-2001; 2001US-00796498.
XX PR 28-FEB-2001; 2001WO-US006520.
XX PR 01-MAR-2001; 2001WO-US006666.
XX PR 09-MAR-2001; 2001US-00802706.
XX PR 14-MAR-2001; 2001US-00808689.
XX PR 22-MAR-2001; 2001US-00816744.
XX PR 05-APR-2001; 2001US-00828366.
XX PR 10-MAY-2001; 2001US-00854208.
XX PR 10-MAY-2001; 2001US-00854280.
XX PR 18-MAY-2001; 2001US-00860216.
XX PR 25-MAY-2001; 2001US-00866028.
XX PR 25-MAY-2001; 2001US-00866034.
XX PR 25-MAY-2001; 2001WO-US017092.
XX PR 01-JUN-2001; 2001US-00872035.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 03-JUN-2001; 2001US-00874503.
XX PR 14-JUN-2001; 2001US-00882636.
XX PR 19-JUN-2001; 2001US-00886342.
XX PR 20-JUN-2001; 2001WO-US019692.
XX PR 21-JUN-2001; 2001US-00887879.
XX PR 22-JUN-2001; 2001WO-US020116.
XX PR 23-JUN-2001; 2001WO-US021066.
XX PR 09-JUL-2001; 2001WO-US021735.
XX PR 18-JUL-2001; 2001US-00908827.
XX PR 06-AUG-2001; 2001US-00924419.
XX PR 09-AUG-2001; 2001US-00927796.
XX PR 16-AUG-2001; 2001US-00931836.
XX PR 19-DEC-2001; 2001US-00028072.
XX PA (GETH) GENENTECH INC.
XX PI Baker KP, Beresini M, Deforge L, Deanoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-466355/44.
XX P-PSDB; ABO25028.
XX PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
XX PRQ4978, useful in molecular biology, chromosome and gene mapping, in
XX PT generating antisense RNA and DNA, and in gene therapy.
XX PS Claim 2; Fig 375; 659pp; English.
XX CC The invention relates to an isolated nucleic acid comprising at least 80%
XX CC sequence identity to a PRO (secreted and transmembrane protein) cDNA
XX CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its
XX CC extracellular domain (with or without its associated signal peptide),
XX CC which comprises any of the 275 120-850 residue amino acid sequences,
XX CC given in the specification; (b) comprising any of the 275 300-3500
XX CC nucleotide sequences, given in the specification; or (c) comprising the
XX CC full-length coding sequence of the nucleotide sequences given in the
XX CC specification, or of the DNA deposited under any of the American Type
XX CC Culture Collection (ATCC) Accession Numbers listed in the specification.
XX CC Also included are a vector comprising the novel nucleic acid, a host cell
XX CC comprising the vector, producing a PRO polypeptide, the isolated PRO
XX CC polypeptides detailed above, a chimaeric molecule comprising the PRO
XX CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
XX CC antibody, detecting a PRO polypeptide in a sample suspected of containing
XX CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a
XX CC PRO polypeptide, modulating at least one biological activity of a cell
XX CC expressing a PRO polypeptide, stimulating the release of tumour necrosis
XX CC factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
XX CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
XX CC modulating the uptake of glucose or FFA by skeletal muscle cells or
XX CC adipocyte cells, stimulating the proliferation or differentiation of
XX CC chondrocyte cells (or proliferation of or gene expression in pericyte
XX CC cells), stimulating the proliferation of inner ear utricular supporting

CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
 CC binding of A-peptide to factor VIIA, or differentiation of adipocyte
 CC cells, detecting the presence of a tumour in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences given
 CC in the specification. The polynucleotide is useful in molecular biology,
 CC including uses as hybridisation probes, in chromosome and gene mapping,
 CC in generating antisense RNA and DNA, and in gene therapy. The
 CC polynucleotide may also be used in preparing PRO polypeptides by
 CC recombinant techniques, and in generating either transgenic animals or
 CC knock-out animals which, in turn, are useful in the development and
 CC screening of therapeutically useful reagents. The PRO polypeptide or the
 CC antibody is used in preparing a medicament for treating a condition
 CC responsive to the polypeptide or antibody, such as tumours, and in
 CC various diagnostic assays. The present sequence encodes a PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTCTCTTCAGCAAAACAGTGGATTAAATCTCTTCGACAAAGTTCGAGGCAAC 60
 DB 1 GTTGTCTCTTCAGCAAAACAGTGGATTAAATCTCTTCGACAAAGTTCGAGGCAAC 60

QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

QY 121 AAGAAAAAAATCATGAAACCATCAGCGCAAAATGCGCAATTCATCTCTTGGGCAAT 180
 DB 121 AAGAAAAAAATCATGAAACCATCAGCGCAAAATGCGCAATTCATCTCTTGGGCAAT 180

QY 181 CTTTCAGGGCTGGCTGCTCTGTGCTCTCTTCAAGGAGTGCCGTCGAGCGGAGATGC 240
 DB 181 CTTTCAGGGCTGGCTGCTCTGTGCTCTCTTCAAGGAGTGCCGTCGAGCGGAGATGC 240

QY 241 CACCTTCCCAAGCTATGACAAACGTGACGGTCCGCGAGGGGAGCGCCACCCCTCAG 300
 DB 241 CACCTTCCCAAGCTATGACAAACGTGACGGTCCGCGAGGGGAGCGCCACCCCTCAG 300

QY 301 GTGCATATGCAACCGGTCACCCGGTGGCTGGCTTAACCGCAGACCATCTCTTA 360
 DB 301 GTGCATATGCAACCGGTCACCCGGTGGCTGGCTTAACCGCAGACCATCTCTTA 360

QY 361 TGTGGGAATGCAAGTGTGCTGTGATCTCTGCGTGGTCTCTTCAGCAACACCCCAAC 420
 DB 361 TGTGGGAATGCAAGTGTGCTGTGATCTCTGCGTGGTCTCTTCAGCAACACCCCAAC 420

QY 421 GCAGTACAGCATGAGATCCAGAACTGTGATGTATGACGAGGGCCCTTACACCTGCTC 480
 DB 421 GCAGTACAGCATGAGATCCAGAACTGTGATGTATGACGAGGGCCCTTACACCTGCTC 480

QY 481 GTGCAGACAGCAACACCCCAAGACCTTAGGTCACCTCATTTGTGCAAGTATCTCC 540
 DB 481 GTGCAGACAGCAACACCCCAAGACCTTAGGTCACCTCATTTGTGCAAGTATCTCC 540

QY 541 CAAAATTGTAGAGATTCTTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTC 600
 DB 541 CAAAATTGTAGAGATTCTTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTC 600

QY 601 CTGCATAGCAACTGGTAGACAGAGCCTACGGTACTTGGAGACACATCTCTCCCAAGC 660
 DB 601 CTGCATAGCAACTGGTAGACAGAGCCTACGGTACTTGGAGACACATCTCTCCCAAGC 660

QY 661 GGTGGCTTTGTGAGTGAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
 DB 661 GGTGGCTTTGTGAGTGAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720

QY 721 AGGGGACTACGAGTGCAGTCCCAATGACGTCGGCGCCCGTGGTACGAGAGTAAA 780
 DB 721 AGGGGACTACGAGTGCAGTCCCAATGACGTCGGCGCCCGTGGTACGAGAGTAAA 780

QY 781 GGTCCCGTGAATATCCACCATACATTTCAAGCCAGGGTACAGGTGTCCCGGTGG 840
 DB 781 GGTCCCGTGAATATCCACCATACATTTCAAGCCAGGGTACAGGTGTCCCGGTGG 840

QY 841 ACAAAGGGGACACATGCGAGTGTGAAGCCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
 DB 841 ACAAAGGGGACACATGCGAGTGTGAAGCCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900

QY 901 CAAGATGACAAAGACTGATTGAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT 960
 DB 901 CAAGATGACAAAGACTGATTGAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT 960

QY 961 CTTCTCAAAATCATCTTCTTCAATGCTCTCAATGCTCTGAAACATGACTATGGAACTACACTTGCCT 1020
 DB 961 CTTCTCAAAATCATCTTCTTCAATGCTCTGAAACATGACTATGGAACTACACTTGCCT 1020

QY 1021 GGCCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGGCCCT 1080
 DB 1021 GGCCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGGCCCT 1080

QY 1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGCGAGCTGCGTCTGCTGCTCTCTTCT 1140
 DB 1081 CAGCGAGGTGAGCAACGGCACGTCGAGGAGGCGAGCTGCGTCTGCTGCTCTCTTCT 1140

QY 1141 GGTCTTGACACCTGCTTCTCAAAATTTTGAATGCCAGCATCATGCTATTGTGTCAGGGCCCT 1200
 DB 1141 GGTCTTGACACCTGCTTCTCAAAATTTTGAATGCCAGCATCATGCTATTGTGTCAGGGCCCT 1200

QY 1201 GCGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1260
 DB 1201 GCGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1260

QY 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGAGGAGGAGAAATTTGAGGGGAGGGAAC 1320
 DB 1261 TATACAAATGAAATTTAGAGAAACACAGCCTCATGAGGAGGAGAAATTTGAGGGGAGGGAAC 1320

QY 1321 AAAGAATACCTTTGGGGGAAAAAGAGTTTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380
 DB 1321 AAAGAATACCTTTGGGGGAAAAAGAGTTTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380

QY 1381 TTTAGTCAATGAGATTTTCTTTTCCAAACGGGAAGAACACAGACACACCCGGCTTGA 1440
 DB 1381 TTTAGTCAATGAGATTTTCTTTTCCAAACGGGAAGAACACAGACACACCCGGCTTGA 1440

QY 1441 CCCACTGCAAGCTGATCGTCAACCTCTTTGTCAGTGTGGGCAAGGGCTCAGCCCTC 1500
 DB 1441 CCCACTGCAAGCTGATCGTCAACCTCTTTGTCAGTGTGGGCAAGGGCTCAGCCCTC 1500

QY 1501 TCTGCCACAGAGTGCCTCCACGTCGAAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
 DB 1501 TCTGCCACAGAGTGCCTCCACGTCGAAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560

QY 1561 GTCCATAGAGACGACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCCTTTG 1620
 DB 1561 GTCCATAGAGACGACAGATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCCTTTG 1620

QY 1621 GTAGACTGTGCCACCAACCGCGTGTCTGTGAAACCTGAAATATAAAGAGCAAAAAA 1679
 DB 1621 GTAGACTGTGCCACCAACCGCGTGTCTGTGAAACCTGAAATATAAAGAGCAAAAAA 1679

RESULT 21

ACA60526

ID ACA60526 standard; cDNA; 1679 BP.

XX ACA60526;

XX 11-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO337 cDNA.

XX Human; secreted and transmembrane polypeptide; PRO;

XX fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;

KW

```
KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
KW toxin; radiolabel; antibody; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tissue typing; gene; ss.
XX
XX Homo sapiens.
XX OS
XX US2002177165-A1.
XX PN
XX
XX 28-NOV-2002.
XX PD
XX
XX 01-FEB-2002; 2002US-00066500.
XX PF
XX 26-AUG-1997; 97US-0056974P.
XX PR 17-SEP-1997; 97US-0059115P.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 19-SEP-1997; 97US-0059588P.
XX PR 17-OCT-1997; 97US-0062285P.
XX PR 24-OCT-1997; 97US-0062816P.
XX PR 27-OCT-1997; 97US-0063082P.
XX PR 27-OCT-1997; 97US-0063329P.
XX PR 29-OCT-1997; 97US-0063733P.
XX PR 21-NOV-1997; 97US-0066364P.
XX PR 25-NOV-1997; 97US-0066840P.
XX PR 16-DEC-1997; 97US-0069694P.
XX PR 09-FEB-1998; 98US-0074086P.
XX PR 09-FEB-1998; 98US-0074092P.
XX PR 25-MAR-1998; 98US-0079294P.
XX PR 08-APR-1998; 98US-0081049P.
XX PR 14-JUL-1998; 98WO-US014552.
XX PR 10-AUG-1998; 98US-0095988P.
XX PR 18-AUG-1998; 98US-0097000P.
XX PR 09-SEP-1998; 98US-0099601P.
XX PR 10-SEP-1998; 98US-0099803P.
XX PR 10-SEP-1998; 98US-0099811P.
XX PR 10-SEP-1998; 98US-0099812P.
XX PR 10-SEP-1998; 98WO-US018824.
XX PR 14-SEP-1998; 98WO-US019093.
XX PR 16-SEP-1998; 98WO-US019330.
XX PR 17-SEP-1998; 98US-0100858P.
XX PR 17-SEP-1998; 98WO-US019437.
XX PR 24-SEP-1998; 98US-0101922P.
XX PR 28-OCT-1998; 98US-0106032P.
XX PR 20-NOV-1998; 98US-0109304P.
XX PR 20-NOV-1998; 98WO-US024855.
XX PR 25-NOV-1998; 98WO-US025190.
XX PR 01-DEC-1998; 98WO-US025108.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 23-MAR-1999; 99US-0125778P.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 15-JUN-1999; 99US-0139695P.
XX PR 20-JUL-1999; 99US-0145070P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 17-AUG-1999; 99US-0149396P.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 15-SEP-1999; 99WO-US021090.
XX PR 15-SEP-1999; 99WO-US021547.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 01-DEC-1999; 99WO-US028301.
XX PR 02-DEC-1999; 99WO-US028565.
XX PR 07-DEC-1999; 99US-0169495P.
XX PR 20-DEC-1999; 99WO-US030999.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 18-FEB-2000; 2000WO-US004342.
XX PR 22-FEB-2000; 2000WO-US004414.
XX PR 01-MAR-2000; 2000WO-US005601.
XX PR 02-MAR-2000; 2000WO-US005841.
XX PR 09-MAR-2000; 2000WO-US006471.
XX PR 20-MAR-2000; 2000WO-US007377.
XX PR 30-MAR-2000; 2000WO-US008439.

PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US0006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Baton DL,
XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
XX Godowski PJ, Gurney AL, Kijavini IU, Mather JP, Napier MA, Pan J,
XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
XX Wood WI, Zhang Z;
XX WPI; 2003-328482/31.
XX P-PSDB; ABU72061.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
XX activity of cell expressing the polypeptide, for identifying agonists or
XX antagonists of polypeptide, and as molecular weight markers.
XX
XX Claim 2; Fig 51; 254pp; English.
XX
XX The invention describes an isolated, secreted and transmembrane
XX polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
XX (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411,
XX PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor
XX (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or
XX PRO951 polypeptide, and for linking a bioactive molecule to a cell
XX expressing the above polypeptides. The bioactive molecule, a toxin,
XX radiolabel or an antibody, causes cell death. PRO is useful in assays to
XX identify other proteins or molecules involved in binding interaction. The
XX polynucleotide (II) encoding (I) is useful in chromosome and gene
XX mapping, in generation of antisense RNA and DNA, for generating
XX transgenic animals or knockout animals which in turn are useful in the
XX development and screening of therapeutically useful reagents, to
XX construct hybridisation probes for mapping the gene which encodes the PRO
XX and for the genetic analysis of individuals with genetic disorders, in
XX gene therapy, for chromosome identification and as a chromosome marker.
XX (I) and (II) are useful for tissue typing. This sequence encodes a novel
XX human secreted and transmembrane PRO polypeptide
XX
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1679; DB 7; Length 1679;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-15;
XX Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTCTGCAACAGCTTGAGAGCAAC 60
Db 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTCTGCAACAGCTTGAGAGCAAC 60
Qy 61 AATCTATCAGGAAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Db 61 AATCTATCAGGAAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Qy 121 AAGAAAAAAATCATGAAACCATCCAGCCAAAATGCAATTTCTTCTGGGCAAT 180
Db 121 AAGAAAAAAATCATGAAACCATCCAGCCAAAATGCAATTTCTTCTGGGCAAT 180
Qy 181 CTTACAGGGGCTGGCTGCTGTGTCTTCTTCCAGGAGTGCCCGTGGCAGCGGATGC 240
Db 181 CTTACAGGGGCTGGCTGCTGTGTCTTCTTCCAGGAGTGCCCGTGGCAGCGGATGC 240
```

Db 181 CTTACGGGGCTGGCTCTCTGTCTCTTCAAGAGTCCCGTCCGACGGAGATGC 240
QY 241 CACCTTCCCAAGCTATGGACAAGTGTGCGTCCGGCAGGGGGAGAGCGCCACCTCTAG 300
Db 241 CACCTTCCCAAGCTATGGACAAGTGTGCGTCCGGCAGGGGGAGAGCGCCACCTCTAG 300
QY 301 GTGCACTATTGACAACCGGGTCAACCGGGTGCCTTGGCTTAACCGCGAGCACCATCTCTA 360
Db 301 GTGCACTATTGACAACCGGGTCAACCGGGTGCCTTGGCTTAACCGCGAGCACCATCTCTA 360
QY 361 TCGTGGGAATGACAAGTGTGCTGATCTCTCGGTGCTTCTTCTGAGCAACACCCAAAC 420
Db 361 TCGTGGGAATGACAAGTGTGCTGATCTCTCGGTGCTTCTTCTGAGCAACACCCAAAC 420
QY 421 GCAGTACAGCTGAGATCCAGAACTGTGATGATGATGAGAGGGCCCTTACACCTGCTC 480
Db 421 GCAGTACAGCTGAGATCCAGAACTGTGATGATGATGAGAGGGCCCTTACACCTGCTC 480
QY 481 GGTGACAGACAGAACCAACCAAGACCTCTTAGGGTCCACCTCATTTGCAAGTATCTCC 540
Db 481 GGTGACAGACAGAACCAACCAAGACCTCTTAGGGTCCACCTCATTTGCAAGTATCTCC 540
QY 541 CAAAATTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCTCAC 600
Db 541 CAAAATTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCTCAC 600
QY 601 CTGCATAGCAACTGTGACAGAGCTACGGTCTTCTTGGAGACACATCTCTCCAAAGC 660
Db 601 CTGCATAGCAACTGTGACAGAGCTACGGTCTTCTTGGAGACACATCTCTCCAAAGC 660
QY 661 GGTGGCTTTGTGAGTGAAGACCAATATCTGAAATTTAGGGCATCACCGGGAGCAGTC 720
Db 661 GGTGGCTTTGTGAGTGAAGACCAATATCTGAAATTTAGGGCATCACCGGGAGCAGTC 720
QY 721 AGGGACTACAGTGCAGTCCCAATGACGTGGCGGCCCTGTGACGAGAGTAA 780
Db 721 AGGGACTACAGTGCAGTCCCAATGACGTGGCGGCCCTGTGACGAGAGTAA 780
QY 781 GGTCACTGAACTATCCACATATATTTCAAGCAAGGTACAGGTGTCCCGTGG 840
Db 781 GGTCACTGAACTATCCACATATATTTCAAGCAAGGTACAGGTGTCCCGTGG 840
QY 841 AAAAAAGGGACACTGCACTGTGAGAGCTTCAAGCTTCCCTCAGCAGAAATTCAGTGTA 900
Db 841 AAAAAAGGGACACTGCACTGTGAGAGCTTCAAGCTTCCCTCAGCAGAAATTCAGTGTA 900
QY 901 CAAGATGACAAAGACTGATTTGAAGAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
Db 901 CAAGATGACAAAGACTGATTTGAAGAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
QY 961 CTTCTCAAACTCATCTTCTCAATGTCTCTGAAATGAGTGGAACTACACTTGGT 1020
Db 961 CTTCTCAAACTCATCTTCTCAATGTCTCTGAAATGAGTGGAACTACACTTGGT 1020
QY 1021 GGCCTCCAAAGCTGGGCAACCAATGCCAGCATATGCTATTTGTCAGGCGCGCT 1080
Db 1021 GGCCTCCAAAGCTGGGCAACCAATGCCAGCATATGCTATTTGTCAGGCGCGCT 1080
QY 1081 CAGCGAGGTGACCAAGCACTCCAGAGGGCAGCTGCGTCTGCTGCTCTCTTCT 1140
Db 1081 CAGCGAGGTGACCAAGCACTCCAGAGGGCAGCTGCGTCTGCTGCTCTCTTCT 1140
QY 1141 GGTCTTGCACTGCTTCTCAATTTTGTGATGAGTGGCACTTCCCGCCGGGAAAGCT 1200
Db 1141 GGTCTTGCACTGCTTCTCAATTTTGTGATGAGTGGCACTTCCCGCCGGGAAAGCT 1200
QY 1201 GCGGCCACCAACCAACCAACCAAGCAATGGCAACCGGACGAAACCAATCAGATA 1260
Db 1201 GCGGCCACCAACCAACCAACCAAGCAATGGCAACCGGACGAAACCAATCAGATA 1260
QY 1261 TATACAAATGAATATAGAGAAACACAGCTCATGGGACAGAAATTTGAGGGAGGGAC 1320
Db 1261 TATACAAATGAATATAGAGAAACACAGCTCATGGGACAGAAATTTGAGGGAGGGAC 1320

QY 1321 AAAGTAATCTTTGGGGGAAAAGAGTTTAAAAAGAAATTTGAAATTTGCCTTGCAGATA 1380
Db 1321 AAAGTAATCTTTGGGGGAAAAGAGTTTAAAAAGAAATTTGAAATTTGCCTTGCAGATA 1380
QY 1381 TTTAGGTACAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGACACACCGGCTTGA 1440
Db 1381 TTTAGGTACAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGACACACCGGCTTGA 1440
QY 1441 CCCACTGAAGTGCATCGTGCACCTCTTTGGTGCCTAGTGTGGCAAGGGCTCAGCTC 1500
Db 1441 CCCACTGAAGTGCATCGTGCACCTCTTTGGTGCCTAGTGTGGCAAGGGCTCAGCTC 1500
QY 1501 TCTGCCACAGAGTCCCGCCACGTGGAGACATCTCTGGAGTGGCCATCCCAATTTCAATCA 1560
Db 1501 TCTGCCACAGAGTCCCGCCACGTGGAGACATCTCTGGAGTGGCCATCCCAATTTCAATCA 1560
QY 1561 GTCCATAGAGACGAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCCTTTG 1620
Db 1561 GTCCATAGAGACGAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCCTTTG 1620
QY 1621 GTAGACTGTGCCACCAACCGCGTGTGTGTGAAAACGTGAAATAAAAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAACCGCGTGTGTGTGAAAACGTGAAATAAAAAGAGCAAAAAA 1679

RESULT 22
ACA04516
ID ACA04516 standard; cDNA; 1679 BP.
XX ACA04516;
XX 28-MAY-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 DNA.
XX
KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW obesity; diabetes; insulinemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032062-A1.
XX
PD 13-FEB-2003.
XX
PF 01-FEB-2002; 2002US-00066273.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066840P.
PR 25-NOV-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.

PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100859P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025190.
 PR 08-MAR-1999; 98WO-US005028.
 PR 23-MAR-1999; 98US-0125778P.
 PR 02-JUN-1999; 98WO-US012252.
 PR 15-JUN-1999; 98US-0139695P.
 PR 20-JUL-1999; 98US-0145070P.
 PR 26-JUL-1999; 98US-0145698P.
 PR 17-AUG-1999; 98US-0149396P.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 30-NOV-1999; 98WO-US028313.
 PR 01-DEC-1999; 98WO-US028301.
 PR 02-DEC-1999; 98WO-US028555.
 PR 07-DEC-1999; 98US-0169493P.
 PR 20-DEC-1999; 98WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001WO-US0002796.
 XX (GETH) GENENTECH INC.
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski FJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood W, Zhang Z;
 XX WPI; 2003-341963/32.
 DR P-P8DB; ABU67162.
 XX
 PT New secreted and transmembrane polypeptide for modulating biological
 PT activity of a cell expressing the polypeptide, identifying agonists or
 PT antagonists of the polypeptide, and as molecular weight markers.
 XX
 PS Claim 2; Fig 51; 254pp; English.

XX The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
 CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (II) Is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (I) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
 CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This sequence encodes a
 CC novel human secreted and transmembrane polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1679; DB 7; Length 1679;
 Best_Local_Similarity 100.0%; Pred. No. 1.5e-15;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTGCAAGCTTGAGACCAAC 60
 DB 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTGCAAGCTTGAGACCAAC 60
 QY 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 DB 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 QY 121 AAGAAAAAATCATGAAACCCATCCAGCAAAATGCAATTCATCTCTTGGGCAAT 180
 DB 121 AAGAAAAAATCATGAAACCCATCCAGCAAAATGCAATTCATCTCTTGGGCAAT 180
 QY 181 CTTACGGGGTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCTGCGAGCGGAGATGC 240
 DB 181 CTTACGGGGTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCTGCGAGCGGAGATGC 240
 QY 241 CACCTTCCCCAAGACTATGACAAACCGTGCCTGGAATCTCTGAGCAACCCCAAC 300
 DB 241 CACCTTCCCCAAGACTATGACAAACCGTGCCTGGAATCTCTGAGCAACCCCAAC 300
 QY 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGCTGCTGAGCAACCCCTCTA 360
 DB 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGCTGCTGAGCAACCCCTCTA 360
 QY 361 TGTGGGAATGACAAAGTGGTGGCTGATCTCTGCGTGGTCTCTTGTGAGCAACCCCAAC 420
 DB 361 TGTGGGAATGACAAAGTGGTGGCTGATCTCTGCGTGGTCTCTTGTGAGCAACCCCAAC 420
 QY 421 GCAGTACAGCATCGAGATCCAGAACCGTGGATGTGTATGACAGGGGCCCTTACACCTGCTC 480
 DB 421 GCAGTACAGCATCGAGATCCAGAACCGTGGATGTGTATGACAGGGGCCCTTACACCTGCTC 480
 QY 481 GGTGACAGACAGCAACCAACCAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCC 540
 DB 481 GGTGACAGACAGCAACCAACCAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCC 540
 QY 541 CAAAATTGTAGAGATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
 DB 541 CAAAATTGTAGAGATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
 QY 601 CTGCATAGCAACTGGTAGACAGAGCCTAGGTTACTTGTGAGACACATCTCTCCCAAGC 660
 DB 601 CTGCATAGCAACTGGTAGACAGAGCCTAGGTTACTTGTGAGACACATCTCTCCCAAGC 660

QY 661 GGTGGCTTTGTGAGTGAAGAGCAATACCTTGGAAATTCAGGCGCATCACCCGGAGCAGTC 720
Db |||||
QY 661 GGTGGCTTTGTGAGTGAAGAGCAATACCTTGGAAATTCAGGCGCATCACCCGGAGCAGTC 720
Db |||||
QY 721 AGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCGCGCGCGTGGTACGGAGAGTAA 780
Db |||||
QY 721 AGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCGCGCGCGTGGTACGGAGAGTAA 780
Db |||||
QY 781 GGTCCCGTGAACCTATCCACCATACATTTTCAGAGCCAAAGGTACAGTGTCCCGTGGG 840
Db |||||
QY 781 GGTCCCGTGAACCTATCCACCATACATTTTCAGAGCCAAAGGTACAGTGTCCCGTGGG 840
Db |||||
QY 841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db |||||
QY 841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db |||||
QY 901 CAAGGATGACAAAGACTGATTTGAAGGAAAGGGGTGAAAGTGGAAACAGACCTTT 960
Db |||||
QY 961 CCTCTCAAACTCATCTTCTCAATGTCTCTGAATGATGATATGGAACTACACTTGGT 1020
Db |||||
QY 961 CCTCTCAAACTCATCTTCTCAATGTCTCTGAATGATGATATGGAACTACACTTGGT 1020
Db |||||
QY 1021 GGCCTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGGT 1080
Db |||||
QY 1021 GGCCTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGGT 1080
Db |||||
QY 1081 CAGCAGGTGAGCAACGGCAGCTCGAGGAGGCGGCTGCTGCTGCTGCTGCTTCTTCT 1140
Db |||||
QY 1081 CAGCAGGTGAGCAACGGCAGCTCGAGGAGGCGGCTGCTGCTGCTGCTGCTTCTTCT 1140
Db |||||
QY 1141 GGTCTTGCACCTGCTTCTCAATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db |||||
QY 1141 GGTCTTGCACCTGCTTCTCAATTTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db |||||
QY 1201 GCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
Db |||||
QY 1201 GCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
Db |||||
QY 1261 TATACAAATGAAATTAGAGAAACACAGCCTCATGGGAAGAAATTTGAGGAGGGGAAAC 1320
Db |||||
QY 1261 TATACAAATGAAATTAGAGAAACACAGCCTCATGGGAAGAAATTTGAGGAGGGGAAAC 1320
Db |||||
QY 1321 AAAGAAATCTTTGGGGGAAAGAGTTTAAAGAAATTCGAAATTCGCTTGCAGATA 1380
Db |||||
QY 1321 AAAGAAATCTTTGGGGGAAAGAGTTTAAAGAAATTCGAAATTCGCTTGCAGATA 1380
Db |||||
QY 1381 TTTAGGTACAATGGAGTTTCTTTTCCCAACGGGAAGAACACAGCACACCCGGCTTGA 1440
Db |||||
QY 1441 CCCACTGCAAGTGCATCGTGCAACCTCTTGGTGCAGTGTGGCAAGGGCTCAGCCCTC 1500
Db |||||
QY 1441 CCCACTGCAAGTGCATCGTGCAACCTCTTGGTGCAGTGTGGCAAGGGCTCAGCCCTC 1500
Db |||||
QY 1501 TCTGCCACACAGAGTGGCCCAAGTGAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
Db |||||
QY 1501 TCTGCCACACAGAGTGGCCCAAGTGAACATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
Db |||||
QY 1561 GTCCATAGAGACGAACAGAAATGAGACTTCCCGCCCAAGCGTGGCGCTCGCGGCACCTTGG 1620
Db |||||
QY 1561 GTCCATAGAGACGAACAGAAATGAGACTTCCCGCCCAAGCGTGGCGCTCGCGGCACCTTGG 1620
Db |||||
QY 1621 GTAGACTGTGCCACCGCGGTGTGTTGAAACGTGAAATTAAGAGAGCAAAAAA 1679
Db |||||
QY 1621 GTAGACTGTGCCACCGCGGTGTGTTGAAACGTGAAATTAAGAGAGCAAAAAA 1679
Db |||||

RESULT 23

ACA66437

ID ACA66437 standard; cDNA; 1679 BP.

XX AC ACA66437;
XX DT 24-JUN-2003 (first entry)
XX DE Human cDNA encoding secreted/transmembrane protein PRO337.
XX KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;
KW leukaemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;
KW infertility; premature aging; psoriasis; inflammatory disease;
KW renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;
KW hepatitis; multiple sclerosis; gene therapy.
XX OS Homo sapiens.
XX PN US2003004102-A1.
XX PD 02-JAN-2003.
XX PF 15-OCT-2001; 2001US-00978189.
XX PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 11-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-0021141.
PR 06-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99US-0000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99US-0005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99US-00051590.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 02-JUN-1999; 99US-00310733.
PR 25-AUG-1999; 99US-00312252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99US-0028313.
PR 02-DEC-1999; 99US-0028551.
PR 02-DEC-1999; 99US-0028555.
PR 16-DEC-1999; 99US-0030035.
PR 30-DEC-1999; 99US-0031243.
PR 30-DEC-1999; 99US-0031274.

05-JAN-2000; 2000WO-US000219.
06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US0003565.
18-FEB-2000; 2000WO-US004341.
24-FEB-2000; 2000WO-US005004.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US006319.
21-MAR-2000; 2000WO-US007532.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000US-00709238.
10-NOV-2000; 2000WO-US030873.
27-NOV-2000; 2000US-00723749.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001WO-US006520.
22-MAR-2001; 2001US-00816744.
22-MAR-2001; 2001US-00816920.
22-MAR-2001; 2001WO-US009552.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
14-JUN-2001; 2001US-00882636.
19-JUN-2001; 2001US-00886342.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
30-JUL-2001; 2001WO-US021855.
(GETH) GENENTECH INC.
PA
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini I, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
DR WPI; 2003-341189/32.
DR P-PSDB; ABU80428.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT PRO1559), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT sclerosis in mammals.
XX
PS Claim 2; Fig 221; 460pp; English.
XX
CC The invention relates to a new isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence encodes a PRO polypeptide
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGCTCTTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAACAC 60
DB 1 GTTGTGCTCTTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAACAC 60
QY 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAAAATCATGAAACCATCCAGCCAAATGCAACATCTCTCTTCTGGCAAT 180
DB 121 AAGAAAAAATCATGAAACCATCCAGCCAAATGCAACATCTCTCTTCTGGCAAT 180
QY 181 CTTCAAGGGGCTGGCTCTCTGTCTCTTCTTCCAGAGAGTGCCTGCGGAGGAGATGC 240
DB 181 CTTCAAGGGGCTGGCTCTCTGTCTCTTCTTCCAGAGAGTGCCTGCGGAGGAGATGC 240
QY 241 CACCTTCCCAAGCTATGACAAACGTGACGCTCCGGAGGGGAGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAGCTATGACAAACGTGACGCTCCGGAGGGGAGAGCGCCACCTCAG 300
QY 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGCTTAAACCGCAGACCATCTCTA 360
DB 301 GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTGCTTAAACCGCAGACCATCTCTA 360
QY 361 TGCTGGGAATGACAAAGTGGTGGATCTCTGCGTGGTCTCTTGTGAGCAACACCCAAAC 420
DB 361 TGCTGGGAATGACAAAGTGGTGGATCTCTGCGTGGTCTCTTGTGAGCAACACCCAAAC 420
QY 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACGAGGGGCCCTTACACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACGAGGGGCCCTTACACCTGCTC 480
QY 481 GGTGACAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
DB 481 GGTGACAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCC 540
QY 541 CAAAATTGTAGAGATTCTTCAGATATCTCCATTAATGAGGAAACAATATTAGCTTCAC 600
DB 541 CAAAATTGTAGAGATTCTTCAGATATCTCCATTAATGAGGAAACAATATTAGCTTCAC 600
QY 601 CTGCATAGCAACTGGTAGACGAGCTACGGTACTTGGAGACATCTCTCCCAAGC 660
DB 601 CTGCATAGCAACTGGTAGACGAGCTACGGTACTTGGAGACATCTCTCTCCCAAGC 660
QY 661 GGTGGCTTTGTGAGTGAAGCAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
DB 661 GGTGGCTTTGTGAGTGAAGCAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTAGAGTGCAGTGCCTTCCAAATGACGTGGGCGGCCCGTGTGAGAGAGTAA 780
DB 721 AGGGGACTAGAGTGCAGTGCCTTCCAAATGACGTGGGCGGCCCGTGTGAGAGAGTAA 780

Db 721 AGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCGCCGCTGGTACGAGAGTARA 780
QY 781 GGTCAACGTTGAATATCCACCATACATTTTCAGAAAGCAAGGTGTACAGGTGTCCCGTGGG 840
Db 781 GGTCAACGTTGAATATCCACCATACATTTTCAGAAAGCAAGGTGTACAGGTGTCCCGTGGG 840
QY 841 ACAAAGGGGACACTGACGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db 841 ACAAAGGGGACACTGACGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
QY 901 CAAGATGACAAAGACTGATTTGAAGAAAGAAAGGGTGAAGTGCAGAAACAGACCTTT 960
Db 901 CAAGATGACAAAGACTGATTTGAAGAAAGAAAGGGTGAAGTGCAGAAACAGACCTTT 960
QY 961 CCTCTCAAACTCATCTTCTCAATGCTCTGAACATGACTATGGAACTACACTTGGCT 1020
Db 961 CCTCTCAAACTCATCTTCTCAATGCTCTGAACATGACTATGGAACTACACTTGGCT 1020
QY 1021 GGCCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT 1080
Db 1021 GGCCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT 1080
QY 1081 CAGCAGGTGAGCAACGCGACGTCGAGGAGGCGAGGCTGCTGCTGCTGCTCTTCT 1140
Db 1081 CAGCAGGTGAGCAACGCGACGTCGAGGAGGCGAGGCTGCTGCTGCTGCTCTTCT 1140
QY 1141 GGTCTTGACCTGCTTCTCAAAATTTTGTGATGTCGATGCCATCTCCACCGGGAAGGCT 1200
Db 1141 GGTCTTGACCTGCTTCTCAAAATTTTGTGATGTCGATGCCATCTCCACCGGGAAGGCT 1200
QY 1201 GCGGCCACCAACCAACCAACCAAGCAATGGCAACCGACAGCAACCAATCAGATA 1260
Db 1201 GCGGCCACCAACCAACCAACCAAGCAATGGCAACCGACAGCAACCAATCAGATA 1260
QY 1261 TATACAAATGAAATTAGAGAAACACAGCCTCATGGGAAGAAATTTGAGGAGGGGAAC 1320
Db 1261 TATACAAATGAAATTAGAGAAACACAGCCTCATGGGAAGAAATTTGAGGAGGGGAAC 1320
QY 1321 AAAGATATCTTTGGGGGAAAGAGTTTAAAGAAAGAAATTCGAAATTCGCTTGCAGATA 1380
Db 1321 AAAGATATCTTTGGGGGAAAGAGTTTAAAGAAAGAAATTCGAAATTCGCTTGCAGATA 1380
QY 1381 TTTAGTACAAATGGAGTTTCTTTTCCCAACCGGAAGAACACAGCACACCGGCTTGA 1440
Db 1381 TTTAGTACAAATGGAGTTTCTTTTCCCAACCGGAAGAACACAGCACACCGGCTTGA 1440
QY 1441 CCCACTGCAAGCTGCATCTGCAACCTTTTGGTGCAGTGTGGCAAGGGCTCAGCCTC 1500
Db 1441 CCCACTGCAAGCTGCATCTGCAACCTTTTGGTGCAGTGTGGCAAGGGCTCAGCCTC 1500
QY 1501 TCTGCCACAGAGTGCCTCCACAGTGGAAATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
Db 1501 TCTGCCACAGAGTGCCTCCACAGTGGAAATTTCTGGAGCTGGCCATCCCAAAATTCATCA 1560
QY 1561 GTCCATAGAGACGAACAGAAATGAGACTTCCCGGCCAACGCTGGGCTCGGGCACTTTG 1620
Db 1561 GTCCATAGAGACGAACAGAAATGAGACTTCCCGGCCAACGCTGGGCTCGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACACGCGGTGTGTGAAACGTGAAATATAAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACACGCGGTGTGTGAAACGTGAAATATAAAGAGCAAAAAA 1679

RESULT 24

AC68559
ID AC68559 standard; cDNA; 1679 BP.

XX AC

XX AC68559;

XX 25-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO337 cDNA.

Human; secreted and transmembrane protein; PRO; cardiant; cytostatic; antiangiogenic; hypotensive; vulnery; antiarteriosclerotic; gene therapy; cardiovascular disorder; endothelial disorder; angiogenic disorder; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; atherosclerosis; hypertension; arterial restenosis; rheumatoid arthritis; angina; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene ss.

XX Homo sapiens.

OS US2003088063-A1.

XX 08-MAY-2003.

XX 12-AUG-2002; 2002US-00219003.

XX 25-JUL-2000; 2000US-0220664P.

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021086.

PR 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX P-PSDB; ABU82110.

DR WPI; 2003-393229/37.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial

XX infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 2; Fig 125; 314pp; English.

XX The invention describes one hundred and eighty seven nucleic acids encoding novel human secreted and transmembrane (PRO) polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

QY Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTTCACAGCTTGAGCAACAC 60

Db 1 GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTTCACAGCTTGAGCAACAC 60

QY 61 AATCTATCAGGAAAGAAAGAAAAAACCAGACCTGCACAAAAAGAAAAAGAAAG 120

Db 61 AATCTATCAGGAAAGAAAGAAAAAACCAGACCTGCACAAAAAGAAAAAGAAAG 120

QY 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCATTTCTCTTGGGCAAT 180

Db 121 AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCATTTCTCTTGGGCAAT 180

QY 181 CTTTCACGGGGCTGGCTGCTCTGTGTCTTCCAGAGTCCCGCCAGCGGAGATGC 240

Db 181 CTTTCACGGGGCTGGCTGCTCTGTGTCTTCCAGAGTCCCGCCAGCGGAGATGC 240

QY 241 CACCTTCCCAAGCTATGGACACAGTGCAGTCCGGCAGGGGGAGAGCGCCACCTCAG 300

Db 241 |CACCTTCCCAAGCTATGGCAACGTCGACGCTCCGCGAGGGGAGAGGGCCACCTCAG 300
QY 301 |GTGCACTATTGCAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCAACATCTCTTA 360
Db 301 |GTGCACTATTGCAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCAACATCTCTTA 360
QY 361 |TGCTGGGAATGACAAAGTGGTGGTCTGGATCCCTCGCGTGGTCCCTCTGAGCAACACCCAAAC 420
Db 361 |TGCTGGGAATGACAAAGTGGTGGTCTGGATCCCTCGCGTGGTCCCTCTGAGCAACACCCAAAC 420
QY 421 |CGAGTACAGATCGAGATCCGAGACGTGGATGTGTATGACGAGGCCCTTACACCTGCTC 480
Db 421 |CGAGTACAGATCGAGATCCGAGACGTGGATGTGTATGACGAGGCCCTTACACCTGCTC 480
QY 481 |GTTGAGACAGACACCAACCCAAAGACCTCTAGGTCACCTCTCTGTCAGATCTCC 540
Db 481 |GTTGAGACAGACACCAACCCAAAGACCTCTAGGTCACCTCTCTGTCAGATCTCC 540
QY 541 |CAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
Db 541 |CAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
QY 601 |CTGCATAGCACTGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC 660
Db 601 |CTGCATAGCACTGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC 660
QY 661 |GTTTGGCTTTGTGAGTGAAGACGAATCTCTGAAATTCAGGSCATCACCCGGGAGCAGTC 720
Db 661 |GTTTGGCTTTGTGAGTGAAGACGAATCTCTGAAATTCAGGSCATCACCCGGGAGCAGTC 720
QY 721 |AGGGGACTACAGTGCAGTGCCTCCATGAGCTGGCGCGCGCTGGTACGAGAGTAAA 780
Db 721 |AGGGGACTACAGTGCAGTGCCTCCATGAGCTGGCGCGCGCTGGTACGAGAGTAAA 780
QY 781 |GGTCACTGTAACATCCACATACATTTAGAGCCGAGGGTACAGTGTCCCGTGGG 840
Db 781 |GGTCACTGTAACATCCACATACATTTAGAGCCGAGGGTACAGTGTCCCGTGGG 840
QY 841 |ACAAAAGGGGACACTGCACTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db 841 |ACAAAAGGGGACACTGCACTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
QY 901 |CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAACACACCTTT 960
Db 901 |CAAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAACACACCTTT 960
QY 961 |CCTCTCAAACTCATCTTCTCAATGCTCTGACATGACTATGGGAACACTACCTTGGGT 1020
Db 961 |CCTCTCAAACTCATCTTCTCAATGCTCTGACATGACTATGGGAACACTACCTTGGGT 1020
QY 1021 |GGCTTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT 1080
Db 1021 |GGCTTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGT 1080
QY 1081 |CAGCGAGGTGAGCAACGCGCAGTGCAGAGGGCAGGCTGGCTGGCTGGCTCTTCT 1140
Db 1081 |CAGCGAGGTGAGCAACGCGCAGTGCAGAGGGCAGGCTGGCTGGCTGGCTCTTCT 1140
QY 1141 |GGTCTTGCACTGCTTCTCAATTTTGAATGAGTGCACCTTCCACCCCGGGAAGGCT 1200
Db 1141 |GGTCTTGCACTGCTTCTCAATTTTGAATGAGTGCACCTTCCACCCCGGGAAGGCT 1200
QY 1201 |GCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260
Db 1201 |GCCGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAATCAGATA 1260
QY 1261 |TATCAATGAAATAGAGAAACACAGCTCTATGGGACAGAAATTTAGGGAGGGGAAAC 1320
Db 1261 |TATCAATGAAATAGAGAAACACAGCTCTATGGGACAGAAATTTAGGGAGGGGAAAC 1320
QY 1321 |AAGAATACTTTGGGGGGAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380
Db 1321 |AAGAATACTTTGGGGGGAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380

Db 1321 |AAGAATACTTTGGGGGGAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380
QY 1381 |TTTAGGTACAAATGAGATTTCTTTTCCAAACCGGAAGAAACACAGCAACCCCGCTTGGGA 1440
Db 1381 |TTTAGGTACAAATGAGATTTCTTTTCCAAACCGGAAGAAACACAGCAACCCCGCTTGGGA 1440
QY 1441 |CCCACTGCAAGCTCATCGTGCACCTCTTTTGGTCCAGTGTGGGCAAGGCTCAGCCTC 1500
Db 1441 |CCCACTGCAAGCTCATCGTGCACCTCTTTTGGTCCAGTGTGGGCAAGGCTCAGCCTC 1500
QY 1501 |TCTCCCAACAGAGTSCCCCAACGTCGAGCAATCTCTGAGCTGGCCATCCCAAAATTCATCA 1560
Db 1501 |TCTCCCAACAGAGTSCCCCAACGTCGAGCAATCTCTGAGCTGGCCATCCCAAAATTCATCA 1560
QY 1561 |GTCCATAGACGCAACAGAAATGAGACCTTCGGGCCCAAGCGTGGCGCTGGGGCAGCTTTG 1620
Db 1561 |GTCCATAGACGCAACAGAAATGAGACCTTCGGGCCCAAGCGTGGCGCTGGGGCAGCTTTG 1620
QY 1621 |GTAGACTGTGCCACCCAGCGGTGTGTGTAAGCTGTAATTAAGAGCAAAAAA 1679
Db 1621 |GTAGACTGTGCCACCCAGCGGTGTGTGTAAGCTGTAATTAAGAGCAAAAAA 1679

RESULT 25
ACA04211
ID ACA04211 standard; cdna; 1679 bp.
XX ACA04211;
AC ACA04211;
DT 27-MAY-2003 (first entry)
XX
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioreactor; tumour.
XX
OS Homo sapiens.
XX
PN US2003032155-A1.
XX
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-00137865.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 17-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 23-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.

PR 05-OCT-1999; 99WO-US0231089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2003-331925/31.
DR P-PSDB; ABU67033.
XX
PT New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 2; Fig 375; 659pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
CC comprises the full-length coding sequence of the DNA deposited under
CC American Type Culture Collection (ATCC) accession number in a list given
CC in the specification. Also included are vectors and host cells for
CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
CC extracellular domains and mature sequences, methods of detecting PRO
CC proteins, methods for stimulating the release of TNF-alpha (tumour
CC necrosis factor alpha) from human blood, (and the proliferation of
CC differentiation of chondrocyte cells, the proliferation of, or gene
CC expression in pericyte cells, the release or proteoglycans from
CC cartilage, proliferation of inner ear utricular supporting cells, the
CC proliferation of T-lymphocyte cells, the release of a cytokine from
CC peripheral blood mononuclear cells (PBMC), or the proliferation of
CC endothelial cells), a method for modulating the uptake of glucose or free
CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
CC cells, a method for detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, AIDS (acquired
CC immunodeficiency syndrome), cancer, or diabetic complications. The
CC nucleic acids are useful as hybridisation probes, in chromosome and gene
CC mapping, and in generating antisense RNA or DNA. The polypeptides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
CC are useful in tissue typing. the present sequence encodes a PRO protein
CC of the invention
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1679; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTCAGCAAGCTTGAGCAACAC 60
DB 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTCAGCAAGCTTGAGCAACAC 60
QY 61 AATCTATCAGGAAGAAGAAGAAAACCGAACCTGCACAAAAGAGAAAAGAG 120
DB 61 AATCTATCAGGAAGAAGAAGAAAACCGAACCTGCACAAAAGAGAAAAGAG 120
QY 121 AAGAAAAAAATCATGAAAAACATCCAGCAAAATGACAAATCTCTCTTGGGCAAT 180
DB 121 AAGAAAAAAATCATGAAAAACATCCAGCAAAATGACAAATCTCTCTTGGGCAAT 180
QY 181 CTTACGGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGAGTCCCGCGCAGCGAGATGC 240
DB 181 CTTACGGGGGCTGGCTGCTGTGTCTCTTCAAGAGAGTCCCGCGCAGCGAGATGC 240
QY 241 CACCTTCCCAAAGCTATGGAACAAGTCGGTCGGCAGGGGGAGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAAGCTATGGAACAAGTCGGTCGGCAGGGGGAGAGCGCCACCTCAG 300

QY 301 GTGCACTATTGACAAACCGGGTCAACCGGTGGCTTAAACCGCAGCACCATCCTCTA 360
Db 301 GTGCACTATTGACAAACCGGGTCAACCGGTGGCTTAAACCGCAGCACCATCCTCTA 360
QY 361 TGCTGGGAATGACAAAGTGGTGGCTTGATCTCGCTGGTTCCTTCGTAGCAACACCCAAAC 420
Db 361 TGCTGGGAATGACAAAGTGGTGGCTTGATCTCGCTGGTTCCTTCGTAGCAACACCCAAAC 420
QY 421 GCAGTACAGCATCGAGATCCAGACGTCGATGTGTATGACGAGGCGCTTACACCTGCTC 480
Db 421 GCAGTACAGCATCGAGATCCAGACGTCGATGTGTATGACGAGGCGCTTACACCTGCTC 480
QY 481 GGTGAGACAGACAAACCCAAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCC 540
Db 481 GGTGAGACAGACAAACCCAAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCC 540
QY 541 CAATAATCTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCAC 600
Db 541 CAATAATCTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCAC 600
QY 601 CTGCATAGCAACTGGTACACAGACGCTAACGGTTACTTGGAGACACATCTCTCCAAAGC 660
Db 601 CTGCATAGCAACTGGTACACAGACGCTAACGGTTACTTGGAGACACATCTCTCCAAAGC 660
QY 661 GGTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Db 661 GGTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
QY 721 AGGGGACTACGAGTGCAGTGCCTCCATGAGCTGGCGCGCCCTGGTACGGAGATGAA 780
Db 721 AGGGGACTACGAGTGCAGTGCCTCCATGAGCTGGCGCGCCCTGGTACGGAGATGAA 780
QY 781 GGTCAACGCTGAACTATCCACCATATCTTCAAGAGCAAGGTACAGGTGTCGCCGCGGG 840
Db 781 GGTCAACGCTGAACTATCCACCATATCTTCAAGAGCAAGGTACAGGTGTCGCCGCGGG 840
QY 841 ACAAAGGGGACACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAATTCAGTGGTA 900
Db 841 ACAAAGGGGACACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAATTCAGTGGTA 900
QY 901 CAAGGATGACAAAGACTGATTGAAGGAAGAAAGGGTGAAGTGAAGTGAAGACACCTTT 960
Db 901 CAAGGATGACAAAGACTGATTGAAGGAAGAAAGGGTGAAGTGAAGTGAAGACACCTTT 960
QY 961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTCGCT 1020
Db 961 CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTCGCT 1020
QY 1021 GGCTCCAAACAGTGGGCGCACACCAATGCCAGATCATGCTATTTGGTCCAGGCGCGT 1080
Db 1021 GGCTCCAAACAGTGGGCGCACACCAATGCCAGATCATGCTATTTGGTCCAGGCGCGT 1080
QY 1081 CAGCGAGTGAAGAAACCGGACGTCGAGAGGCGAGGCTGCTGGCTGCTGCTCTTCT 1140
Db 1081 CAGCGAGTGAAGAAACCGGACGTCGAGAGGCGAGGCTGCTGGCTGCTGCTCTTCT 1140
QY 1141 GGTCTTGCACTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCAACCCGGGAAAGGCT 1200
Db 1141 GGTCTTGCACTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCAACCCGGGAAAGGCT 1200
QY 1201 GCGCCACACCAACCAACAGCAATGCGAATGCGAATGCGAATGCGAATGCGAATGCGAAT 1260
Db 1201 GCGCCACACCAACCAACAGCAATGCGAATGCGAATGCGAATGCGAATGCGAATGCGAAT 1260
QY 1261 TATACAAATGAAATTAGAAGAAACACAGCTCTATGGGACAGAAATTTGAGGGGGGGAAC 1320
Db 1261 TATACAAATGAAATTAGAAGAAACACAGCTCTATGGGACAGAAATTTGAGGGGGGGAAC 1320
QY 1321 AAGAATATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380
Db 1321 AAGAATATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380

QY 1381 TTTAGGTACATGAGTTCCTTTTCCAAACGGGAAGAACACAGCACACCCGGCTTGGG 1440
Db 1381 TTTAGGTACATGAGTTCCTTTTCCAAACGGGAAGAACACAGCACACCCGGCTTGGG 1440
QY 1441 CCCACTGCAAGCTGCATCGTGGCAACCTTTTGGTGGCAGTGTGGGCAAGGCTCAGCCTC 1500
Db 1441 CCCACTGCAAGCTGCATCGTGGCAACCTTTTGGTGGCAGTGTGGGCAAGGCTCAGCCTC 1500
QY 1501 TCTGCCACAGAGTGGCCCCACCGTGGAAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
Db 1501 TCTGCCACAGAGTGGCCCCACCGTGGAAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560
QY 1561 GTCCATAGAGAGCAAGCAAGATGAGACCTTCGGGCCCAAGCGTGGCGTGGGGCACTTTG 1620
Db 1561 GTCCATAGAGAGCAAGCAAGATGAGACCTTCGGGCCCAAGCGTGGCGTGGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCGCGGTGTGTGTGAACCTGTAACCTGTAACCTGTAACCTGTAACCT 1679
Db 1621 GTAGACTGTGCCACCGCGGTGTGTGTGAACCTGTAACCTGTAACCTGTAACCTGTAACCT 1679
RESULT 26
ACA65657
ID ACA65657 standard; cDNA; 1679 BP.
XX ACA65657;
AC ACA65657;
XX
DT 19-JUN-2003 (first entry)
XX
DE DE
XX
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW genetic disorder; gene therapy.
XX Homo sapiens.
OS
XX
PN US2003032057-A1.
XX
PD 13-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00002796.
XX 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 29-OCT-1997; 97US-0063329P.
PR 21-NOV-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.

20-NOV-1998; 98WO-US024855.
 25-NOV-1998; 98WO-US025190.
 01-DEC-1998; 98WO-US025108.
 08-MAR-1999; 99WO-US0005028.
 23-MAR-1999; 99WO-US0125778P.
 02-JUN-1999; 99US-0139695P.
 15-JUN-1999; 99US-0145070P.
 20-JUL-1999; 99US-0145698P.
 26-JUL-1999; 99US-0149396P.
 17-AUG-1999; 99US-04902011.
 01-SEP-1999; 99WO-US020594.
 08-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 30-NOV-1999; 99WO-US028313.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028565.
 07-DEC-1999; 99US-0169495P.
 20-DEC-1999; 99WO-US030999.
 05-JAN-2000; 2000WO-US000219.
 18-FEB-2000; 2000WO-US004341.
 18-FEB-2000; 2000WO-US004342.
 22-FEB-2000; 2000WO-US004414.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 09-MAR-2000; 2000WO-US006471.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 15-MAY-2000; 2000WO-US013358.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 11-AUG-2000; 2000WO-US022031.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032678.
 28-FEB-2001; 2001WO-US006520.
 30-MAY-2001; 2001WO-US017443.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 (GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Baton DL,
 Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J,
 Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
 Wood WI, Zhang Z;
 WPI; 2003-341960/32.
 P-PSDB; ABU79804.
 Novel secreted and transmembrane polypeptide for modulating biological
 activity of cell expressing the polypeptide, identifying agonists or
 antagonists of polypeptide, and as molecular weight markers.
 Claim 2; Fig 51; 255pp; English.
 The invention relates to an isolated, secreted/transmembrane polypeptide,
 termed PRO polypeptide, having at least 80% sequence identity to a
 sequence selected from any one of the 37 sequences appearing as ABU79779
 -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
 under any one of the ATCC numbers given in the specification. Also
 included are an isolated nucleic acid molecule having at least 80%
 sequence identity to a sequence selected from any one of the 37 cDNA
 sequences defined in the specification (or encoding the mature PRO
 protein or a PRO protein extracellular domain), a PRO expression vector,
 a host cell comprising the vector, PRO fusion proteins, anti-PRO
 antibodies and a method for linking a bioactive molecule to a cell
 expressing the above PRO polypeptides, the bioactive molecule is a toxin,

radiolabel or an antibody and causes the death of the cell. PRO or the
 antibody is useful for modulating at least one biological activity of
 cell expressing the above polypeptides. PRO is useful for identifying
 agonists or antagonists of PRO, for preparing a variant of PRO, as
 molecular weight markers for protein electrophoresis purpose and PRO
 nucleic acid is useful for recombinantly expressing those markers. PRO is
 also useful as therapeutic agent. PRO is useful in assays to identify
 other proteins or molecules involved in binding interaction. PRO nucleic
 acid is useful as hybridisation probes, in chromosome and gene mapping,
 in generation of antisense RNA and DNA, in the preparation of PRO
 polypeptide, in gene therapy, for generating transgenic animals or
 knockout animals which in turn are useful in the development and
 screening of therapeutically useful reagents, to construct hybridisation
 probes for mapping the gene which encodes the PRO and for the genetic
 analysis of individuals with genetic disorders, for chromosome
 identification, as a chromosome marker, and for generating probes for
 polymerase chain reaction (PCR), Northern analysis, Southern analysis and
 Western analysis. The antibody is useful in diagnostic assays for PRO,
 e.g. detecting its expression in specific cells, tissues or serum, for
 affinity purification of PRO from recombinant cell culture or natural
 sources. PRO or Ab is useful for the preparation of medicament for
 treating conditions which is responsive to the PRO polypeptide or anti-
 PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
 present sequence encodes a PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1679; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 1.5e-15;
 Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGTGCTCTTTCAGCAAAACAGTGGATTAAATCTCTTTCGCAACAGCTTGAGAGCAAC 60
 DB 1 GTTGTGCTCTTTCAGCAAAACAGTGGATTAAATCTCTTTCGCAACAGCTTGAGAGCAAC 60
 QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
 QY 121 AAGAAAAAAATCATGAAAAACCATCAGCAAAATTCATCTCTTTGGGCAAT 180
 DB 121 AAGAAAAAAATCATGAAAAACCATCAGCAAAATTCATCTCTTTGGGCAAT 180
 QY 181 CTTTCAGGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGTGCCTGCGGAGCGAGATGC 240
 DB 181 CTTTCAGGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGTGCCTGCGGAGCGAGATGC 240
 QY 241 CACCTTCCCAAGCTATGGAACAAGTACGCTCGGAGGGGGAGAGCGCCACCTCAG 300
 DB 241 CACCTTCCCAAGCTATGGAACAAGTACGCTCGGAGGGGGAGAGCGCCACCTCAG 300
 QY 301 GTGCACTATTGCAACCCGGGTCAACCCGGGTGCTGCTTAAACCGCAGCACCCTCTTA 360
 DB 301 GTGCACTATTGCAACCCGGGTCAACCCGGGTGCTGCTTAAACCGCAGCACCCTCTTA 360
 QY 361 TCGTGGGATGCAAGTGTGCTGGATCTCGGCTGCTCTTCTGAGCAACACCAAC 420
 DB 361 TCGTGGGATGCAAGTGTGCTGGATCTCGGCTGCTCTTCTGAGCAACACCAAC 420
 QY 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACCTGCTC 480
 DB 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACCTGCTC 480
 QY 481 GGTGAGAGAGCAACACCAAGAGCTCTAGGGTCCACCTCAATTTGCAAGTATCTCC 540
 DB 481 GGTGAGAGAGCAACACCAAGAGCTCTAGGGTCCACCTCAATTTGCAAGTATCTCC 540
 QY 541 CAATTTCTAGAGATTTCTTTCAGATATCTCCATTAATGAGGGAACAATATAGCTCAC 600
 DB 541 CAATTTCTAGAGATTTCTTTCAGATATCTCCATTAATGAGGGAACAATATAGCTCAC 600
 QY 601 CTGCATAGCAACTGGTAGACAGAGCCCTACGGTACTTCTGGAGACACATCTCTCCCAAGC 660
 DB 601 CTGCATAGCAACTGGTAGACAGAGCCCTACGGTACTTCTGGAGACACATCTCTCCCAAGC 660

601	CTGCATAGCAAACTGGTATAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAAGC	660	
Qy	661	GGTTGGCTTTTGAGTGAAGACGAATACTTTGGAAATTCAGGGCATACCCGGGAGCAATC	720
	661	GGTTGGCTTTTGAGTGAAGACGAATACTTTGGAAATTCAGGGCATACCCGGGAGCAATC	720
	661	GGTTGGCTTTTGAGTGAAGACGAATACTTTGGAAATTCAGGGCATACCCGGGAGCAATC	720
Qy	721	AGGGGACTACGAGTGCAGTGGCTCCATGACGTGGCCGGCCCGTGGTACGGAGAGTAAA	780
	721	AGGGGACTACGAGTGCAGTGGCTCCATGACGTGGCCGGCCCGTGGTACGGAGAGTAAA	780
	721	AGGGGACTACGAGTGCAGTGGCTCCATGACGTGGCCGGCCCGTGGTACGGAGAGTAAA	780
Qy	781	GGTCACCGTGAACCTATCCACCATACATTTAGAAAGCCAAAGGATACAGTGTCCCGGTGGG	840
	781	GGTCACCGTGAACCTATCCACCATACATTTAGAAAGCCAAAGGATACAGTGTCCCGGTGGG	840
	781	GGTCACCGTGAACCTATCCACCATACATTTAGAAAGCCAAAGGATACAGTGTCCCGGTGGG	840
Qy	841	ACAAAAGGGAGACATGCGAGTGTGAAGCCTCAGCAGTCCCTCTACGAGAAATTCAGTGGTA	900
	841	ACAAAAGGGAGACATGCGAGTGTGAAGCCTCAGCAGTCCCTCTACGAGAAATTCAGTGGTA	900
	841	ACAAAAGGGAGACATGCGAGTGTGAAGCCTCAGCAGTCCCTCTACGAGAAATTCAGTGGTA	900
Qy	901	CAAGGATGACAAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTGTGAAGAACAGACCTTT	960
	901	CAAGGATGACAAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTGTGAAGAACAGACCTTT	960
	901	CAAGGATGACAAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTGTGAAGAACAGACCTTT	960
Qy	961	CCTCTCAAACTCATCTTTCTCAATGTCTCTGAAACATGACTATGGGAACTACACTTCGGT	1020
	961	CCTCTCAAACTCATCTTTCTCAATGTCTCTGAAACATGACTATGGGAACTACACTTCGGT	1020
	961	CCTCTCAAACTCATCTTTCTCAATGTCTCTGAAACATGACTATGGGAACTACACTTCGGT	1020
Qy	1021	GGCCTCAACAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTCGTTCAGGGCCGT	1080
	1021	GGCCTCAACAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTCGTTCAGGGCCGT	1080
	1021	GGCCTCAACAAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTCGTTCAGGGCCGT	1080
Qy	1081	CAGCGAGTGAAGCAACGGCAGCTCGAGAGGGCAGGCTGCGTCTGGCTGTGCTCTTCT	1140
	1081	CAGCGAGTGAAGCAACGGCAGCTCGAGAGGGCAGGCTGCGTCTGGCTGTGCTCTTCT	1140
	1081	CAGCGAGTGAAGCAACGGCAGCTCGAGAGGGCAGGCTGCGTCTGGCTGTGCTCTTCT	1140
Qy	1141	GGTCTTGCACTGCTTCTCAAAATTTTGATGTAGTGCACCTTCCCCACCCGGGAAAGCT	1200
	1141	GGTCTTGCACTGCTTCTCAAAATTTTGATGTAGTGCACCTTCCCCACCCGGGAAAGCT	1200
	1141	GGTCTTGCACTGCTTCTCAAAATTTTGATGTAGTGCACCTTCCCCACCCGGGAAAGCT	1200
Qy	1201	GGCCGCCACCCACCCACACACAGCATGGCAACCGACAGACAGCAACCAATCAGATA	1260
	1201	GGCCGCCACCCACCCACACACAGCATGGCAACCGACAGACAGCAACCAATCAGATA	1260
	1201	GGCCGCCACCCACCCACACACAGCATGGCAACCGACAGACAGCAACCAATCAGATA	1260
Qy	1261	TATACAAATGAAATTTAGAAGAAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC	1320
	1261	TATACAAATGAAATTTAGAAGAAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC	1320
	1261	TATACAAATGAAATTTAGAAGAAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAC	1320
Qy	1321	AAAGAAATCTTTGGGGGAAAAGAGTTTAAAAAGAAATTTGAAAAATTCGCTTCAGATA	1380
	1321	AAAGAAATCTTTGGGGGAAAAGAGTTTAAAAAGAAATTTGAAAAATTCGCTTCAGATA	1380
	1321	AAAGAAATCTTTGGGGGAAAAGAGTTTAAAAAGAAATTTGAAAAATTCGCTTCAGATA	1380
Qy	1381	TTTAGGTACAAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGCACACCCGGCTTGGGA	1440
	1381	TTTAGGTACAAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGCACACCCGGCTTGGGA	1440
	1381	TTTAGGTACAAATGGAGTTTCTTTTCCAAACGGGAAGAACACAGCACACCCGGCTTGGGA	1440
Qy	1441	CCCACTGCAAGCTGCATGTGCACACTTTTGGTGCCAGTGTGGGCAAGGCTCAGCCTC	1500
	1441	CCCACTGCAAGCTGCATGTGCACACTTTTGGTGCCAGTGTGGGCAAGGCTCAGCCTC	1500
	1441	CCCACTGCAAGCTGCATGTGCACACTTTTGGTGCCAGTGTGGGCAAGGCTCAGCCTC	1500
Qy	1501	TCTGCCACACAGAGTGCCTCCACGCTGGACATCTCTGGAGCTGGCCATCCCAATTCATCA	1560
	1501	TCTGCCACACAGAGTGCCTCCACGCTGGACATCTCTGGAGCTGGCCATCCCAATTCATCA	1560
	1501	TCTGCCACACAGAGTGCCTCCACGCTGGACATCTCTGGAGCTGGCCATCCCAATTCATCA	1560
Qy	1561	GTCCATAGAGACGAACGAATAGACACTTCCGGGCCAAGCGTGGCGTGGGGCAGCTTGG	1620
	1561	GTCCATAGAGACGAACGAATAGACACTTCCGGGCCAAGCGTGGCGTGGGGCAGCTTGG	1620
	1561	GTCCATAGAGACGAACGAATAGACACTTCCGGGCCAAGCGTGGCGTGGGGCAGCTTGG	1620
Qy	1621	GTAGACTGTGCCACACAGCGCTGTGTGTGAAACGTGAAATATAAAGAGCAAAAAAAA	1679
	1621	GTAGACTGTGCCACACAGCGCTGTGTGTGAAACGTGAAATATAAAGAGCAAAAAAAA	1679
	1621	GTAGACTGTGCCACACAGCGCTGTGTGTGAAACGTGAAATATAAAGAGCAAAAAAAA	1679

24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005746.
02-MAR-2000; 2000WO-US005841.
10-MAR-2000; 2000WO-US005819.
15-MAR-2000; 2000WO-US006884.
20-MAR-2000; 2000WO-US007377.
21-MAR-2000; 2000WO-US007532.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
28-JUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023528.
08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000US-00747259.
20-DEC-2000; 2000WO-US034956.
28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00828366.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
18-MAY-2001; 2001US-00860216.
25-MAY-2001; 2001US-0086028.
25-MAY-2001; 2001US-00865034.
25-MAY-2001; 2001WO-US017092.
01-JUN-2001; 2001US-00872035.
01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
14-JUN-2001; 2001US-00882636.
19-JUN-2001; 2001US-00886342.
20-JUN-2001; 2001WO-US019692.
21-JUN-2001; 2001US-00887879.
22-JUN-2001; 2001WO-US020116.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
18-JUL-2001; 2001US-00908827.
06-AUG-2001; 2001US-00924419.
09-AUG-2001; 2001US-00927796.
16-AUG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00028072.
(GETH) GENENTECH INC.
Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
WPI; 2003-584997/55.
P-PSDB; ADA45895.
Novel secreted and transmembrane polypeptide for modulating biological
activity of cell expressing the polypeptide, identifying agonists or
antagonists of polypeptide, and as molecular weight markers.
Claim 2; Fig 375; 659pp; English.
The invention describes 305 nucleic acids encoding PRO (secreted and
transmembrane) polypeptides (I). (I) is useful for stimulating the
release of TNF-alpha from human blood, for modulating the uptake of
glucose or FFA by skeletal muscle cells or adipocyte cells, for
stimulating the proliferation or differentiation of chondrocyte cells,
for stimulating the proliferation of or gene expression in pericyte

CC cells, for stimulating the release of proteoglycans from cartilage, for
stimulating the proliferation of inner ear utricular supporting cells,
for stimulating the proliferation of T-lymphocyte cells, for stimulating
the release of a cytokine from BMC cells, for inhibiting the binding of
A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
cells, for stimulating proliferation of endothelial cells, for detecting
the presence of tumour in a mammal. The tumour is lung, colon, breast,
prostate, rectal, cervical or liver tumour. The oligonucleotide probes
are useful for isolating genomic and cDNA nucleotide sequences or
antisense probes. (I) is also useful as therapeutic agent. PRO is useful
in assays to identify other proteins or molecules involved in binding
interaction. A polynucleotide (II) encoding (I) is useful in chromosome
and gene mapping, in generation of antisense RNA and DNA, in the
preparation of PRO polypeptide, for generating transgenic animals or
knockout animals which in turn are useful in the development and
screening of therapeutically useful reagents, in gene therapy, for
chromosome identification, as chromosome marker, and for generating
probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
detecting its expression in specific cells, tissues or serum, and for
affinity purification of PRO from recombinant cell culture or natural
sources. (I) and (II) are useful for tissue typing. This sequence encodes
a novel human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAACTTGAGAGCAACAC 60
DB 1 GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTGACAACTTGAGAGCAACAC 60
QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
QY 121 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180
DB 121 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 180
QY 181 CTTACGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGAGTCCCGTGGCAGCGAGATGC 240
DB 181 CTTACGGGGCTGGCTGCTCTGTGTCTCTTCAAGAGAGTCCCGTGGCAGCGAGATGC 240
QY 241 CACCTTCCCAAGCTATGAGCAACAGTGCCTCGGAGAGGGGAGAGCGCCACCTCAG 300
DB 241 CACCTTCCCAAGCTATGAGCAACAGTGCCTCGGAGAGGGGAGAGCGCCACCTCAG 300
QY 301 GTGCACATATTGACAAACCGGGTCAACCGGGTCCCGTGGCTTAACCGCAGCACCCTCTTA 360
DB 301 GTGCACATATTGACAAACCGGGTCAACCGGGTCCCGTGGCTTAACCGCAGCACCCTCTTA 360
QY 361 TGCTGGGAATGCAAGTGGTGGTCTCTGCGTGGTCTCTTCTGAGCAACACCCAAAC 420
DB 361 TGCTGGGAATGCAAGTGGTGGTCTCTGCGTGGTCTCTTCTGAGCAACACCCAAAC 420
QY 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACGTGGATGTATGACGAGGGCCCTTACCTGCTC 480
QY 481 GGTGAGAGCAACACCCAGCAACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
DB 481 GGTGAGAGCAACACCCAGCAACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
QY 541 CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCAC 600
DB 541 CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCTCAC 600
QY 601 CTGATAGCAACTGGTAGACAGAGCTTACGGTTACTTGGAGACACATCTCTCCAAAGC 660
DB 601 CTGATAGCAACTGGTAGACAGAGCTTACGGTTACTTGGAGACACATCTCTCCAAAGC 660

661 GGTGGCTTTGTGAGTGAAGCAATCTTGGAAATTCAGGSCATCACCCGGGAGCAGTC 720
661 GGTGGCTTTGTGAGTGAAGCAATCTTGGAAATTCAGGSCATCACCCGGGAGCAGTC 720
721 AGGGGACTACAGTGCAGTGCCTCAATGACGCTGGCCCGCCGCGTGGTACGGAGAGTAAA 780
721 AGGGGACTACAGTGCAGTGCCTCAATGACGCTGGCCCGCCGCGTGGTACGGAGAGTAAA 780
781 GGTCAACCTGAACTATCCACCATATCTTCAAGAGCCCAAGGTTAGAGTGGTCCCGGTGGG 840
781 GGTCAACCTGAACTATCCACCATATCTTCAAGAGCCCAAGGTTAGAGTGGTCCCGGTGGG 840
841 ACAAAGGGGACACTGAGTGTGAAGCTCCAGCTCCCTCAGCAGAAATTCAGTGGTA 900
841 ACAAAGGGGACACTGAGTGTGAAGCTCCAGCTCCCTCAGCAGAAATTCAGTGGTA 900
901 CAAGATGACAAAGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
901 CAAGATGACAAAGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
961 CCTCTCAAACTCATCTTCTTCAATGCTCTGAATGCTATGGAATGGAATCACTTGGT 1020
961 CCTCTCAAACTCATCTTCTTCAATGCTCTGAATGCTATGGAATGGAATCACTTGGT 1020
1021 GGCCTCCAAAGCTGGGCCACACAAATGCGAGCATATGCTATTTGGTCCAGGCGCGT 1080
1021 GGCCTCCAAAGCTGGGCCACACAAATGCGAGCATATGCTATTTGGTCCAGGCGCGT 1080
1081 CAGGAGGTGAGCAACGCGCAGTGCAGGAGGCGGCTGCTGCTGCTGCTGCTTCT 1140
1081 CAGGAGGTGAGCAACGCGCAGTGCAGGAGGCGGCTGCTGCTGCTGCTGCTTCT 1140
1141 GGTCTTGCACCTGCTTCTCAAAATTTGATGTGAGTGCACCTTCCGCCACCCGGGAAAGCT 1200
1141 GGTCTTGCACCTGCTTCTCAAAATTTGATGTGAGTGCACCTTCCGCCACCCGGGAAAGCT 1200
1201 GCGCGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
1201 GCGCGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1260
1261 TATCAAAATGAATTTAGAGAAACACAGCCTCTATGGGACAGAAATTTGAGGGGGGAA 1320
1261 TATCAAAATGAATTTAGAGAAACACAGCCTCTATGGGACAGAAATTTGAGGGGGGAA 1320
1321 AAGAAATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTGCAGATA 1380
1321 AAGAAATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTGCAGATA 1380
1381 TTTAGGTACATGAGTGTCTTTTCCCAACCGGAGAGAACACAGACACCCGGCTTGA 1440
1381 TTTAGGTACATGAGTGTCTTTTCCCAACCGGAGAGAACACAGACACCCGGCTTGA 1440
1441 CCCACTGCAAGTGCATGCTGCAACCTCTTTGGTGGCCAGTGTGGCAAGGCTCAGCCTC 1500
1441 CCCACTGCAAGTGCATGCTGCAACCTCTTTGGTGGCCAGTGTGGCAAGGCTCAGCCTC 1500
1501 TCTGCCACAGAGTGCCTCCACAGTGGAACTTTTGGAGCTGGCCATCCCAAAATTCATCA 1560
1501 TCTGCCACAGAGTGCCTCCACAGTGGAACTTTTGGAGCTGGCCATCCCAAAATTCATCA 1560
1561 GTCCATAGACAGCAAGATGAGACCTTCCGCCCAAGGCTGCGCTGCGGCACTTTG 1620
1561 GTCCATAGACAGCAAGATGAGACCTTCCGCCCAAGGCTGCGCTGCGGCACTTTG 1620
1621 GTAGACTGTGCCACCAAGGCTGTGTTGTGAACCTGAAATTAAGAGCAAAAAA 1679
1621 GTAGACTGTGCCACCAAGGCTGTGTTGTGAACCTGAAATTAAGAGCAAAAAA 1679

RESULT 28
ADA76325
ID ADA76325 standard; cDNA; 1679 BP.
XX

AC ADA76325;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human PRO polynucleotide #188.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW liver; microvascular endothelial cell; glucose; PFA;
KW skeletal muscle cell; adipocyte cell; pericyte cell;
KW inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell tube formation; bone disorder; cartilage disorder;
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW immune system cell infiltration.
XX Homo sapiens.
XX
EN US2003073212-A1.
XX
PD 17-APR-2003.
XX
PF 16-APR-2002; 2002US-00123903.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUN-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US021089.
PR 23-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 2000WO-US000219.
PR 05-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.

24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PR (GETH) GENENTECH INC.
XX
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-687639/65.
DR P-PSDB; ADA76326.
XX
PT New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 2; Fig 375; 659pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for

CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC the proliferation of or gene expression in pericyte cells, for stimulating
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polynucleotide of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

	Query Match	Best Local Similarity	100.0%;	Score 1679;	DB 8;	Length 1679;
	Matches 1679;	Conservative	0;	Mismatches	0;	Gaps
QY	1	GTGTGTCTCTCAGCAAAACAGTGGATTAAATCTCTTGTGCACAAAGCTTGAGCAACAC	60			
DB	1	GTGTGTCTCTCAGCAAAACAGTGGATTAAATCTCTTGTGCACAAAGCTTGAGCAACAC	60			
QY	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120			
DB	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120			
QY	121	AAGAAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAAAATTCATCTCTTGGGCAAT	180			
DB	121	AAGAAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAAAATTCATCTCTTGGGCAAT	180			
QY	181	CTTACGGGGTGGTGTCTGTGTCTCTTCAAGAGAGTGTCCCGGCGGAGGAGATGC	240			
DB	181	CTTACGGGGTGGTGTCTGTGTCTCTTCAAGAGAGTGTCCCGGCGGAGGAGATGC	240			
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DB	301	GTGCACTATTGACAAACCGGGTCACCCGGTGGCTGGCTGCTAAACCGCAGCAACATCCTCTA	360			
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DB	421	GCAGTACAGATCCAGATCCAGAGCTGGATGTGTATGACGAGGGCCCTTACCTGTCTC	480			
QY	481	GGTGACAGACAAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540			
DB	481	GGTGACAGACAAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540			
QY	541	CAAAATTTAGAGATTTCTTCCAGATATCTCCATTAATGAAGGAACAATATTAGCTCAC	600			
DB	541	CAAAATTTAGAGATTTCTTCCAGATATCTCCATTAATGAAGGAACAATATTAGCTCAC	600			

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Db 781 GGTCAACCGTGAATCTCCACCATATCTTCAAGAGCCAAAGGGTACAGGTGTCCCGTGGG 840
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Db 841 ACAAAAGGGGACCTGAGTGTGAAGCTCAGCTAGCTGCCCTCAGCAGAAATTCAGTGGTA 900
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Db 901 CAAGGATGACAAAAGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACACACTTT 960
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ABT44288
ID ABT44288 standard; cDNA; 1679 BP.

XX AC
AC ABT44288;

DT 06-NOV-2003 (first entry)

XX Human PRO337 cDNA.

DE XX
XX PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; ss;
differentiation; dermal fibroblast; tumour; gene therapy; gene;

XX KW
KW cytosstatic.

XX OS
OS Homo sapiens.

XX US2003050448-A1.

XX PD
PD 13-MAR-2003.

XX XX
XX 28-AUG-2002; 2002US-00230414.

XX XX
XX 01-JUN-2001; 2001WO-US017800.

XX PR
PR 29-JUN-2001; 2001WO-US021066.

XX PR
PR 09-APR-2002; 2002US-00119480.

XX PA
(GETH) GENENTECH INC.

XX XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX PI
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX DR
DR WPI; 2003-521818/49.

XX DR
DR P-PSDB; ABU72290.

XX PT
PT New nucleic acid encoding for a PRO protein, useful for the manufacture

XX PT
PT of a medicament for diagnosing or treating tumors or for measuring or

XX PT
PT detecting expression of an associated gene.

XX PS
PS Claim 2; Fig 125; 315pp; English.

XX CC
CC The invention relates to a novel isolated nucleic acid encoding a fully

XX CC
CC defined PRO polypeptide. The molecules of the invention may be useful for

XX CC
CC stimulating proliferation or gene expression in pericyte cells or the

XX CC
CC release of TNF-alpha from human blood. Other possible uses include the

XX CC
CC stimulation or inhibition of chondrocyte proliferation or

XX CC
CC differentiation, the stimulation of human dermal fibroblast cell

XX CC
CC proliferation and the detection of the presence of a tumour within a

XX CC
CC mammal. Furthermore, the nucleic acid may be useful for the manufacture

XX CC
CC of a medicament for diagnosing or treating a tumour within a mammal or

XX CC
CC for measuring or detecting the expression of an associated gene, as well

XX CC
CC as during gene therapy. The current sequence is that of the human PRO

XX CC
CC cDNA of the invention

XX SQ
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1679; DB 8; Length 1679;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

QY 121 AAGAAAAAAATCATGAAACCATCCAGCCAAATTCATCTCTTGGCAAT 180

Db 121 AAGAAAAAAATCATGAAACCATCCAGCCAAATTCATCTCTTGGCAAT 180

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1621 GTAGACTGTGCCACCAACCGCGCTGTGTGTGAAACCTGAAATAAAAAGAGCAAAAAAAA 1679
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Search completed: May 28, 2004, 15:50:35
Job time : 751.61 secs

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3	1679	100.0	1679	9	US-09-978-192A-522		Sequence 522, App
4	1679	100.0	1679	9	US-09-939-932A-522		Sequence 522, App
5	1679	100.0	1679	10	US-09-978-189-522		Sequence 522, App
6	1679	100.0	1679	10	US-09-978-608A-522		Sequence 522, App
7	1679	100.0	1679	10	US-09-978-585A-522		Sequence 522, App
8	1679	100.0	1679	10	US-09-978-191A-522		Sequence 522, App
9	1679	100.0	1679	10	US-09-978-403A-522		Sequence 522, App
10	1679	100.0	1679	10	US-09-978-564A-522		Sequence 522, App
11	1679	100.0	1679	10	US-09-999-833A-522		Sequence 522, App
12	1679	100.0	1679	10	US-09-981-915A-522		Sequence 522, App
13	1679	100.0	1679	10	US-09-978-824-522		Sequence 522, App
14	1679	100.0	1679	10	US-09-918-585A-522		Sequence 522, App

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 89 1679 100.0 1679 15 US-10-066-193-103 Sequence 103, App
 90 1679 100.0 1679 15 US-10-230-338-125 Sequence 125, App
 91 1679 100.0 1679 15 US-10-142-419-375 Sequence 125, App
 92 1679 100.0 1679 15 US-10-218-631-125 Sequence 125, App
 93 1679 100.0 1679 15 US-10-017-081A-522 Sequence 522, App
 94 1679 100.0 1679 15 US-10-123-262-375 Sequence 375, App
 95 1679 100.0 1679 15 US-10-142-423-375 Sequence 375, App
 96 1679 100.0 1679 15 US-10-230-414-125 Sequence 125, App
 97 1679 100.0 1679 15 US-10-230-050-375 Sequence 375, App
 98 1679 100.0 1679 15 US-10-141-755-375 Sequence 375, App
 99 1679 100.0 1679 15 US-10-167-749-522 Sequence 522, App
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ALIGNMENTS

RESULT 1

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 ; Patent No. US20020156006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C11
 ; CURRENT APPLICATION NUMBER: US/09/978,295A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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Best Local Similarity 100.0%; Pred. No. 7, 8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 AATCTATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
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QY 241 CACCTTCCCAAGCTATGGAACAAACGTGACGGTCCCGGAGGGGAGAGCGCAACCTCAG 300
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QY	1021	GGCTCCAAAGCTGGCCACACCAATGCGAGCATCATGCTATTGGTCCAGGCGCCCT	1080	APPLICANT: Shelton, David L.
Db	1021	GGCTCCAAAGCTGGCCACACCAATGCGAGCATCATGCTATTGGTCCAGGCGCCCT	1080	APPLICANT: Stewart, Timothy A.
QY	1081	CAGCGAGGTAGCAAGCGACGTCGAGGAGGCGAGGCTGGCTGGCTGCTCTTCT	1140	APPLICANT: Tumas, Daniel
Db	1081	CAGCGAGGTAGCAAGCGACGTCGAGGAGGCGAGGCTGGCTGGCTGCTCTTCT	1140	APPLICANT: Williams, P. Mickey
QY	1141	GGTCTTGACCTGCTTCTCAAAATTTGATGAGTGCCATTCGCCACCCGGGAAAGGCT	1200	APPLICANT: Wood, William J.
Db	1141	GGTCTTGACCTGCTTCTCAAAATTTGATGAGTGCCATTCGCCACCCGGGAAAGGCT	1200	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
QY	1201	GCGGCCACCCACCCACCAACACACAGCAATGCAACCCGAGCAACCAATCAGATA	1260	FILE REFERENCE: P2630PIC27
Db	1201	GCGGCCACCCACCCACCAACACACAGCAATGCAACCCGAGCAACCAATCAGATA	1260	CURRENT APPLICATION NUMBER: US/09/978,697
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Db	1261	TATCAAAATGAATAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGAAC	1320	PRIOR APPLICATION NUMBER: 09/918585
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RESULT 2

US-09-978-697-522

Sequence 522, Application US/09978697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

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Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 100.0%; Score 1679; DB 9; Length 1679;

Best Local Similarity 100.0%; Pred. No. 7.8e-22;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

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US-09-999-832A-522
; Sequence 522, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Destoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secured and Trans
; FILE REFERENCE: P2630FIC63
; CURRENT APPLICATION NUMBER: US/09/999
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311

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1	PRIOR FILING DATE: 1997-11-13	2	PRIOR APPLICATION NUMBER: 60/081819
3	PRIOR APPLICATION NUMBER: 60/066364	4	PRIOR FILING DATE: 1998-04-15
5	PRIOR FILING DATE: 1997-11-21	6	PRIOR APPLICATION NUMBER: 60/081952
7	PRIOR APPLICATION NUMBER: 60/077450	8	PRIOR FILING DATE: 1998-04-15
9	PRIOR FILING DATE: 1998-03-10	10	PRIOR APPLICATION NUMBER: 60/081838
11	PRIOR APPLICATION NUMBER: 60/077632	12	PRIOR FILING DATE: 1998-04-15
13	PRIOR FILING DATE: 1998-03-11	14	PRIOR APPLICATION NUMBER: 60/082568
15	PRIOR APPLICATION NUMBER: 60/077641	16	PRIOR FILING DATE: 1998-04-21
17	PRIOR FILING DATE: 1998-03-11	18	PRIOR APPLICATION NUMBER: 60/082569
19	PRIOR APPLICATION NUMBER: 60/077649	20	PRIOR FILING DATE: 1998-04-21
21	PRIOR FILING DATE: 1998-03-11	22	PRIOR APPLICATION NUMBER: 60/082704
23	PRIOR APPLICATION NUMBER: 60/077791	24	PRIOR FILING DATE: 1998-04-22
25	PRIOR FILING DATE: 1998-03-12	26	PRIOR APPLICATION NUMBER: 60/082804
27	PRIOR APPLICATION NUMBER: 60/078004	28	PRIOR FILING DATE: 1998-04-22
29	PRIOR FILING DATE: 1998-03-13	30	PRIOR APPLICATION NUMBER: 60/082700
31	PRIOR APPLICATION NUMBER: 60/078886	32	PRIOR FILING DATE: 1998-04-22
33	PRIOR FILING DATE: 1998-03-20	34	PRIOR APPLICATION NUMBER: 60/082797
35	PRIOR APPLICATION NUMBER: 60/078936	36	PRIOR FILING DATE: 1998-04-22
37	PRIOR FILING DATE: 1998-03-20	38	PRIOR APPLICATION NUMBER: 60/082796
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47	PRIOR APPLICATION NUMBER: 60/079294	48	PRIOR FILING DATE: 1998-04-28
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61	PRIOR FILING DATE: 1998-03-27	62	PRIOR APPLICATION NUMBER: 60/083499
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81	PRIOR FILING DATE: 1998-03-30	82	PRIOR APPLICATION NUMBER: 60/083500
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93	PRIOR FILING DATE: 1998-03-31	94	PRIOR APPLICATION NUMBER: 60/084414
95	PRIOR APPLICATION NUMBER: 60/080194	96	PRIOR FILING DATE: 1998-05-06
97	PRIOR FILING DATE: 1998-03-31	98	PRIOR APPLICATION NUMBER: 60/084441
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101	PRIOR FILING DATE: 1998-04-01	102	PRIOR APPLICATION NUMBER: 60/084637
103	PRIOR APPLICATION NUMBER: 60/080328	104	PRIOR FILING DATE: 1998-05-07
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113	PRIOR FILING DATE: 1998-04-01	114	PRIOR APPLICATION NUMBER: 60/084598
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125	PRIOR FILING DATE: 1998-04-08	126	PRIOR APPLICATION NUMBER: 60/084643
127	PRIOR APPLICATION NUMBER: 60/081195	128	PRIOR FILING DATE: 1998-05-07
129	PRIOR FILING DATE: 1998-04-08	130	PRIOR APPLICATION NUMBER: 60/085339
131	PRIOR APPLICATION NUMBER: 60/081203	132	PRIOR FILING DATE: 1998-05-13
133	PRIOR FILING DATE: 1998-04-09	134	PRIOR APPLICATION NUMBER: 60/085338
135	PRIOR APPLICATION NUMBER: 60/081229	136	PRIOR FILING DATE: 1

[illegible]

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366

[illegible]

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Db	1561	GTCCATAGAGACGAACAGAAATGAGACCTTCCGGGCCAAGCGTGGCGCTGGGGGACACTTGG	1620
Qy	1621	GTGACTGTGGCCACACGGCGTGTGTGTGAAACGTGAATATAAAAGAGCAAAAAAAA	1679
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RESULT 6

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US-09-978-608A-522
; Sequence 522, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-608A-522

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[illegible]

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Db 1081 CAGCGAGGTGAGCAACGGCAGCTCGAGGAGGCGAGGCTGCGTGTGGCTGCTGCCTCTTCT 1140
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Db 1141 GGTCTTGCACTGCTTCTCAAAATTTGATGTGAGTGCCACTTCCCAACCGCGGAAAGGCT 1200
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QY 1261 TATACAAATGAAATTTAGAGAAACACAGCTTCATGGGACAGAAATTTGAGGAGGGGAAC 1320
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QY 1621 GTAGACTGTGCCACCAACGCGGCTGTGTGTGAAACGTGAAATTTAAAGAGCAAAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAACGCGGCTGTGTGTGAAACGTGAAATTTAAAGAGCAAAAAAAA 1679

RESULT 8

US-09-978-191A-522
; Sequence 522, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTGCTCTCAGCAAAACAGTGGATTAAATCTCTTGCACAACTTGAGGCAACAC 60
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DB 61 AATCTATCAGAAAGAAAGAAAGAAACCGAACCTGACAAAAGAAAGAAAGAAAG 120
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QY 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGGAGTGCCCGTCCGCGAGATGC 240
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DB 361 TGCTGGGAATGACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 GCAGTACAGCATCGAGATCCAGAACCTGATGTGTATGAGAGGGGCTTACACCTGCTC 480
DB 421 GCAGTACAGCATCGAGATCCAGAACCTGATGTGTATGAGAGGGGCTTACACCTGCTC 480
QY 481 GGTGCAGACAGCAACACCGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
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DB 541 CAAAATTGTAGAGATTCTTTAGATATCTCCATTAATGAAGGAAACAATATTAGCTTAC 600
QY 601 CTGCATAGCAACTGGTAGACAGAGCGGTACCTTGGAGACACATCTCTCCCAAGC 660
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Db 601 CTGATAGCAACTGGTAGACAGAGCCCTACGTTACTTGGAGACACATCTCTCCCAAGC 660
QY 661 GGTGGCTTTGTAGTGAAGACGAATACTTGGAAATTCAGGGCATACCCGGGAGCAGTC 720
Db 661 GGTGGCTTTGTAGTGAAGACGAATACTTGGAAATTCAGGGCATACCCGGGAGCAGTC 720
QY 721 AGGGGACTACAGTGCAGTGCTCCATGATGAGTGGCCGCGCCGCTGTACGGAGGTAAA 780
Db 721 AGGGGACTACAGTGCAGTGCTCCATGATGAGTGGCCGCGCCGCTGTACGGAGGTAAA 780
QY 781 GGTCAACCGTGAACATATCACCATATCATTTAGAGCCCAAGGGTACAGGTGTCCCGGTGGG 840
Db 781 GGTCAACCGTGAACATATCACCATATCATTTAGAGCCCAAGGGTACAGGTGTCCCGGTGGG 840
QY 841 ACAAAGGGGACATGCGAGTGTGAAGCCTCAGAGTGTCCCTCAGCAGAAATTCAGAGTGATA 900
Db 841 ACAAAGGGGACATGCGAGTGTGAAGCCTCAGAGTGTCCCTCAGCAGAAATTCAGAGTGATA 900
QY 901 CAAGGATCACAAAGACTGATTGAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTT 960
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QY 961 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGT 1020
Db 961 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGT 1020
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Db 1081 CAGGAGGTGAGCAACGCGACGTCGAGGAGGCGCTGCGTCTGCTGCTCTTCT 1140
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QY 1621 GTAGACTGTGCCACACGCGCTGTGTGTGAACGTGAATATAAAGAGCAAAAAA 1679
Db 1621 GTAGACTGTGCCACACGCGCTGTGTGTGAACGTGAATATAAAGAGCAAAAAA 1679

US-09-978-403A-522
; Sequence 522, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austen L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978.403A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 7, 8e-22;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTGTCTCTTCAGCAAAAACAGTGGATTAAATCTCTTGCACAACTTGAGAGCAAC 60
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QY 121 AAGAAAAAATCATGAAACCATCAGCAAAAATGCAAAATTCATCTCTTGGCAAT 180
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Db 361 TGCTGGGAATGACAAAGTGGTGGATCTCGCTGGTGGTCTTCTGAGCAACACCCCAAC 420
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RESULT 10

US-09-978-564A-522

; Sequence 522, Application US/0978564A

; Publication No. US20030050241A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tunas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630PIC25

; CURRENT APPLICATION NUMBER: US/09/978,564A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Garney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljanin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Query Match      100.0%; Score 1679; DB 10; Length 1679;
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DB      1 GTTGTGCTCTTCAGCAAAACAGTGGATTTAAATCTCTTGCAAGACTTTGAGACCAAC 60

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DB      61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

QY      121 AAGAAAGAAATCATGAAACCATCAGCCAAATGCAATTTCTATCTTTGGGCAAT 180
DB      121 AAGAAAGAAATCATGAAACCATCAGCCAAATGCAATTTCTATCTTTGGGCAAT 180

QY      181 CTTTACGGGGCTGGCTGTCTGTCTCTTCCAGAGAGTCCCGTCCGAGGGAGATGC 240
DB      181 CTTTACGGGGCTGGCTGTCTGTCTCTTCCAGAGAGTCCCGTCCGAGGGAGATGC 240

QY      241 CACCTTCCCAAGTATGGACAAAGTACGCTGCGGAGGGGGAGCGCCACCTCAG 300
DB      241 CACCTTCCCAAGTATGGACAAAGTACGCTGCGGAGGGGGAGCGCCACCTCAG 300

QY      301 GTGCACTATTGCAACCGGGTCAACCGGGTGGCTTAAACCGGAGCACCCTCTTA 360
DB      301 GTGCACTATTGCAACCGGGTCAACCGGGTGGCTTAAACCGGAGCACCCTCTTA 360

QY      361 TCGTGGGAATGCAAGTGTGCTGTGATCTCTCGCGTGGCTTCTTGAGCAACACCAAC 420
DB      361 TCGTGGGAATGCAAGTGTGCTGTGATCTCTCGCGTGGCTTCTTGAGCAACACCAAC 420

QY      421 GCAGTACAGATCGAGATCCAGAAAGTGTATGACGAGGGCCCTTACACCTGCTC 480
DB      421 GCAGTACAGATCGAGATCCAGAAAGTGTATGACGAGGGCCCTTACACCTGCTC 480

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481 GGTGCAGACAGACAAACCAACCAAGAGCCTCTAGGGTCCACCTCATTTGTGGAAGTATCTCC 540
481 GGTGCAGACAGACAAACCAACCAAGAGCCTCTAGGGTCCACCTCATTTGTGGAAGTATCTCC 540
541 CAAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACATATTTAGCCTCAC 600
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661 GGTTCGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
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721 AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCCCGTGGTACGAGAGTAAA 780
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781 GGTCAACCGTGAACCTATCCACCATATATTTCAAGAGCCAAAGGTTACAGGTGTCCTCGTGG 840
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1081 CAGCGAGTGTAGCAACCGCAGCTCGAGGAGGCGAGCTGCTGCTGGCTGCTCTTCTTCT 1140
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1321 AAGAAATCTTTGGGGGAAAGAGTTTTTAAAGAAATTTGAAATTTGAAATTTGAAATTTGAA 1380
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1441 CCCACTGCAAGCTGCATCGTGCACCTCTTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTC 1500
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181  CTTTCAAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
181  CTTTCAAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
241  CACCTTCCCAAGCTATGGACAAAGCTATGGACAAAGCTATGGACAAAGCTATGGACAA 300
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421  GCAGTACAGCATCGAGATCCAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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481  GGTGCAGACAGCAACCAACCGGGTCAACCGGGTCAACCGGGTCAACCGGGTCAACCG 540
481  GGTGCAGACAGCAACCAACCGGGTCAACCGGGTCAACCGGGTCAACCGGGTCAACCG 540
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Db 1 GTTGTGCTCTTCAGCAAAACAGTGGATTAAATCTCTTCCTTGCAACAGCTTGAGACAAC 60

Qy 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACTTGCAAAAAAGAGAAAGAAAG 120
Db 61 AATCTATCAGGAAGAAAGAAAGAAACCGAACTTGCAAAAAAGAGAAAGAAAG 120

Qy 121 AAGAAAAAATCATGAAAAACCATCCAGCAAAATGCAAAATCTATCTTTGGCAAT 180
Db 121 AAGAAAAAATCATGAAAAACCATCCAGCAAAATGCAAAATCTATCTTTGGCAAT 180

Qy 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGAGTGGCCGTGCGCAGCGAGATGC 240
Db 181 CTTACGGGGCTGGCTGCTGTGTCTCTTCAAGAGTGGCCGTGCGCAGCGAGATGC 240

Qy 241 CACCTTCCCAAGCTATGGACAACGTGACGCTCGGAGGGGGAGAGCGCCACCTCAG 300
Db 241 CACCTTCCCAAGCTATGGACAACGTGACGCTCGGAGGGGGAGAGCGCCACCTCAG 300

Qy 301 GTGCACATTTGACAACCGGTCACCCGGGTGCGCTGGCTTAAACCGCAGCACCATCTCTA 360
Db 301 GTGCACATTTGACAACCGGTCACCCGGGTGCGCTGGCTTAAACCGCAGCACCATCTCTA 360

Qy 361 TGCTGGGAATGCAAGTGGTGTCTCGGTGCTCTCGGTGCTCTTCTGAGCAACACCAAC 420
Db 361 TGCTGGGAATGCAAGTGGTGTCTCGGTGCTCTCGGTGCTCTTCTGAGCAACACCAAC 420

Qy 421 GCAGTACAGCATCGAGATCCAGAACTGTGATGTGATGAGGGGGCTTACACCTGCTC 480
Db 421 GCAGTACAGCATCGAGATCCAGAACTGTGATGTGATGAGGGGGCTTACACCTGCTC 480

Qy 481 GGTGCAAGCAGACAACACCCAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
Db 481 GGTGCAAGCAGACAACACCCAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540

Qy 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTAC 600
Db 541 CAAAATTGTAGAGATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTAC 600

Qy 601 CTGCATAGCACTGGTAGACAGCGCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660
Db 601 CTGCATAGCACTGGTAGACAGCGCTACGGTTACTTGGAGACACATCTCTCCCAAGC 660

Qy 661 GGTGGCTTTGTGAGTGAAGACGAATACTTTGAAATTTAGGGCATCACCCGGGAGCAGTC 720
Db 661 GGTGGCTTTGTGAGTGAAGACGAATACTTTGAAATTTAGGGCATCACCCGGGAGCAGTC 720

QY	721	AGGGGACTACGAGTGCAGTGCCCTCCAATGACGTGGCCGGCCCGTGGTACGGAGAGTAAA	780
Db	721	AGGGGACTACGAGTGCAGTGCCCTCCAATGACGTGGCCGGCCCGTGGTACGGAGAGTAAA	780
QY	781	GGTCAACGGTGAACTAATCCACATACATTTTCAGAACCAAGGGTACAGGTGTCCCCGTGGG	840
Db	781	GGTCAACGGTGAACTAATCCACATACATTTTCAGAACCAAGGGTACAGGTGTCCCCGTGGG	840
QY	841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCCTCAGCAGAAATTCAGTGGTA	900
Db	841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCCCTCAGCAGAAATTCAGTGGTA	900
QY	901	CAAGGATGACAAAAGACTGATTGAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTT	960
Db	901	CAAGGATGACAAAAGACTGATTGAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTT	960
QY	961	CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAATTCACACTTGCCT	1020
Db	961	CCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAATTCACACTTGCCT	1020
QY	1021	GGCCTCAACAAGCTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGT	1080
Db	1021	GGCCTCAACAAGCTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGT	1080
QY	1081	CAGCGAGGTGACAAACGGCAGTGCAGGAGGGCAGGCTGGCTGCGGTGCTGCTCTTCT	1140
Db	1081	CAGCGAGGTGACAAACGGCAGTGCAGGAGGGCAGGCTGGCTGCGGTGCTGCTCTTCT	1140
QY	1141	GGTCTTGCACTGCTTCTCAAATTTTGATGTAGTGGCCACTTCCCAACCCGGGAAAGGCT	1200
Db	1141	GGTCTTGCACTGCTTCTCAAATTTTGATGTAGTGGCCACTTCCCAACCCGGGAAAGGCT	1200
QY	1201	GCCGCGACACGACCAACACAAACAGCAATGCGAACACCGACAGCAACCAATCAGATA	1260
Db	1201	GCCGCGACACGACCAACACAAACAGCAATGCGAACACCGACAGCAACCAATCAGATA	1260
QY	1261	TATACAAATGAAATTTAGAAGAAACACAGCCCTCATGGGACAGAAATTTGAGGGAGGGGAAC	1320
Db	1261	TATACAAATGAAATTTAGAAGAAACACAGCCCTCATGGGACAGAAATTTGAGGGAGGGGAAC	1320
QY	1321	AAAGAATACTTTGGGGGAAAGAGTTTAAAAAAGAAATTTGAAATTTGCCCTTCAGATA	1380
Db	1321	AAAGAATACTTTGGGGGAAAGAGTTTAAAAAAGAAATTTGAAATTTGCCCTTCAGATA	1380
QY	1381	TTTAGGTACAATGGAGTTTCTTTTCCAAACGGGAGAAACACAGCACACCCCGCTTGGGA	1440
Db	1381	TTTAGGTACAATGGAGTTTCTTTTCCAAACGGGAGAAACACAGCACACCCCGCTTGGGA	1440
QY	1441	CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGGCTC	1500
Db	1441	CCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAAGGGCTCAGGCTC	1500
QY	1501	TCTGCCACAGAGTGCCTCCACAGTGGAACTCTGGAGCTGGCCATCCCAATTCATCA	1560
Db	1501	TCTGCCACAGAGTGCCTCCACAGTGGAACTCTGGAGCTGGCCATCCCAATTCATCA	1560
QY	1561	GTCCATAGAGCGAAAGAAATGAGACCTTCGGGCCCAAGCGTGGCGCTCGGGGCACTTTG	1620
Db	1561	GTCCATAGAGCGAAAGAAATGAGACCTTCGGGCCCAAGCGTGGCGCTCGGGGCACTTTG	1620
QY	1621	GTAGACTGTGCCACACGCGGTGTGTGTGAAACGTGAAATTAAGAGCAAAAAAAA	1679
Db	1621	GTAGACTGTGCCACACGCGGTGTGTGTGAAACGTGAAATTAAGAGCAAAAAAAA	1679

RESULT 14

RESULT 14
US-09-918-585A-522

US-09-318-383A-322
: Sequence 522, Application US/09918585A

; sequence 322, Application US/03
; Publication No. US20030060406A1

: GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: ASIKEMAZI, AVI
APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David	
APPLICANT: Desnoyers, Luc	
APPLICANT: Eaton, Dan	
APPLICANT: Ferrara, Napoleon	
APPLICANT: Filvaroff, Ellen	
APPLICANT: Fong, Sherman	
APPLICANT: Gao, Wei-Qiang	
APPLICANT: Gerber, Hanspeter	
APPLICANT: Gerritsen, Mary E.	
APPLICANT: Goddard, Audrey	
APPLICANT: Godowski, Paul J.	
APPLICANT: Grimaldi, J. Christopher	
APPLICANT: Gurney, Austin L.	
APPLICANT: Hillan, Kenneth J.	
APPLICANT: Kijavini, Ivar J.	
APPLICANT: Kuo, Sophia S.	
APPLICANT: Napier, Mary A.	
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APPLICANT: Paoni, Nicholas F.	
APPLICANT: Roy, Margaret Ann	
APPLICANT: Shelton, David L.	
APPLICANT: Stewart, Timothy A.	
APPLICANT: Tumas, Daniel	
APPLICANT: Williams, P. Mickey	
APPLICANT: Wood, William I.	
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	
FILE REFERENCE: P2630PJC1	
CURRENT APPLICATION NUMBER: US/09/318,585A	
CURRENT FILING DATE: 2001-07-30	
PRIOR APPLICATION NUMBER: 60/062250	
PRIOR FILING DATE: 1997-10-17	
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47	PRIOR APPLICATION NUMBER: 60/085697
48	PRIOR FILING DATE: 1998-05-15
49	PRIOR APPLICATION NUMBER: 60/086023
50	PRIOR FILING DATE: 1998-05-15

	Query Match	100.0%;	Score 1679;	DB 10;	Length 1679;
	Best Local Similarity	100.0%;	Pred. No. 7.8e-22;		
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Qy	61	AATCTATCAGAAAGAAAGAAAAAACCAGACCTGACAAAAAGAAAAAGAAAAAGAAAG	120		
Db	61	AATCTATCAGAAAGAAAGAAAAAACCAGACCTGACAAAAAGAAAAAGAAAAAGAAAG	120		
Qy	121	AAGAAAAAAATCATGAAAAACCATCCAGGCCAAAAATGCACAAATTTCTATCTCTTGGGCAAT	180		
Db	121	AAGAAAAAAATCATGAAAAACCATCCAGGCCAAAAATGCACAAATTTCTATCTCTTGGGCAAT	180		
Qy	181	CTTCACGGGCTGGCTGCTCTGTGTCTTCTCCAGGAGTCCCTGTGCGACGGAGATGC	240		
Db	181	CTTCACGGGCTGGCTGCTCTGTGTCTTCTCCAGGAGTCCCTGTGCGACGGAGATGC	240		
Qy	241	CACCTTCCCAAGCTATGGACAACTGTACGGTCCGGCAGGGGGAGAGCGCACCTCTAG	300		
Db	241	CACCTTCCCAAGCTATGGACAACTGTACGGTCCGGCAGGGGGAGAGCGCACCTCTAG	300		

QY 301 GTGCACATTGACAAACGGGCTCACCCGGGTGGCTGCTGCTAAACCGCAGCACCATCTCTCTA 360
Db 301 GTGCACATTGACAAACGGGCTCACCCGGGTGGCTGCTGCTAAACCGCAGCACCATCTCTCTA 360
QY 361 TGCTGGGAATGACAAGTGGTGGCTGAGTCTCGCTGGTCTCTCTGAGCAACACCCAAAC 420
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QY 421 GCAGTACAGCATCAGATCCAGATCCAGATCGGATGTGTATGACGAGGGCCCTTACACCTGCTC 480
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QY 841 AAAAAAGGGGACATGAGTGTGAAGCTCAGAGTCCCTCAGCAGAAATTCAGTGGTA 900
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QY 961 CCTCTCAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTGCTTGGT 1020
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RESULT 15

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; Sequence 522, Application US/09978423A

; Publication No. US20030069178A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

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; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C21

; CURRENT APPLICATION NUMBER: US/09/978,423A

; CURRENT FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

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;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 7.8e-22;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTTGCCACAGCTTGAGAGCAAC	60
Db	1	GTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCTTGCCACAGCTTGAGAGCAAC	60
Qy	61	AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120
Db	61	AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120
Qy	121	AAGAAAAAATCATGAAACCATCCAGCCAAAATGCAAAATCTCTTTGGGCAAT	180
Db	121	AAGAAAAAATCATGAAACCATCCAGCCAAAATGCAAAATCTCTTTGGGCAAT	180
Qy	181	CTTCACGGGCTGGCTCTCTGTCTCTTCCAGAGAGTCCCGTGGCGAGGAGATGC	240
Db	181	CTTCACGGGCTGGCTCTCTGTCTCTTCCAGAGAGTCCCGTGGCGAGGAGATGC	240
Qy	241	CACCTTCCCAAGCTATGCAACAGTGAAGTCCCGCAGGGGAGAGCGCCCTCTCAG	300
Db	241	CACCTTCCCAAGCTATGCAACAGTGAAGTCCCGCAGGGGAGAGCGCCCTCTCAG	300
Qy	301	GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTTGAACCGCGAGCCATCTCTTA	360
Db	301	GTGCACATATTGACAAACCGGGTCAACCGGGTGGCTTGAACCGCGAGCCATCTCTTA	360
Qy	361	TGCTGGGAATGCAAGTGGTGGCTGGATCTCTCGGCTGGCTCTCTGAGCAACCCAAAC	420
Db	361	TGCTGGGAATGCAAGTGGTGGCTGGATCTCTCGGCTGGCTCTCTGAGCAACCCAAAC	420
Qy	421	GCAGTACAGCATCAGATCCAGAAACGTGGATGTGTATGAGAGGCGCTTACACCTGCTC	480
Db	421	GCAGTACAGCATCAGATCCAGAAACGTGGATGTGTATGAGAGGCGCTTACACCTGCTC	480
Qy	481	GGTCAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGAGATCTCC	540
Db	481	GGTCAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGAGATCTCC	540
Qy	541	CAAAATTGTAGATTTCTTCAGATATCTCCATTAATGAAGGAAACATATTAGCCTCAC	600
Db	541	CAAAATTGTAGATTTCTTCAGATATCTCCATTAATGAAGGAAACATATTAGCCTCAC	600
Qy	601	CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC	660
Db	601	CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC	660
Qy	661	GGTGGCTTTGTAGTGAAGCAATATCTGGAATTCAGGGCATCACCCGGGAGCAGTC	720
Db	661	GGTGGCTTTGTAGTGAAGCAATATCTGGAATTCAGGGCATCACCCGGGAGCAGTC	720
Qy	721	AGGGACTACAGTGCAGTGGCTCCAAATGAGTGGCGCGCGCTGGTACGGAGATATA	780
Db	721	AGGGACTACAGTGCAGTGGCTCCAAATGAGTGGCGCGCGCTGGTACGGAGATATA	780
Qy	781	GGTCAACGGTGAATTCACCATATCATTTTGAAGCCAAAGGATCAGGTGTCCTGGGG	840
Db	781	GGTCAACGGTGAATTCACCATATCATTTTGAAGCCAAAGGATCAGGTGTCCTGGGG	840
Qy	841	ACAAAGGGGACACTGCAAGTGGAGCTCAGAGTCCCTCAGCAGAAATTCAGTGGTA	900
Db	841	ACAAAGGGGACACTGCAAGTGGAGCTCAGAGTCCCTCAGCAGAAATTCAGTGGTA	900
Qy	901	CAAGGATGACAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT	960
Db	901	CAAGGATGACAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTT	960

RESULT 16

US-09-978-193A-522

Sequence 522, Application US/09978:93A

Publication No. US20030073624A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Geritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Kenneth L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C6
CURRENT APPLICATION NUMBER: US/09/978,193A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/077791
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; PRIOR FILLING DATE: 1998-05-15									
; PRIOR APPLICATION NUMBER: 60/085697									
Query Match 100.0%; Score 1679; DB 10; Length 1679;									
Best Local Similarity 100.0%; Pred. No. 7.8e-22;									
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GTGTGTCCTTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTCAGAGCAACAC	60						
Db	1	GTGTGTCCTTTCAGCAAAACAGTGGATTAAATCTCTTGACAAAGCTTCAGAGCAACAC	60						
Qy	61	AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120						
Db	61	AATCTATCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120						
Qy	121	AAGAAAGAAATCATGAAACCATCCAGCCCAATATGCAATTCATCTCTTGGGCAAT	180						
Db	121	AAGAAAGAAATCATGAAACCATCCAGCCCAATATGCAATTCATCTCTTGGGCAAT	180						
Qy	181	CTTCACGGGGCTGGCTGCTGTGTCTCTTCCAGAGAGTGCCTGCGCAGCGGAGATGC	240						
Db	181	CTTCACGGGGCTGGCTGCTGTGTCTCTTCCAGAGAGTGCCTGCGCAGCGGAGATGC	240						
Qy	241	CACCTTCCCAAGCTATGGAACACGTCAGCGTCCGGCAGGGGAGAGCGCACCCCTCAG	300						
Db	241	CACCTTCCCAAGCTATGGAACACGTCAGCGTCCGGCAGGGGAGAGCGCACCCCTCAG	300						
Qy	301	GTGCACCTATTGACAAACCGGGTCACCCGGTGGCTGCTTAAACCGCAGCAATCTCTTA	360						
Db	301	GTGCACCTATTGACAAACCGGGTCACCCGGTGGCTGCTTAAACCGCAGCAATCTCTTA	360						
Qy	361	TGCTGGGAATGACAAGTGGTGGCTGGATCCCTGCGTGGTCTTCTGAGCAACCCCAAC	420						
Db	361	TGCTGGGAATGACAAGTGGTGGCTGGATCCCTGCGTGGTCTTCTGAGCAACCCCAAC	420						
Qy	421	GCAGTACAGCATCCAGATCCAGATGGATGTGTATGACAGGGGCCCTTACACTGCTC	480						
Db	421	GCAGTACAGCATCCAGATCCAGATGGATGTGTATGACAGGGGCCCTTACACTGCTC	480						
Qy	481	GGTCAGACAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	540						
Db	481	GGTCAGACAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	540						
Qy	541	CAAAATGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCTCAC	600						
Db	541	CAAAATGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCTCAC	600						
Qy	601	CTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC	660						
Db	601	CTGCATAGCAACTGGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGC	660						
Qy	661	GGTTGGCTTTGTAGTGAAGACGAATCTTGAATTCAGGGCATCACCCGGAGAGTC	720						
Db	661	GGTTGGCTTTGTAGTGAAGACGAATCTTGAATTCAGGGCATCACCCGGAGAGTC	720						
Qy	721	AGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCGGCCCGCTGGTACGAGAGTAAA	780						
Db	721	AGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCGGCCCGCTGGTACGAGAGTAAA	780						
Qy	781	GGTCAACCGTGAATATCCACCATACATTTTCAAGAGCCAAAGGGTACAGGTGTCCCGTGG	840						
Db	781	GGTCAACCGTGAATATCCACCATACATTTTCAAGAGCCAAAGGGTACAGGTGTCCCGTGG	840						
Qy	841	ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900						
Db	841	ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900						
Qy	901	CAAGGATGACAAAGACTGATTTGAAGAAAGAAAGGGGTGAAGTGGAAACAGACCTTT	960						
Db	901	CAAGGATGACAAAGACTGATTTGAAGAAAGAAAGGGGTGAAGTGGAAACAGACCTTT	960						
Qy	961	CTTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCT	1020						
Db	961	CTTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCT	1020						
Qy	1021	GGCTCTCAACAGCTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGCGGCCGT	1080						
Db	1021	GGCTCTCAACAGCTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGCGGCCGT	1080						
Qy	1081	CAGCGAGGTGAGCAACCGCACGTCGAGGAGGGCAGGCTCGCTGCTGCTCTTCT	1140						
Db	1081	CAGCGAGGTGAGCAACCGCACGTCGAGGAGGGCAGGCTCGCTGCTGCTCTTCT	1140						
Qy	1141	GGTCTTGCACCTGCTTCTCAATTTTGTGTGAGTGCCTTCCACCCGGGAAAGGCT	1200						
Db	1141	GGTCTTGCACCTGCTTCTCAATTTTGTGTGAGTGCCTTCCACCCGGGAAAGGCT	1200						
Qy	1201	GCCGCCACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	1260						
Db	1201	GCCGCCACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	1260						
Qy	1261	TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGAAC	1320						
Db	1261	TATACAAATGAAATTTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGGAGGGAAC	1320						
Qy	1321	AAAGAAATCTTTGGGGGAAAGAGTTTAAAGAAAGAAATTTGAAATTTGCTTTCAGATA	1380						
Db	1321	AAAGAAATCTTTGGGGGAAAGAGTTTAAAGAAAGAAATTTGAAATTTGCTTTCAGATA	1380						
Qy	1381	TTTAGGTACAAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCCCGGCTTGA	1440						
Db	1381	TTTAGGTACAAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGCACACCCCGGCTTGA	1440						
Qy	1441	CCCACTGCAAGCTGCATCGTGCACCTCTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC	1500						
Db	1441	CCCACTGCAAGCTGCATCGTGCACCTCTTTGGTGCAGTGTGGGCAAGGGCTCAGCCTC	1500						
Qy	1501	TCCTGCCACAGAGTGGCCCACTCGTGAACATCTCGAGCTGGCCATCCCAAAATTCATCA	1560						
Db	1501	TCCTGCCACAGAGTGGCCCACTCGTGAACATCTCGAGCTGGCCATCCCAAAATTCATCA	1560						
Qy	1561	GTCCATAGACGCAACAGAAATGAGACCTTCGGGCCCAAGCGTGGCGTGGCGGACCTTTG	1620						
Db	1561	GTCCATAGACGCAACAGAAATGAGACCTTCGGGCCCAAGCGTGGCGTGGCGGACCTTTG	1620						
Qy	1621	GTAGACTGTGCCACACCGCGGTGTGTGTGAAACGTTGAAATATAAAGAGCAAAAAAAA	1679						
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Db      1621 GTAGACTGTGCCACCGCGTGTGTGTGAACGTGAATATAAAGACAAAAA 1679
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RESULT 17
US-09-999-830A-522
; Sequence 522, Application US/09999830A
; Publication No. US20030077700A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC70
; CURRENT APPLICATION NUMBER: US/09/999,830A
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/083392
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Tue Jun 1 09:37:49 2004

[illegible]

Db 1201 GCCGCCACACACACACACACACAGCAATGGCAACACGACAGCAACCAATCAGATA 1260
QY 1261 TATACAAATGAAATAGAGAAACACACAGCCTCATGGGACAGAAATTTGAGGGAGGGAAAC 1320
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QY 1321 AAAGAAATCTTTGGGGGAAAGAGATTTTAAAGAAATTTGAAATTTGCCCTTGAGATA 1380
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QY 1441 CCCACTGCAAGCTGCATCGTCAACCTCTTTTGGTCCCAAGTGTGGCAAGGGCTCAGCCTC 1500
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QY 1501 TCTGCCACAGAGTGGCCCCCAGTGGAAATCTCTGGAGCTGCCATCCCAATTTCAATCA 1560
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QY 1561 GTCCATAGAGAGAAACAGAAATCAGACCTTCCCGGCCCAAGCTGGCGCTCGCGGCACTTTG 1620
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QY 1621 GTAGACTGTGCCACCAAGCGCGTGTGTGTGAACGTGAAATTTAAAGAGCAAAAAAAA 1679
Db 1621 GTAGACTGTGCCACCAAGCGCGTGTGTGTGAACGTGAAATTTAAAGAGCAAAAAAAA 1679

RESULT 18

US-09-978-757A-522
; Sequence 522, Application US/09978757A
; Publication No. US20030083248A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C26
; CURRENT APPLICATION NUMBER: US/09/978,757A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AATCTATCAGGAAAGAAAGAAAGAAACCCGAACTGCAAAAAGAAAGAAAGAAAG 120
Db 61 AATCTATCAGGAAAGAAAGAAAGAAACCCGAACTGCAAAAAGAAAGAAAGAAAG 120
Qy 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATGCAAAATTCATCTCTTTGGGCAAT 180
Db 121 AAGAAAAAATCATGAAACCATCCAGCCAAAATGCAAAATTCATCTCTTTGGGCAAT 180
Qy 181 CTTCAAGGGCTGGCTGCTCTCTCTCTTCAAGGAGTGCCTGCGAGCGGAGATGC 240
Db 181 CTTCAAGGGCTGGCTGCTCTCTCTCTTCAAGGAGTGCCTGCGAGCGGAGATGC 240
Qy 241 CACCTTCCCAAGCTATGACAAACGTCGTCGGGTCGGGAGAGCGGAGAGCCCTCAG 300
Db 241 CACCTTCCCAAGCTATGACAAACGTCGTCGGGTCGGGAGAGCGGAGAGCCCTCAG 300
Qy 301 GTGCACCTATTGACAAACCGGTCACCGGGTGGCTGCTCTCTCTCTGAGCAACCCCAAC 420
Db 301 GTGCACCTATTGACAAACCGGTCACCGGGTGGCTGCTCTCTCTGAGCAACCCCAAC 420
Qy 361 TGCTGGGAATGACAAAGTGGTGCCTGGATCTCTCGGTCGTCCTCTCTGAGCAACCCCAAC 480
Db 361 TGCTGGGAATGACAAAGTGGTGCCTGGATCTCTCGGTCGTCCTCTCTGAGCAACCCCAAC 480
Qy 421 GCAGTACAGCATCGAGATCCAGAACGTCGATGTCGATGTCGATGTCGATGTCGATGTC 540
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Qy 481 GGTGCAGACAGCAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC 540
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Db 601 CTGCATAGCAACTCGGTAGACAGAGCCCTACGGTTACTTGAGAGACATCTCTCCCAAGC 660
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Db 721 AGGGGACTTACGAGTGCAGTGCCTCAATGAGCGTGGCGCGCCCTGGTACGGAGAGTAA 780
Qy 781 GGTCAACCGTGAACATTCACCAATACATTTCAAGAGCCAGGGTACAGGTGCCCGTGGG 840

Db 781 GGTACCGTGAACATATCCACCATATTTTCCAGAGCGGTACAGGTGTCCCGTGGG 840
QY 841 ACAAAGGGGACACTGCGAGTGAAGCCCTCAGCAGTCCCTCAGCAGATTTCCAGTGTGA 900
Db 841 ACAAAGGGGACACTGCGAGTGAAGCCCTCAGCAGTCCCTCAGCAGATTTCCAGTGTGA 900
QY 901 CAAGATGACAAAGACACTGATTGAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTT 960
Db 901 CAAGATGACAAAGACACTGATTGAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTT 960
QY 961 CCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGT 1020
Db 961 CCTCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGT 1020
QY 1021 GGCCTCCACAGCTGGGACACCAATGCGAGCATCATGCTATTTGGTCCAGGCGCGT 1080
Db 1021 GGCCTCCACAGCTGGGACACCAATGCGAGCATCATGCTATTTGGTCCAGGCGCGT 1080
QY 1081 CAGCAGGTGAGCAACGCGACGTCGAGGAGGCGAGGCTGCTGCTGCTCTTCT 1140
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QY 1441 CCCACTGCAAGCTGATCGTGCAACCTCTTTGCTGCGGCAAGGCTCAGCCTC 1500
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QY 1501 TCTGCCCCACAGTGTCCCACTGCGAATTTCTGAGAGTGGCCATCCCAATTCATCA 1560
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Db 1621 GTAGACTGTGCCACCGGCTGTGTGTGAACGTGAATTAAGAGAGCAAAAAA 1679

RESULT 19

US-09-978-187B-522

; Sequence 522, Application US/09978187B

; Publication No. US20030096744A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Hillan, Kenneth J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C5
CURRENT APPLICATION NUMBER: US/09/978, 187B
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCTTGCACAAAGCTTGAGAGCAACAC 60

QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Db 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

QY 121 AAGAAAAAAATCATGAAAAACATCCAGCCAAAAATGACAAATTCATTCTTTGGGCAAT 180
Db 121 AAGAAAAAAATCATGAAAAACATCCAGCCAAAAATGACAAATTCATTCTTTGGGCAAT 180

QY 181 CTTACGGGGCTGGCTGCTGTGTCTCTCCAGAGTGCCTGCGCAGCGGAGATGC 240
Db 181 CTTACGGGGCTGGCTGCTGTGTCTCTCCAGAGTGCCTGCGCAGCGGAGATGC 240

QY 241 CACCTTCCCAAGCTATGGAACCAATCCAGCCAAAAATGACAAATTCATTCTTTGGGCAAT 300
Db 241 CACCTTCCCAAGCTATGGAACCAATCCAGCCAAAAATGACAAATTCATTCTTTGGGCAAT 300

QY 301 GTGCACATTTGACAAACCGGGTCAACCGGGTGGCTGGCTTAAACCGCAGCACCATTCTCTA 360
Db 301 GTGCACATTTGACAAACCGGGTCAACCGGGTGGCTGGCTTAAACCGCAGCACCATTCTCTA 360

QY 361 TGTGGAATGACAAAGTGGTGGCTGATCTCTCGCTGGTCTCTTCTGAGCAACACCAAC 420
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; ORGANISM: Homo sapiens									
US-09-978-375A-522									
Query Match 100.0%; Score 1679; DB 10; Length 1679;									
Best Local Similarity 100.0%; Pred. No. 7.8e-22;									
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	GTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTCGACAAAGCTTGAGAGCAAC	60						
Db	1	GTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCTTCGACAAAGCTTGAGAGCAAC	60						
Qy	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120						
Db	61	AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	120						
Qy	121	AAGAAAAAATCATGAAAAATCCAGCCAAATGCAAAATTCATCTCTTTGGGCAAT	180						
Db	121	AAGAAAAAATCATGAAAAATCCAGCCAAATGCAAAATTCATCTCTTTGGGCAAT	180						
Qy	181	CTTCACGGGGCTGGCTGTGTCTCTCTCCAGAGTGCCTGCGCAGCGGAGATGC	240						
Db	181	CTTCACGGGGCTGGCTGTGTCTCTCTCCAGAGTGCCTGCGCAGCGGAGATGC	240						
Qy	241	CACCTTCCCAAGCTATGGACACGTCACGGTCCCGCAGGGGAGAGCGCCCTCAG	300						
Db	241	CACCTTCCCAAGCTATGGACACGTCACGGTCCCGCAGGGGAGAGCGCCCTCAG	300						
Qy	301	GTGCACTATTGCAACCGGGTCAACCGGGTGGCTTAAACCGGAGCACCATCTCTA	360						
Db	301	GTGCACTATTGCAACCGGGTCAACCGGGTGGCTTAAACCGGAGCACCATCTCTA	360						
Qy	361	TGCTGGGATGACAGTGGTGGCTCGATCTCGCTGCTTCTGAGCAACACCAAC	420						
Db	361	TGCTGGGATGACAGTGGTGGCTCGATCTCGCTGCTTCTGAGCAACACCAAC	420						
Qy	421	GCAGTACAGCATCGAGATCCAGAACTGGATGTGATGACAGGGGCCCTTACACCTGTC	480						
Db	421	GCAGTACAGCATCGAGATCCAGAACTGGATGTGATGACAGGGGCCCTTACACCTGTC	480						
Qy	481	GGTGACAGACAAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540						
Db	481	GGTGACAGACAAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCC	540						
Qy	541	CAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCTAC	600						
Db	541	CAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCTAC	600						
Qy	601	CTGCATAGCAACTGTGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCAAAGC	660						
Db	601	CTGCATAGCAACTGTGTAGACAGAGCTACGGTTACTTTGGAGACACATCTCTCCAAAGC	660						
Qy	661	GGTTGGCTTTGTGAGTGAAGACAAATCTTGGAAATTCAGGGCATCACCGGGAGCAGTC	720						
Db	661	GGTTGGCTTTGTGAGTGAAGACAAATCTTGGAAATTCAGGGCATCACCGGGAGCAGTC	720						
Qy	721	AGGGGACTAGCTGAGTGCCTCCCAATGACGTCGCGCGCGCTGTGACGAGAGTAA	780						
Db	721	AGGGGACTAGCTGAGTGCCTCCCAATGACGTCGCGCGCGCTGTGACGAGAGTAA	780						
Qy	781	GGTCACCGTGAACTATCCACATACATTTTCAAGAGCCAAAGGTACAGGTGTCTCCCGTGG	840						
Db	781	GGTCACCGTGAACTATCCACATACATTTTCAAGAGCCAAAGGTACAGGTGTCTCCCGTGG	840						
Qy	841	ACAAAGGGGACACTGAGTGTGAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900						
Db	841	ACAAAGGGGACACTGAGTGTGAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA	900						
Qy	901	CAAGGATGACAAAGACTGATTGAAGAAAGAGGGGTGAAAGTGGAAACACAGCCTTT	960						
Db	901	CAAGGATGACAAAGACTGATTGAAGAAAGAGGGGTGAAAGTGGAAACACAGCCTTT	960						
Qy	961	CTCTCTCAAACTCATCTTCTCAATGTCTCTGAAACATGACTATGGGAACCTACCTTGGCT	1020						
Db	961	CTCTCTCAAACTCATCTTCTCAATGTCTCTGAAACATGACTATGGGAACCTACCTTGGCT	1020						

RESULT 22
US-09-978-298A-522
; Sequence 522, Application US/09978298A
; Publication No. US20030134785A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desmoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C2
CURRENT APPLICATION NUMBER: US/09/978,298A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-04-01
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PRIOR APPLICATION NUMBER: 60/081049
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
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PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
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PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640

[illegible]

RESULT 23

US-09-978-188A-522
Sequence 522, Application US/09978188A

Publication No. US20030139328A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: KJavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C8
CURRENT APPLICATION NUMBER: US/09/978,188A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079664
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495

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181	CTTCAACGGGGCTGGCTGCTCTGTGTCTCTTCCAAAGAGTGCCTGGCGAGCGAGATGC	240
181	CTTCAACGGGGCTGGCTGCTCTGTGTCTCTTCCAAAGAGTGCCTGGCGAGCGAGATGC	240
241	CACCTTCCCAAGAGCTATGACAAACGTCAGCGTCCGCGAGGGGAGAGCGCCACCTCTCAG	300
241	CACCTTCCCAAGAGCTATGACAAACGTCAGCGTCCGCGAGGGGAGAGCGCCACCTCTCAG	300
301	GTGCACCTATTGACAAACCGGGTCCACCCCGGGTGGCTTGGCTAAACCCGAGCACCCTCTCTA	360
301	GTGCACCTATTGACAAACCGGGTCCACCCCGGGTGGCTTGGCTAAACCCGAGCACCCTCTCTA	360
361	TGCTGGGGAATGACAAAGTGGTGGCTTGGATCTCGCGTGGTCTTCTGAGCAACACCCAAAC	420
361	TGCTGGGGAATGACAAAGTGGTGGCTTGGATCTCGCGTGGTCTTCTGAGCAACACCCAAAC	420
421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTC	480
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481	GGTGACAGACAAACCCAAAGACCTCTAGGGTCCACTCATTTGAAGGGAAACAAATATAGCCTCAC	540
481	GGTGACAGACAAACCCAAAGACCTCTAGGGTCCACTCATTTGAAGGGAAACAAATATAGCCTCAC	540
541	CAAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAAACAAATATAGCCTCAC	600
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661	GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATACCCCGGAGACGATC	720
661	GGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATACCCCGGAGACGATC	720
721	AGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCCCTGGTATCGAGAGTAAA	780
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781	GGTCAACGTGAACACTATCCACATACATTTGAGAGCCAGGGTACAGGTGTCCTGGTGGG	840
781	GGTCAACGTGAACACTATCCACATACATTTGAGAGCCAGGGTACAGGTGTCCTGGTGGG	840
841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTTCCAGTGGTA	900
841	ACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTTCCAGTGGTA	900
901	CAAGGATGACAAAAGCTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAACAGACCTTT	960
901	CAAGGATGACAAAAGCTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAACAGACCTTT	960
961	CTCTCAAAACCTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACCTACATTCGCT	1020
961	CTCTCAAAACCTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACCTACATTCGCT	1020
1021	GGCCTCCAAACAGCTGGGCCAACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGT	1080
1021	GGCCTCCAAACAGCTGGGCCAACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGT	1080
1081	CAGCGAGGTGACCAACGCGACGTGAGGAGGGCAGGTGGCTCTGGTCTGGCTCTCTCT	1140
1081	CAGCGAGGTGACCAACGCGACGTGAGGAGGGCAGGTGGCTCTGGTCTGGCTCTCTCT	1140
1141	GGTCTTGCACCTGCTTCTCAAAATTTTGTGTGAGTGCCACTTCCCCACCCGGGAAAGCT	1200
1141	GGTCTTGCACCTGCTTCTCAAAATTTTGTGTGAGTGCCACTTCCCCACCCGGGAAAGCT	1200
1201	GGCGCCACCAACCAACCAACAGCAATGGCAACACCGACAGCAACCAATCAGATA	1260
1201	GGCGCCACCAACCAACCAACAGCAATGGCAACACCGACAGCAACCAATCAGATA	1260
121	AAGAAAAAATCATGAAACCATCCAGCCAAAAATGCAAAATTCCTATCTCTGGGCAAT	180

QY	1261	TATACAAATGAATTAAGAAACACAGACCTCTATGGGACAGAAATTTGAGGGAGGGGAAC	1320	;	PRIOR APPLICATION NUMBER: 60/065311
				;	PRIOR FILING DATE: 1997-11-13
Db	1261	TATACAAATGAATTAAGAAACACAGACCTCTATGGGACAGAAATTTGAGGGAGGGGAAC	1320	;	PRIOR APPLICATION NUMBER: 60/066364
				;	PRIOR FILING DATE: 1997-11-21
QY	1321	AAAGTAATCTTGGGGGAAAGAGTTTAAAGAAATTTGAAATTTGCTTTGCAGATA	1380	;	PRIOR APPLICATION NUMBER: 60/077450
				;	PRIOR FILING DATE: 1998-03-10
Db	1321	AAAGTAATCTTGGGGGAAAGAGTTTAAAGAAATTTGAAATTTGCTTTGCAGATA	1380	;	PRIOR APPLICATION NUMBER: 60/077632
				;	PRIOR FILING DATE: 1998-03-11
QY	1381	TTTAGGTACAAATGAGTTTCTTTTCCCAAACGGGAAGAACACAGACACACCCCGCTTGA	1440	;	PRIOR APPLICATION NUMBER: 60/077641
				;	PRIOR FILING DATE: 1998-03-11
Db	1381	TTTAGGTACAAATGAGTTTCTTTTCCCAAACGGGAAGAACACAGACACACCCCGCTTGA	1440	;	PRIOR APPLICATION NUMBER: 60/077791
				;	PRIOR FILING DATE: 1998-03-12
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				;	PRIOR FILING DATE: 1998-03-13
Db	1441	CCCACTGCAAGCTGCATCGTGCACCTCTTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTC	1500	;	PRIOR APPLICATION NUMBER: 60/078886
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QY	1501	TTTGCCCAAGAGTGGCCCAAGTGAACATCTCTGAGCTGGCCATCCCAAAATTCATCA	1560	;	PRIOR APPLICATION NUMBER: 60/078910
				;	PRIOR FILING DATE: 1998-03-20
Db	1501	TTTGCCCAAGAGTGGCCCAAGTGAACATCTCTGAGCTGGCCATCCCAAAATTCATCA	1560	;	PRIOR APPLICATION NUMBER: 60/078939
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QY	1561	GTCCATAGACAGCAACAGAAATGAGACCTTCGGGCCCAAGCGTGGCGGACCTTTG	1620	;	PRIOR APPLICATION NUMBER: 60/079294
				;	PRIOR FILING DATE: 1998-03-25
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				;	PRIOR FILING DATE: 1998-03-26
QY	1621	GTAGACTGTCCCAAGCAGCGGTGTGTGTGAAAGTGAATTAAGAAAGCAAAAAA	1679	;	PRIOR APPLICATION NUMBER: 60/079664
				;	PRIOR FILING DATE: 1998-03-27
Db	1621	GTAGACTGTCCCAAGCAGCGGTGTGTGTGAAAGTGAATTAAGAAAGCAAAAAA	1679	;	PRIOR APPLICATION NUMBER: 60/079689
				;	PRIOR FILING DATE: 1998-03-27

RESULT 24

US-09-978-681A-522

; Sequence 522, Application US/09978681A

; Publication No. US20030195148A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630PIC18

; CURRENT APPLICATION NUMBER: US/09/978,681A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

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RESULT 25

US-09-978-194A-522
; Sequence 522, Application US/09978194A
; Publication No. US2003019533A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C10
; CURRENT APPLICATION NUMBER: US/09/978,194A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 7.8e-22;

Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	121	AAGAAAAAAATCATGAAACCATCAGCAAAATGCAATTTCTCTTGGCAAT	180
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DB	181	CTTCAGGGGGTGGCTGTCTGTCTCTTCAAGAGTGCCTGCGCAGGGGAGATGC	240
QY	241	CACCTTCCCAAGAGCTATGGAACAACTGACGGTCCGGCAGGGGGAGCGCCACCTCAG	300
DB	241	CACCTTCCCAAGAGCTATGGAACAACTGACGGTCCGGCAGGGGGAGCGCCACCTCAG	300
QY	301	GTGCACTATTGACAAACCGGGTCAACCGGGTGGCTTGGCTTAAACCGCAGCAATCTCTA	360
DB	301	GTGCACTATTGACAAACCGGGTCAACCGGGTGGCTTGGCTTAAACCGCAGCAATCTCTA	360
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Db 841 ACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
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RESULT 26
US-09-999-829A-522
; Sequence 522, Application US/09999829A
; Publication No. US20030195344A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C61
; CURRENT APPLICATION NUMBER: US/09/999,829A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-999-829A-522

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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7	PRIOR APPLICATION NUMBER:	60/081195	
7	PRIOR FILING DATE:	1998-04-08	
7	PRIOR APPLICATION NUMBER:	60/081203	
7	PRIOR FILING DATE:	1998-04-09	
7	PRIOR APPLICATION NUMBER:	60/081229	
7	PRIOR FILING DATE:	1998-04-09	
7	PRIOR APPLICATION NUMBER:	60/081955	
7	PRIOR FILING DATE:	1998-04-15	
7	PRIOR APPLICATION NUMBER:	60/081817	
7	PRIOR FILING DATE:	1998-04-15	

[illegible]

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PLC13
CURRENT APPLICATION NUMBER: US/09/978,544A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
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PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366

1 PRIOR FILING DATE: 1998-05-05
1 PRIOR APPLICATION NUMBER: 60/084414
1 PRIOR FILING DATE: 1998-05-06
1 PRIOR APPLICATION NUMBER: 60/084441
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1 PRIOR APPLICATION NUMBER: 60/085689
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085579
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085580
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085573
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085704
1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7.9e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GTTGTGCTTCAGCAAAACAGTGGATTAAATCTCCTTGACAGCTTGAGAGCAAC 60
Qy 61 AATCTATCAGCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Db 61 AATCTATCAGCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
Qy 121 AAGAAAAAATCATGAAAAACATCCAGCCAAAATGCAAAATGCAATCTCTCTGGGCAAT 180
Db 121 AAGAAAAAATCATGAAAAACATCCAGCCAAAATGCAAAATGCAATCTCTCTGGGCAAT 180
Qy 181 CTTACGGGGTGGCTGCTGTGTCTCTTCAAGAGTGCCGCGCAGCGGAGATGC 240
Db 181 CTTACGGGGTGGCTGCTGTGTCTCTTCAAGAGTGCCGCGCAGCGGAGATGC 240
Qy 241 CACCTTCCCAAGCTATGGACAAAGTACCGTCCGGCAGGGGGAGAGCGCCCTCAG 300
Db 241 CACCTTCCCAAGCTATGGACAAAGTACCGTCCGGCAGGGGGAGAGCGCCCTCAG 300
Qy 301 GTGCACTATTGACACCGGGTCAACCGGGTGGCTGGCTAAACCGGAGCAATCTCTTA 360
Db 301 GTGCACTATTGACACCGGGTCAACCGGGTGGCTGGCTAAACCGGAGCAATCTCTTA 360
Qy 361 TGCTGGGAATGACAGTGGTGGTCTGATCCCTCGCTGCTCTTCTGAGCAACCCCAAC 420
Db 361 TGCTGGGAATGACAGTGGTGGTCTGATCCCTCGCTGCTCTTCTGAGCAACCCCAAC 420

Qy 421 GCAGTACAGCATCGAGATCCAGAAACGCTGATGTGTATGACAGGGCCCTTACACCTGCTC 480
Db GCAGTACAGCATCGAGATCCAGAAACGCTGATGTGTATGACAGGGCCCTTACACCTGCTC 480
Qy 481 GGTGCGAGACAGCAACCCAAAGACCTCTAGGGTCCACTTATGTGCAAGTATCTCC 540
Db GGTGCGAGACAGCAACCCAAAGACCTCTAGGGTCCACTTATGTGCAAGTATCTCC 540
Qy 541 CAAAAATTGTAGAGATTCTTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTCAC 600
Db CAAAAATTGTAGAGATTCTTCAGATATCTCCATTATGAAGGGAACAATATTAGCCTCAC 600
Qy 601 CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC 660
Db CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGC 660
Qy 661 GGTGGCTTTGTGAGTGAAGACGAAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Db GGTGGCTTTGTGAGTGAAGACGAAATACCTTGGAAATTCAGGGCATCACCCGGGAGCAGTC 720
Qy 721 AGGGGACTACGAGTGCAGTCCCTCAATGACGTGGCGCGCCCGTGTACGGAGAGTAAA 780
Db AGGGGACTACGAGTGCAGTCCCTCAATGACGTGGCGCGCCCGTGTACGGAGAGTAAA 780
Qy 781 GGTCAACCGTGAACCTATCCACATATTTTCCAGAAAGCCAGGGTACAGGTGTCCCGTGGG 840
Db GGTCAACCGTGAACCTATCCACATATTTTCCAGAAAGCCAGGGTACAGGTGTCCCGTGGG 840
Qy 841 AAAAAAGGACACTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Db AAAAAAGGACACTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTA 900
Qy 901 CAAGGATGACAAAAAGACTGATTGAAGGAAAGAGGGGTGAAAGTGGAAACAGACCTTT 960
Db CAAGGATGACAAAAAGACTGATTGAAGGAAAGAGGGGTGAAAGTGGAAACAGACCTTT 960
Qy 961 CCTCTAAAACTCATCTTCTTCAATGTCTGAAATGCTCTGAAATGCTATGGGAACTACCTGCGT 1020
Db CCTCTAAAACTCATCTTCTTCAATGTCTGAAATGCTCTGAAATGCTATGGGAACTACCTGCGT 1020
Qy 1021 GGCTCTCAACAGCTGGGCGCACCAATGCCAGCATCATCTATTTGCTCCAGCGCGCT 1080
Db GGCTCTCAACAGCTGGGCGCACCAATGCCAGCATCATCTATTTGCTCCAGCGCGCT 1080
Qy 1081 CAGCGAGTGCAGCAACCGGCACGCTCGAGAGGGCAGGCTGCTGCTGGCTGCTCTCTTCT 1140
Db CAGCGAGTGCAGCAACCGGCACGCTCGAGAGGGCAGGCTGCTGCTGGCTGCTCTCTTCT 1140
Qy 1141 GGTCTTGCACTGCTTCTCAAAATTTTGAATGTGAGTGCCACTTCCCGCACCAGGAAAGGCT 1200
Db GGTCTTGCACTGCTTCTCAAAATTTTGAATGTGAGTGCCACTTCCCGCACCAGGAAAGGCT 1200
Qy 1201 GCCGCCACCCACCCACCAACACAGCAATGCAACACCGAGCAACAGCAACCAATCAGATA 1260
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Qy 1261 TATACAAATGAAATAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGAGGAAAC 1320
Db TATACAAATGAAATAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGAGGAAAC 1320
Qy 1321 AAAGAAATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380
Db AAAGAAATCTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAATTTGCTTTCAGATA 1380
Qy 1381 TTTAGGTACATGAGTTTCTTTTCCCAACCGGAAAGAACACAGCAGCACCCCGGCTTGA 1440
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Qy 1441 CCCACTGCAAGCTCATGTCACCTCTTTGGTGGCAGTGTGGGAGGAGGCTCAGGCTC 1500
Db CCCACTGCAAGCTCATGTCACCTCTTTGGTGGCAGTGTGGGAGGAGGCTCAGGCTC 1500
Qy 1501 TCTGCCCAACAGAGTGGCCCGCACGTGGGAAACATTTCTGGAGCTGGCCATCCCAATTCATCA 1560

Db 1501 TCTGCCACAGAGTCCCGCCACAGTGGAAACATCTCTGGAGCTGGCCATCCCAATTCATCA 1560
QY 1561 GTCCATAGAGACGAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
Db 1561 GTCCATAGAGACGAACAGAAATGAGACCTTCCGGCCCAAGCGTGGCGCTCGGGCACTTTG 1620
QY 1621 GTAGACTGTGCCACCGAGCGGTGTGTGTAACGTTGAATATAAAAGACAAAAAAA 1679
Db 1621 GTAGACTGTGCCACCGAGCGGTGTGTGTAACGTTGAATATAAAAGACAAAAAAA 1679

RESULT 29

US-09-978-665A-522
; Sequence 522, Application US/09978665A
; Publication No. US20030199437A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C19
; CURRENT APPLICATION NUMBER: US/09/978,665A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
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; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
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; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797

1	PRIOR FILING DATE: 1998-04-22	QY	1	GTGTGCTCTTTCAGCAAAACAGTGGATTTAAATCTCTCTGCAAGCTTGAGAGCAACAC	60
2	PRIOR APPLICATION NUMBER: 60/082796				
3	PRIOR FILING DATE: 1998-04-23	Db	1	GTGTGCTCTTTCAGCAAAACAGTGGATTTAAATCTCTCTGCAAGCTTGAGAGCAACAC	60
4	PRIOR APPLICATION NUMBER: 60/083336				
5	PRIOR FILING DATE: 1998-04-27	QY	61	AATCTATCAGGAAAGAAAGAAACCGAACCTGACAAAAAGAAAAAGAAAAAGAAAG	120
6	PRIOR APPLICATION NUMBER: 60/083322				
7	PRIOR FILING DATE: 1998-04-28	Db	61	AATCTATCAGGAAAGAAAGAAACCGAACCTGACAAAAAGAAAAAGAAAAAGAAAG	120
8	PRIOR APPLICATION NUMBER: 60/083392				
9	PRIOR FILING DATE: 1998-04-29	QY	121	AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAATCTATCTCTTGGGCAAT	180
10	PRIOR APPLICATION NUMBER: 60/083495				
11	PRIOR FILING DATE: 1998-04-29	Db	121	AAGAAAAAATCATGAAAAACCATCCAGCCAAAAATGCAATCTATCTCTTGGGCAAT	180
12	PRIOR APPLICATION NUMBER: 60/083496				
13	PRIOR FILING DATE: 1998-04-29	QY	181	CTTTCAGGGGCTGGCTCTCTGTGTCTCTTCCAGAGAGTCCCGTGGCGAGCGAGATGC	240
14	PRIOR APPLICATION NUMBER: 60/083499				
15	PRIOR FILING DATE: 1998-04-29	Db	181	CTTTCAGGGGCTGGCTCTCTGTGTCTCTTCCAGAGAGTCCCGTGGCGAGCGAGATGC	240
16	PRIOR APPLICATION NUMBER: 60/083545				
17	PRIOR FILING DATE: 1998-04-29	QY	241	CACCTTCCCAAGCTATGGAACACGTGACGGTCCGGCAGGGGAGAGCGCCACCTTCAG	300
18	PRIOR APPLICATION NUMBER: 60/083554				
19	PRIOR FILING DATE: 1998-04-29	Db	241	CACCTTCCCAAGCTATGGAACACGTGACGGTCCGGCAGGGGAGAGCGCCACCTTCAG	300
20	PRIOR APPLICATION NUMBER: 60/083558				
21	PRIOR FILING DATE: 1998-04-29	QY	301	GTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGGCTTAAACCGGAGACCATCTCTA	360
22	PRIOR APPLICATION NUMBER: 60/083559				
23	PRIOR FILING DATE: 1998-04-29	Db	301	GTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGGCTTAAACCGGAGACCATCTCTA	360
24	PRIOR APPLICATION NUMBER: 60/083500				
25	PRIOR FILING DATE: 1998-04-29	QY	361	TGCTGGGAATGACAAAGTGGTGGCTGGATCTCTGGTGGTCTCTTCTGAGCAACACCCAAAC	420
26	PRIOR APPLICATION NUMBER: 60/083742				
27	PRIOR FILING DATE: 1998-04-30	Db	361	TGCTGGGAATGACAAAGTGGTGGCTGGATCTCTGGTGGTCTCTTCTGAGCAACACCCAAAC	420
28	PRIOR APPLICATION NUMBER: 60/084366				
29	PRIOR FILING DATE: 1998-05-05	QY	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGGCGCTTACACCTGCTC	480
30	PRIOR APPLICATION NUMBER: 60/084414				
31	PRIOR FILING DATE: 1998-05-06	Db	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGGCGCTTACACCTGCTC	480
32	PRIOR APPLICATION NUMBER: 60/084441				
33	PRIOR FILING DATE: 1998-05-06	QY	481	GGTGCAGACAGAAACCAACCGGAGACCTCTAGGGTCCACTTCTTGTGCAAGTATCTCC	540
34	PRIOR APPLICATION NUMBER: 60/084637				
35	PRIOR FILING DATE: 1998-05-07	Db	481	GGTGCAGACAGAAACCAACCGGAGACCTCTAGGGTCCACTTCTTGTGCAAGTATCTCC	540
36	PRIOR APPLICATION NUMBER: 60/084639				
37	PRIOR FILING DATE: 1998-05-07	QY	541	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	600
38	PRIOR APPLICATION NUMBER: 60/084640				
39	PRIOR FILING DATE: 1998-05-07	Db	541	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	600
40	PRIOR APPLICATION NUMBER: 60/084598				
41	PRIOR FILING DATE: 1998-05-07	QY	601	CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTTACTTGGAGACACATCTCTCCCAAAGC	660
42	PRIOR APPLICATION NUMBER: 60/084600				
43	PRIOR FILING DATE: 1998-05-07	Db	601	CTGCATAGCAACTGGTAGACAGAGCCCTACGGTTTACTTGGAGACACATCTCTCCCAAAGC	660
44	PRIOR APPLICATION NUMBER: 60/084627				
45	PRIOR FILING DATE: 1998-05-07	QY	661	GGTTGGCTTTGTGAGTGAAGACGATCTTGGAAATTCAGGGGATCACCCGGGAGCAGTC	720
46	PRIOR APPLICATION NUMBER: 60/084643				
47	PRIOR FILING DATE: 1998-05-07	Db	661	GGTTGGCTTTGTGAGTGAAGACGATCTTGGAAATTCAGGGGATCACCCGGGAGCAGTC	720
48	PRIOR APPLICATION NUMBER: 60/085339				
49	PRIOR FILING DATE: 1998-05-13	QY	721	AGGGGACTACGAGTGCAGTGCCTCCATGACGTGGCGCGCGCGCTGTGTACGAGAGTAAA	780
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51	PRIOR FILING DATE: 1998-05-13	Db	721	AGGGGACTACGAGTGCAGTGCCTCCATGACGTGGCGCGCGCGCTGTGTACGAGAGTAAA	780
52	PRIOR APPLICATION NUMBER: 60/085323				
53	PRIOR FILING DATE: 1998-05-13	QY	781	GGTCAACCGTGAACCTATCCACCATATCATTTGAGAACCCAAAGGATACAGTGTCCCGTGGG	840
54	PRIOR APPLICATION NUMBER: 60/085582				
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56	PRIOR APPLICATION NUMBER: 60/085700				
57	PRIOR FILING DATE: 1998-05-15	QY	841	ACAAAGGGGACATGCGAGTGTGAGCCTCAGCAGTCCCTCAGCAGATTTCCAGTGTGA	900
58	PRIOR APPLICATION NUMBER: 60/085689				
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67	PRIOR FILING DATE: 1998-05-15	Db	961	CCTCTCAAAAATCATCTTTCAATGTCTGTGAACATGATATATGGGAACTACATTTGGT	1020
68	PRIOR APPLICATION NUMBER: 60/085697				
69	PRIOR FILING DATE: 1998-05-15	QY	1021	GGCTTCCAAAGCTGGGGCCACCAATGCCAGCATCATGCTATTGTTCAGGGCGCGT	1080
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71	PRIOR FILING DATE: 1998-05-15	Db	1021	GGCTTCCAAAGCTGGGGCCACCAATGCCAGCATCATGCTATTGTTCAGGGCGCGT	1080
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Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 30

US-09-978-802A-522

; Sequence 522, Application US/09978802A

; Publication No. US20030199674A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC20
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1679; DB 10; Length 1679;
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QY 181 CTTACGGGGCTGGCTGCTCTGTGTCTTCAAGAGAGTCCCGTCCGAGCGGAGATGC 240
DB |||||
181 CTTACGGGGCTGGCTGCTCTGTGTCTTCAAGAGAGTCCCGTCCGAGCGGAGATGC 240
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QY 301 GTGCATATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGGAGCAACATCTCTTA 360
DB |||||
301 GTGCATATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGGAGCAACATCTCTTA 360
QY 361 TGCTGGGATGACAGTGGTGGCTCGCTGATCCTCGCTGGTCTTCTGAGCAACACCAAC 420
DB |||||
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DB |||||
421 GCAGTACAGATCGAGATCCAGAACGTGTATGATGATGATGATGATGATGATGATGATGAT 480
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DB |||||
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QY 601 CTGCATAGCAACTGGTAGACAGAGCTACGGTACTTGGAGACACATCTCTCCCAAGC 660
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 15:29:05 ; Search time 144.763 Seconds
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6436.482 Million cell updates/sec

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	704.6	42.0	6075	4	US-09-023-655-1366
5	703	41.9	7000	4	US-09-851-896-3
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8	700.9	41.7	14770	4	US-09-220-132-30
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53	692.8	41.3	9535	4	US-09-562-702A-1
54	692.8	41.3	39982	4	US-09-820-924-3
55	692.7	41.3	7316	4	US-09-976-594-16
56	692.7	41.3	7705	6	5455158-2
57	692.6	41.3	8078	4	US-09-702-251-3
58	692.5	41.2	11673	4	US-09-334-220-3
59	692.5	41.2	13993	4	US-09-220-132-20
60	692.3	41.2	4131	3	US-08-726-214-11
61	692.3	41.2	6156	3	US-08-891-640-1
62	692.3	41.2	6378	4	US-09-620-312D-332
63	692.3	41.2	9848	4	US-09-385-222A-3
64	692.2	41.2	9164	4	US-09-205-817A-2
65	692.1	41.2	7679	4	US-09-220-132-38
66	692.1	41.2	7680	4	US-09-023-655-1289
67	692.1	41.2	7680	5	PCT-US95-09819-6
68	692.1	41.2	7705	1	US-08-259-569-16
69	692.1	41.2	7705	2	US-08-826-885-16
70	692	41.2	5421	1	US-08-118-441-28
71	692	41.2	5421	3	US-08-338-579A-28
72	692	41.2	5421	5	PCT-US94-09851-28
73	692	41.2	5433	4	US-09-562-702A-15
74	692	41.2	5433	4	US-09-561-818A-15
75	692	41.2	5613	4	US-09-562-702A-13
76	692	41.2	5613	4	US-09-561-818A-13
77	692	41.2	5613	4	US-09-561-709B-10
78	692	41.2	26664	4	US-09-564-805-28
79	691.9	41.2	13977	4	US-09-484-970B-60
80	691.8	41.2	14044	3	US-08-652-877-89
81	691.8	41.2	14080	3	US-08-652-877-87
82	691.8	41.2	14083	3	US-08-476-515A-83
83	691.8	41.2	14086	3	US-08-652-877-83
84	691.7	41.2	4003	3	US-08-991-840A-3
85	691.7	41.2	4610	4	US-09-417-822-4
86	691.7	41.2	7326	1	US-08-194-468-1
87	691.7	41.2	7326	4	US-09-514-247A-7
88	691.7	41.2	7326	4	US-09-686-316-1
89	691.7	41.2	7344	3	US-08-961-739-1
90	691.7	41.2	13146	2	US-08-724-354D-3
91	691.7	41.2	13146	3	US-09-270-984A-3
92	691.5	41.2	4648	4	US-09-620-312D-464
93	691.5	41.2	4651	4	US-09-417-822-3
94	691.5	41.2	14070	4	US-09-108-006C-2
95	691.4	41.2	12222	4	US-09-328-925-42
96	691.3	41.2	13930	4	US-09-976-594-1011
97	691	41.2	6951	4	US-09-023-655-1265
98	691	41.2	6951	6	5256642-1
99	691	41.2	6951	6	5472939-1
100	691	41.2	7313	4	US-09-620-312D-259

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Sequence 464, App
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Sequence 42, Appli
Sequence 1011, Ap
Sequence 1265, Ap
Patent No. 5256642
Patent No. 5472939
Sequence 259, App

ALIGNMENTS

RESULT 1

US-09-700-397-2
; Sequence 2, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIORITY APPLICATION NUMBER: JP 10-131815
; PRIORITY FILING DATE: 1998-05-14
; PRIORITY APPLICATION NUMBER: PCT/JP99/02485
; PRIORITY FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone OC001 derived from human brain
; NAME/KEY: CDS
; LOCATION: (130)..(1161)
; NAME/KEY: sig_peptide
; LOCATION: (130)..(213)
; NAME/KEY: mat_peptide
; LOCATION: (214)..()
US-09-700-397-2

Query Match 99.5%; Score 1671.3; DB 4; Length 1693;
Best Local Similarity 99.9%; Pred. No. 5.7e-26;
Matches 1673; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY	6	GTCTCTCAGCAAAACAGTGGATTTAAATCTCTCTTGGCAGACAGCTTGAGAGCAGCAATCT	65
DB	1	GTCTCTCAGCAAAACAGTGGATTTAAATCTCTCTTGGCAGACAGCTTGAGAGCAGCAATCT	60
QY	66	ATCAGGAAAGAAAGAAAG-AAAAAAGCGAACCTGCACAAAAAGAAAGAAAGAAAGAAAGAA	124
DB	61	ATCAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA	120
QY	125	AAAAAATCATGAAACCATCCAGCCAAATGCAATTTCTATCTCTTGGGCAATCTTC	184
DB	121	AAAAAATCATGAAACCATCCAGCCAAATGCAATTTCTATCTCTTGGGCAATCTTC	180
QY	185	ACGGGGCTGGCTGCTCTGTGTCTCTTCCAGGAGTGCCTGCGCGAGGGAGATGCCACC	244
DB	181	ACGGGGCTGGCTGCTCTGTGTCTCTTCCAGGAGTGCCTGCGCGAGGGAGATGCCACC	240
QY	245	TTCCCCAAGAGTATGGACAAAGTGAACGTCGCGGAGGGGAGAGCGCCACCTCAGGTGC	304
DB	241	TTCCCCAAGAGTATGGACAAAGTGAACGTCGCGGAGGGGAGAGCGCCACCTCAGGTGC	300
QY	305	ACTATTGACACCGGGTCAACCGGGTGGCTGGGTAAACCGCAGCAACATCTCTATGCT	364
DB	301	ACTATTGACACCGGGTCAACCGGGTGGCTGGGTAAACCGCAGCAACATCTCTATGCT	360
QY	365	GGGAATGACAGTGTGCTGGATCTCTGCGGTGCTCTCTGAGCAACACCCCAACGAG	424
DB	361	GGGAATGACAGTGTGCTGGATCTCTGCGGTGCTCTCTGAGCAACACCCCAACGAG	420
QY	425	TACAGCATCGAGATCCAGAAAGTGGATGTATGACGAGGGCCCTTACCTGCTCGGTG	484
DB	421	TACAGCATCGAGATCCAGAAAGTGGATGTATGACGAGGGCCCTTACCTGCTCGGTG	480
QY	485	CAGACAGACACACCCCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAA	544

DB	481	CAGACAGACACACCCCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAA	540
QY	545	ATTGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCACCTGC	604
DB	541	ATTGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCACCTGC	600
QY	605	ATAGCAACTGGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTT	664
DB	601	ATAGCAACTGGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTT	660
QY	665	GGCTTTGTGAGTGAAGACGAATACTTTGGAATTTAGGGCATCACCCGGGAGCAGTCAAGG	724
DB	661	GGCTTTGTGAGTGAAGACGAATACTTTGGAATTTAGGGCATCACCCGGGAGCAGTCAAGG	720
QY	725	GACTAGAGTGCAAGTGCCTCCAATGAGTGGCGCGCCCTGGTACGAGAGTAAGGTC	784
DB	721	GACTAGAGTGCAAGTGCCTCCAATGAGTGGCGCGCCCTGGTACGAGAGTAAGGTC	780
QY	785	ACCGTGAACCTATCCACATACATTTCCAGAGCCAAAGGTACAGGTGTCCCGTGGGCAA	844
DB	781	ACCGTGAACCTATCCACATACATTTCCAGAGCCAAAGGTACAGGTGTCCCGTGGGCAA	840
QY	845	AAGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAG	904
DB	841	AAGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAG	900
QY	905	GATGACAAAGACTGATTGAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTCTCTC	964
DB	901	GATGACAAAGACTGATTGAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTCTCTC	960
QY	965	TCAAAACTCATCTTCTTCAATGTCCTGAACATGACTATGGAAGTACACTTCGCTGGCC	1024
DB	961	TCAAAACTCATCTTCTTCAATGTCCTGAACATGACTATGGAAGTACACTTCGCTGGCC	1020
QY	1025	TCCAAAGCTGGGSCACACCAATGCCAGCATCATGTTTGGTCCAGGCGCGTCAGC	1084
DB	1021	TCCAAAGCTGGGSCACACCAATGCCAGCATCATGTTTGGTCCAGGCGCGTCAGC	1080
QY	1085	GAGGTAGCAACCGGCGAGTGCAGAGGGGCGGCTGCTGCTGCTCTCTCTCTCTCTCT	1144
DB	1081	GAGGTAGCAACCGGCGAGTGCAGAGGGGCGGCTGCTGCTGCTCTCTCTCTCTCTCT	1140
QY	1145	TTGCACCTGCTCTCAAAATTTGATGTAGTGCACCTTCCACCCCGGAAAGGCTGCCG	1204
DB	1141	TTGCACCTGCTCTCAAAATTTGATGTAGTGCACCTTCCACCCCGGAAAGGCTGCCG	1200
QY	1205	CCACCAACCAACCAACAGCAATGGCAACCGCAGCAACCAATCAGATATATA	1264
DB	1201	CCACCAACCAACCAACAGCAATGGCAACCGCAGCAACCAATCAGATATATA	1260
QY	1265	CAATGAAATAGAAAGAAACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAACAAAG	1324
DB	1261	CAATGAAATAGAAAGAAACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAACAAAG	1320
QY	1325	AATACTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAAAATTTGCTTGCAGATATTA	1384
DB	1321	AATACTTTGGGGGAAAGAGTTTAAAAAGAAATTTGAAAAATTTGCTTGCAGATATTA	1380
QY	1385	GGTACAATGAGTTTCTTTTCCAAACCGGAAAGAAACAGCAACACCCCGCTTGGACCCA	1444
DB	1381	GGTACAATGAGTTTCTTTTCCAAACCGGAAAGAAACAGCAACACCCCGCTTGGACCCA	1440
QY	1445	CTCAGAGTGCATCGTGCACCTTTTGGTGCAGTGTGGGCAAGGCTCAGCTCTCTCTG	1504
DB	1441	CTCAGAGTGCATCGTGCACCTTTTGGTGCAGTGTGGGCAAGGCTCAGCTCTCTCTG	1500
QY	1505	CCACAGAGTGCCTCCACCGTGGAACTTTGAGAGTGGCCATCCCAAAATTCATCAGTCC	1564
DB	1501	CCACAGAGTGCCTCCACCGTGGAACTTTGAGAGTGGCCATCCCAAAATTCATCAGTCC	1560
QY	1565	ATAGAGACGAAAGATGAGACCTTCGGGCCCAAGCGTGGCGTGGGCGACCTTCTGTAG	1624

Db 181 AGCAACACCCAAACGAGTACAGATCAGATCAGAACTGGATGTGTATGACGGGC 240
QY 467 CTTTACACCTGCTGGTGCAGACAGACACACCCAAAGACCTCTAGGGTCCACCTCAT 526
Db 241 CTTTACACCTGCTGGTGCAGACAGACACACCCAAAGACCTCTAGGGTCCACCTCAT 300
QY 527 GTGCAAGTATCTCCAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 586
Db 301 GTGCAAGTATCTCCAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 360
QY 587 AATATTAGCTTCACTGCATAGCAACTGGTAGACAGAGCCTAGGTTACTTTGAGACAC 646
Db 361 AATATTAGCTTCACTGCATAGCAACTGGTAGACAGAGCCTAGGTTACTTTGAGACAC 420
QY 647 ATCTCTCCCAAGGGTGGTGTGTAGTGAAGACGAATCTTGGAAATTCAGGGGCATC 706
Db 421 ATCTCTCCCAAGGGTGGTGTGTAGTGAAGACGAATCTTGGAAATTCAGGGGCATC 480
QY 707 ACCGGGAGCAGTCAGGGGACTACAGTGCAGTGCCTCCCAATGACGTGGCGGCCCGGTG 766
Db 481 ACCGGGAGCAGTCAGGGGACTACAGTGCAGTGCCTCCCAATGACGTGGCGGCCCGGTG 540
QY 767 GTACGGAGTAAAGGTCAACGTTGAACTATCCACATACATTTGAGAAAGCAAGGTACA 826
Db 541 GTACGGAGTAAAGGTCAACGTTGAACTATCCACATACATTTGAGAAAGCAAGGTACA 600
QY 827 GGTCTCCCGTGGGACAAAGGGGACACTGAGTGCAGTGCCTCCCAATGACGTGGCGGCCCGGTG 886
Db 601 GGTCTCCCGTGGGACAAAGGGGACACTGAGTGCAGTGCCTCCCAATGACGTGGCGGCCCGGTG 660
QY 887 GAATTCAGTGGTACAAAGGATGACAAAGAGCTGATTGAAGAAAGAGGGGTGAAAGTG 946
Db 661 GAATTCAGTGGTACAAAGGATGACAAAGAGCTGATTGAAGAAAGAGGGGTGAAAGTG 720
QY 947 GAAACAGACCTTTCCTCTCAAACTCATCTCTTCAATGTCTCTGAAACATGACTATGG 1006
Db 721 GAAACAGACCTTTCCTCTCAAACTCATCTCTTCAATGTCTCTGAAACATGACTATGG 780
QY 1007 AACTACACTTTCGCTGGCTCCCAAGCTGGGACACACCAATGCCAGCATCATCTATTT 1066
Db 781 AACTACACTTTCGCTGGCTCCCAAGCTGGGACACACCAATGCCAGCATCATCTATTT 840
QY 1067 GGTCCAGGCGCGTCAGCGAGGTGAGCAACGGCAGCTGCGAGGGGCGAGGCTGGCTGG 1126
Db 841 GGTCCAGGCGCGTCAGCGAGGTGAGCAACGGCAGCTGCGAGGGGCGAGGCTGGCTGG 900
QY 1127 CTGCTGCTCTTCTGCTTGCACCTGCTTCTCAATTT 1165
Db 901 CTGCTGCTCTTCTGCTTGCACCTGCTTCTCAATTT 939

RESULT 4

US-09-023-655-1366
; Sequence 1366, Application US/09023655
; Patent No. 6607879

GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HEREWITH

CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1366:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6075 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENE BANK

; CLONE: G35787

; US-09-023-655-1366

Query Match 42.0%; Score 704.6; DB 4; Length 6075;

Best Local Similarity 36.8%; Pred. No. 0.00033;

Matches 1443; Conservative 0; Mismatches 159; Indels 2320; Gaps 411;

QY 1 GT-----TGCTCTCTTCAG-----CAAAAC 20
Db 2110 GTGAGAGATGT-TCTTCAGCTCCCTCAGCCAGCGCGCTCTACCGTGACCATTAAC 2168
QY 21 -----AGTGG-----ATTTAAT--CTCCTTGCA--CAAG-----CT----- 48
Db 2169 TACAAGGAGTGGCAAGTATGAAATCACTCTT-CAGCCAGAGCGGACAGTCCCTGACA 2227
QY 49 ---T-----GAG-----AGCAACACA-----A-T-CTAT----- 67
Db 2228 AAGTCCAGGAGTCAGCTGTGTAGCACTCAGCCAGGAGTACTATTTAAGGGTATCTCGGG 2287
QY 68 -----CA--GGAAA--GA-----AAG-----AAAGAAAAAACCGAACCT 98
Db 2288 TGATGCCACTGGAGACTTTGATCACTATGAAGTCACTTAAACAAAAAC--AACTT 2345
QY 99 GA--CAA--AAAAG-----A--AGAAAAAGAA----- 119
Db 2346 CATTCAAACTAAAGGCAATCCCAAGTCAGAAAAAGAAATGTGTATTTTTCAGCTAGTCCC 2405
QY 120 --GA-----AG-----AAAAA--A-AATCATGA-----AAC 141
Db 2406 TGGACGGTTGTACAGTGTCTACTTTACTACAAAGTGGACAAT-ATGAAGCCCAATGAAC 2464
QY 142 -----CA--TCC--AGCC--AA-----AA-AT--GC-ACA-----A 162
Db 2465 AAGGGAATGGAGAACAAATTCAGAGCCTCTTAAGGATCTAACATTTGCCAACAGGACA 2524
QY 163 TT-----CT---ATCT--CTTGGGCA--ATCTTCACGGGGCTG----- 193
Db 2525 CTGAGGACTTGCATGTGACTTGTGTGAGGAGC-TAATGGGGATGTGACCAATATGATC 2583
QY 194 --GCTGCTCT--GTGT--CTC--TTC-----CAA-G 215
Db 2584 CAGTCTCTCAATGACATGAAGATTTCTCTCTTTTTCCTTTTGTAAATACCGAAC 2643
QY 216 GAGT-----GCC-----CGTG-GCG-- 229
Db 2644 GAGTATGATTTACTTCCCTTAACACAGCGCGCCCAATACAAATTTCTTGTCTTGAGATT 2703
QY 230 AGCGGAGAT-----GC--CA-CCTTC-----CC-----CAAA 253

Db 2704 AGCGGGATGTACAGCAGTCTTCAITTAGGGCTTACAGTCTCTAGTGTGTCAAA 2763
QY 254 -----GCT-----ATGCA-CAAC-----G-TGACGGT-----CCGGCA-----279
Db 2764 AATAATTCACATTTCTCCATGAGCAACAGATAGCTTACGGTGAAGTGG-ACTCCTGG 2822
QY 280 -GGGGAGAGCG-----CC-ACCC-----TCAGG-----TG-----303
Db 2823 TGGGGGAGA-CGTTGATTCTACACGGTGTGCGCAATTCAGGCACAGTCAAAAGTTGACT 2881
QY 304 --C--ACTATT-----G-----ACA-----A-CCGGG-----320
Db 2882 CTCAGACTATTCCAAGCAGCTCTTTGAGCACAGCTTCCACAGCTGGAGGCGGGGAGC 2941
QY 321 -----TCA-----CC-----CGGGTGGCTG-----GCTAAA-----342
Db 2942 AGTACCAGATCATGTTGCTCAGTCAGCGGT-CCCTGAAGATCAGATTAATGTGGTT 3000
QY 343 ---CCG-CAG---CACATC-CTC-----TA-TGCTGGGAATG---ACA-AGT-----377
Db 3001 GGGCGACAGTTCACGATCTGTCCAAAGGAGTAATTGCAGACAAATGCATACAGCAGTTAT 3060
QY 378 -----G--GT-----GC-CTGG-----ATCCCTGCG-394
Db 3061 TCCCTTAATAGTAGTTGGCAAAAGCTGTGTGGTGGCAAGATATATATCTCT-GCT 3119
QY 395 -----G-----TGG-TCTTCTGAGCAACAC-----CCA-----AAC-420
Db 3120 TCTAAGTAAATGGAATCTTCTGCGCAACATCAGAGCCAGCCACCACTAAGCAACA 3179
QY 421 -----CGAG---TA-CA-GC-----AT-CGAGATCCAGA-----AC-----GTGG-449
Db 3180 CAAATTTGAAGATCTAAACACCGGCAAGAAATACAGATACAGATCTCTAACTGTCTAGTGG 3239
QY 450 A---TGCTATGACGAGG-GCCCTTACACT---GCTCG-----GT-----GCAG-----487
Db 3240 AGGCTCTTTA-G-CAAGAGAGCCC---AGA-CTGAAGGC---CGAACAGTCCCGAGCAGTGT 3293
QY 488 -----ACAGACAA---CCACCCAAAG---ACCT-----CTAGGGTCC 518
Db 3294 CACCGACCTGAGGATCAGAGAGACTCCACC---AGGCACCTGTCTCTCCGT---GGACC 3348
QY 519 ACCTCA-----TTGTGCAAGTATCT-----CCCA-A-----AAT-T 547
Db 3349 GCCTCAGAGGGGAGCTCAGCTGGTACAA-CATCTTTTGTACAAACCCAGATGGGAATCT 3407
QY 548 ---GTAGAGA-T---TT---CT---T-CAGA---TATC---TCCATTAA-TG-----578
Db 3408 CCAGGAGAGAGCTCAGTTGACCCACTAGTCAGAGCTTCTCTTTCCA-GAACTTGTCTAC 3466
QY 579 AAGG-GA---ACAAATAT-----TAGCCTCAC-----CTG-C--AT-AG---608
Db 3467 AAGGCAGAAATGTACAAGATGGTATGTGA-ACTCAGTGGGGAGCTGTCTAATGAGTCT 3525
QY 609 --CA-A-CTGGTAGACCAG---AGCTTACGGTTACTTGGAGACATCTC-----TCC 654
Db 3526 TTCATATTGGTAGAACAGTCCAGCCT-CTGT-----GAG--TCATCTCAGGGGGTCC 3576
QY 655 CAAAGCGG-----TTGGCTT---TGTGAGTGAAGAC-----GAAT-686
Db 3577 --AATCGGNACAGCAGACAGCAGCTTTGG-TTCAACTG-GAGTCCAGCCTCTGGGGACTT 3632
QY 687 ---ACTT-----G-GA-----AATTC---AGGCATC-----ACCCGGGAGC 716
Db 3633 TCACITTTTATGAGTGAATCTCTATTAATCCCAATGGCA-CAAAGAAGGAATCTGAA--3689
QY 717 AGTCAGGGGACT-AC-GAGT-GCAGT-----GCC-----TCC---AATG-----AGTGGC 756
Db 3690 AGACAAGGACCTGACGGAGTGGCGGTTTCAAGGCTTGTCTCTGGAAGGAAGTACGT-GC 3748
QY 757 CGCGCCCGTGGT-----AC---GGAG-----AG---TAAAGCTCAC---CG-----TGAA 792
Db 3749 TGTG-GGTGGTAACTCACAGTGGAGATCTAGCAATAAA-GTCACGCGGAGAGCAGAA 3805

QY 793 CTA-TCCA-----CCA---TA---CATTT---CA-G-AA-----GCC 817
Db 3806 C-AGTCCCAAGTCTCTCCAGTCTTATGTCAITTTGCTGACATTCACAAACATCTCTTGGCC 3864
QY 818 A-A-GGGTACAGGTGTCTCCC-G-TGG---GAC-AAAAGGGGAC---A-CTGCAAGTGT 862
Db 3865 ATCAGTGGAAAGG-GCCCCAGACTGGACAGACTACAA-CGACTTTGAGCTGCAAGT-3920
QY 863 GAAGCCTCA-GCA-----GT-----CCCCCT---CAGCAG-AAATTC-----892
Db 3921 GTTGGC-CAGAGATGCATCTTACTGTCTTCAACCCCTTACAAACACAGAAATCAGAGGAC 3979
QY 893 -CA-GTG-----GTACAAGATGA-----CAA-----AAGAC-----917
Db 3980 GCATTTGTATAGTCTTGTCTCCAGGA-GATCTATCAATCAACGTCAAGATGTCTCACT 4038
QY 918 --TGATT---GAAGGAA---AG-AAA-----GGG-----GTG-----AAG--TG 946
Db 4039 GGTGATTCCTGGAA-AACTTACAGCAACCAATTTTGGATCTGTGAGGACAAAGCCTG 4096
QY 947 ---GA---AAACAGACTT---TT-CC---TCTCAAAACT-----CAT---C---TTCTT 981
Db 4097 ACAAGATACAAA---ACCTGCAATTCGGCCTCAGAACTCCACGGCCATTTGCTGTCTT 4153
QY 982 CAATGTCT-CTGA-----AC-----ATG-----ACTAT-----GGGAAT-ACAC--1014
Db 4154 GGATCCCTCTCTGATCTGACTTTGTATGTTATAGTATTAATGCGCGGAAATGAGACACC 4213
QY 1015 ---TTGCTGGCTCCACAAAGCTGG-GCCACACAA---TGC-CAGCATC---AT 1059
Db 4214 AAGAAAGTTGAGT--TTTCCAGAAAGCTGGAGAAAGAAATCTCTGCTCAACATCATGAT 4271
QY 1060 GCTATT-----TG-GTCC-----AG-GC-----GCGG---T---CAG 1083
Db 4272 GCTAGTGGCCCATAGAGGTACTGTGTCTTCCATCAAGTGCAGTGGCGGCGCATGACCAG 4331
QY 1084 CGAGGTG---AGCAACGGGACGT---CGAGGAGGGCAG---GC-----1117
Db 4332 CGAGGTGGTTGAG-ACAGCAC-TATCAATGA---TAGACCGCCGCCCTCTCCACG 4385
QY 1118 ---TGCGTCTG-----GCTGCT---GC---CT-----CTT---1138
Db 4386 CCCACACATTCGTGTGAATGAAAGGATG-TGCTAATTAGCAAGTCTTCCATCAACTTTA 4444
QY 1139 CTGGTC---TTGCACCTGTCTC-----TCAAT-TT-----1165
Db 4445 CT-GTCAACTGCAGCTGTTTTCAGCGACACCAATGGAGCTGTGAATACTTTCACAGTGGT 4503
QY 1166 ---TGATG---TGAG-T---GCCA-----CT-TCC---CC 1186
Db 4504 GTGAGAGAGGCTGTGCGCAGTGTGAGTGTGAAGCCAGACAGCAGCAGCCTCTCCCTCC 4563
QY 1187 -ACCCGG-G-AAAGC---TGCGGCCA-----CCACC 1212
Db 4564 TACCTGGAGTACAGCAACATGCTTCCATTCGGGTGTATCAGACTAATTTATTTTGGCAGC 4623
QY 1213 A-----CC---A-CC-AACA-CAAC-----AGCA---1230
Db 4624 AATGTGCCGAAATCTTAACAGCAACTCCAAGAGTTTAAACATTAAGCTTTGGAGCAGAG 4683
QY 1231 ATGG---C-----AACAC-CGA-----CAGCAA-----1249
Db 4684 ATGGAGACTTAGGTGGAAAGCGATCCCACTCAGCAAAATTTCTGTGTGAGGACCACTG 4743
QY 1250 -----CC-----AATCAG-AT-A---TATACA-A-----ATGA---1271
Db 4744 AAGCCACACACTGCTCAGAAATCAGCATTCAGAGCTTTTACACAGCTCTTGTATGAGGAC 4803
QY 1272 -----AATT-----AG-----A---AGAAACA-----1285
Db 4804 CTGAAGGAATTCACAAAGCCACTCTATTTCAGACACATTTTTTTTCTTTTACCATCACTACT 4863

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QY 1286 ---CAG---CCT-----C 1292
Db 4864 GAATCAGAGCCCTTGTGGAGCTATTGAAGTGTGAGTGTGCTGCTGCTTTTAAATTGGC 4923
QY 1293 ATG-----G-GACAGAAATT-----TG----- 1308
Db 4924 ATGCTAGTGGCTGTGTTGGCTTATTGATCTGCGACAGAGAAAGTGAGCCATGTCGAGAA 4983
QY 1309 AG-----G-CAG-----GGGAACAAGA-----AT-----ACTT----- 1331
Db 4984 AGACCTCTGCCGCTCTGAGCATTCGTAGGATC--GACCATTAATGTGTCCTTAAC 5040
QY 1332 -TGG-----GGAA-----AAGATT-TT-----A-AAAAAGAA-----TTGAA--- 1364
Db 5041 CTGGCCAGAGAAGGTAAACGGAAACTTCTTGTCCATAAATAAATCACTTTGAAGGG 5100
QY 1365 -AATT-----GC-----CT--TGCAGATA--TT--T--AGG--TAC----- 1389
Db 5101 CATTTCAAGCTACAGGCTGACTCCAACTACCTTCTATCCNAGGAATACGAGGATTA 5160
QY 1390 AA-----TGG-----AGT-----TT-----TCTT----- 1403
Db 5161 AAAGAGTGGCCGGAACCACTCATGTGACATTCGACTCTTCCGGAGATAGAGGAAA 5220
QY 1404 -----TT-CCCA-----ACGGGA-----AGA- 1419
Db 5221 AATCGATACAAATATATTGCCCTATGATGCCAGCGAGTGAAGCTCTCCAATGTAGAT 5280
QY 1420 -----ACA-----CAGC-ACA-CCC-GGC----- 1435
Db 5281 GATGATCTTGTCTGACTACATCAATGCCAGCTACATCCCTGGCAACAACCTCAGAAGA 5340
QY 1436 -----TT-----GGACC-----CACTG-----CAAG-----CTG-----CATCGT 1460
Db 5341 GAATACATTTGCTACTCAGGACCGCTTC-CTGGACCACAGGATGACTTCTGGAAATGGT 5399
QY 1461 G-----CAACTCTT--TGGTG--CCAGTGT-----GGGC----- 1486
Db 5400 GTGGGAACAAACGTTCAACAATCGTCTGATGGTGACCCAGTGTGTTGAGAAGGCCGAGT 5459
QY 1487 -AAG-----GGCTCAG-----CCTCT-----C 1502
Db 5460 AAGTGTGACCATTTACTTGGC-CAGCGACACAGGATTCCTCTACTATGGGACCTCATCC 5518
QY 1503 TGC-----C-CACAGAT--GCC--CC--ACGTGGAACATTTCTGG----- 1536
Db 5519 TGCAGATGCTCTCAGAGTCGCTGCTGCTGA-GTGGACCATCCGGAGTTTAAGATATGC 5577
QY 1537 -----AGC-TG-GC-----CATC--CCAAATTCA--AT-----CA 1560
Db 5578 GTGAGGAACAGCTTTGATGACACAGACTCATCGGCCACTTTCATATACGGTGTGGCCA 5637
QY 1561 GTCCATAGAGAC--GAA-----CA-----GA--A-----TGAGACCT----- 1588
Db 5638 GACCATGAGTCCAGAGAACCCACCTGCTCTGATCCAGTTTGTGAGAACTGTCAAGGAC 5697
QY 1589 --TC-----C-GGCCCAAGC-GTG--GCCGTGC-----GG 1612
Db 5698 TACATCAACAGAACCCGGGTGCTGGGCCCA--CTGTGGTGCACTGCAGTGCTGGTGG 5755
QY 1613 GCA-----CT-----TTGG-----TAGACT----- 1627
Db 5756 GTAGGACTGGAACCTTTATTGCAATTTGAGCCGAATCTCCAGAGTTAGACTCCAAAGACT 5815
QY 1628 -----GTGC-----CAC-----CAC--GG----- 1639
Db 5816 CTGTGGACATTTATGAGCAGTGCAGGACCTTAAGACTTCACAGGGTTCACTGGTCCAGA 5875
QY 1640 C---GTGT--GT-TGTGAA---AC-----GTGAATAAAA-----AGACAA-AA 1674
Db 5876 CTGAGTGTCAAGTATGTCTACTACATCAGTGTG--TAAGATGTCTCTCAGAGCAAGAA 5932
QY 1675 A-----AAAA 1679
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Db 5933 AGCTACGGAGTGAACAAGAAA 5954

RESULT 5

US-09-851-896-3/c
; Sequence 3, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RIS-0220
; CURRENT APPLICATION NUMBER: US/09/851,896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
; LENGTH: 70000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-851-896-3

Query Match 41.9%; Score 703; DB 4; Length 70000;

Best Local Similarity 40.5%; Pred. No. 0.031;

Matches 1394; Conservative 0; Mismatches 196; Indels 1854; Gaps 388;

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QY 1 GTTG-----TG-----TCCT-----TCAG-----CAA 17
Db 49493 GTTGGCCAGGCTGCTCTCGAATCTCTGGCTCAGGTGATCTGACCATCTTGGCCTCCAA 49434
QY 18 A-----A-----CAG-TGG-----ATTT-----AAAT 33
Db 49433 AGTGTGTTGTACACGAGCCACTGACAGCTGGCCAGTTATTTTAAAGTTTTTAAAAAAT 49374
QY 34 CTCCTT-----GCACA-----A-GC-----TTG----- 50
Db 49373 TT--TTAATTTTAATTTTGTGGGTACATAGTAGGCATATATATTATTATTATTATTT 49316
QY 51 ---A-CA-----GCA-----ACAC-----AA--TCTATCA-GG-AA--AG-- 75
Db 49315 TAAATGAATTAATTTTGAATTTTCAACATTTTAAATTTCTAAATGTTAAATATAGAT 49256
QY 76 AAGAAA-----GA-AAAAACC-----GAACCTGACAAAA--AGAAGAA 114
Db 49255 AAGAAAAATCCAGATGATTAATAAATCTTTGTGATCTT--CAATAATTTTTCAGAGTATA 49198
QY 115 AAGAAGAAAGAA-----AAAAATCATGAAAC-----CA-TCCA-----GCC- 150
Db 49197 AAG-GGATCAATAGAGCCAAAGAACTTGAGAACTGCTGAGTTAGATCATTCNAGGGCCC 49139
QY 151 -----AAAAATG--CAAAAT-----CTAT-----CTCTT 173
Db 49138 ACCAGTGTCAAAATGTCCACAGTTTCAAAATGAATAATTTATAGTTTCAGCCTTTT 49079
QY 174 GGGCAA-----TCTTC-ACG-----G-----CTGGCTG-CTC--TGT 203
Db 49078 GGGCAACAACTCTCTTCCAGTTTGTGACCTTTGGTATATAAAACAGGATGTCTCTGAATGT 49019
QY 204 GTCTCT--TCCAAG-----GAGTGCCCGTG-----CGCA-----G--CGAGATGC 240
Db 49018 GTC-CTGATC--AGCTTTTAGAT--CCCGGGGTCTCTCATGTTCTGTCATCTAGA--C 48965
QY 241 -C-----AC--CTTC--CCCAAA-----GCTATGGACAACGTG--ACGGT--C- 274
Db 48964 TCAGTAAACAGACTTCTGTACATACGGTATTCTATAGAAAACGTGCACACGGTGGGGC 48905
QY 275 CGS-----CAG-----GGGG-----AGAGCG-----CCACCTTC 298
Db 48904 CGGTGGCTCACGCCCTGTATCCACAGACTTTGGGGTGCCAG-GCGGGTGGATCA---TG 48849
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QY 299 AGGTGCACTA--TTGA-----CAAC-CGGG--TC---ACCGGGTGGCC--- 334
Db 48848 AGGT-CAGGAGTTTGAGACAGCCTGGCCACACACAGAGTTTCAGACACAGCCTGGCCAAAC 48790
QY 335 -TGG-----CTAA-----AC-----C-----GCA-----GCAC----- 351
Db 48789 GTGGTGAACCCCGTCTCTACTAAAAATACAAAATTAGCTGGGCATGGTGGCAGCTGCC 48730
QY 352 --CA-TC---CT-CT---ATGCTG-GGAATGACAA----- 375
Db 48729 TGCAGTCCAGCTACTTGGAGGCTGAGGAGGAGAAATCGCTTGAACCTGGGAGCGGAG 48670
QY 376 ---GTGGT-GCCTGGATC-----CTC--GCCTGG-----TCCT 402
Db 48669 GTTGTGGTGGCGGAGATCGCGCACTGCACCTCCAGCCTGGGCGACAGTGGCGAGACTCCA 48610
QY 403 TCT-G-----AG--CA--ACACCA-----AACGCACTA----- 426
Db 48609 TCTCGAAAAAAGAAATACATGCACACACATATGTCTGTAAACACAGTAACGTCCTCTCT 48550
QY 427 -C-AG-----CA--TCGAGAT-----CCAGAACCT----- 447
Db 48549 GCTAGGTTAATATGTTCTACTCTAGATGTGTAAACACACAGTAAGGCTTTGAGGGCA 48490
QY 448 GGA--TGCTG---AT-----GACGA--G---GGC-CCTTACAC---CTGCTCGG- 482
Db 48489 GGAACCTGTGTTCTATAATAAACAACGAATATGCTTGGCAGCTGCGACAGGCTGCTGGGC 48430
QY 483 TGCA-----GACAG-----ACACACACCA---AAGA----- 506
Db 48429 TGCACACTCAGGCTTGGCTGCGAGGATCTTACAGCCTCCAGGGAAGATGAGAGCAACA 48370
QY 507 -----C-----CT--CTAGGGTC-----CACCT- 522
Db 48369 CCGGACCACTGAGGAGACAGGATGCTCTACCTGGGCCAGGTACTGCGTGTGTCACTTA 48310
QY 523 --CAIT-----GTG--CAAGTATCTCCA-AAATTTGAGAGATTTCTT--CAGATA- 566
Db 48309 GACATTTCTGTAGAGGTGACCAAGTGTCCACCATTAATTTTCCACAACCTTTCCAGATAA 48250
QY 567 ---T---CTCCATT--A-ATGA-----AGG-GA-----ACA----- 587
Db 48249 GTATTGACACCACTTTTCCAGATGAGGAAATCGAGGCTGACAGGTGACATGGCTGTCT 48190
QY 588 -----A---TAT-----TAG-----CCTCACCTG-CAT--AG--CA--- 610
Db 48189 CAGGCGCAGTCTATGCCAGAGCTGTCATTTTCTCTCTGTCGCAATGAGTGCCTCAAT 48130
QY 611 -----ACTGGT-----AG--ACCGAGCCTAC-----G-GTTACTT---G-GAGA 643
Db 48129 GGGGACACAGGTGGAAAAAGGTACCAACAGCACAGAGGAGTGTGTATTTTGGGCTGAGA 48070
QY 644 ----CACAT-----CTCTCCCAA-----AG-C-GGT-----TG-GCTTT--GTG-- 673
Db 48069 GGGGACCTTGGAGGCT-TCCTGAGGAGGAGTCAAGGCTCACTGAGCTTTGGGTGGG 48011
QY 674 -AG-TGA-----A--GACGA-----ATAC--TTGAA-----ATTGAG 700
Db 48010 AAGATGATTGGAGCAGCTGACATAGGAGGAGGACAGTGGGAGGAGGCTCCAGTCCG 47951
QY 701 G-----GCAT---CACCGGG-----A-GCA-GTCA--GG-----GSACT-A 729
Db 47950 GACAGCCCTCTGCTATTTCCACCGGGGCCCCACAGGCGAGCAGACACGCGCTCGGCTCA 47891
QY 730 -CGA-----GTGCA-----GTGC-CTCCAATGACGTGG-----CCGCG--- 760
Db 47890 CCGCATGCGCCAGGTGACGGGGGTGTTCCTCGTCTCTCC-----G-CG-GGCATCGCGGT 47836
QY 761 ---CCGCTGG-----TACGG-AGAGT-AAAG-----G--TCAC-----CGTG 790
Db 47835 GGGCCCGTGGGTGACGAGCACTATGACAGTCAAGCGGTGTCGATCAGCGCACCGCAGCTG 47776
QY 791 AA-----CTATCCACCACATACA-----TTTCAGAA----- 814

Db 47775 CAGGGCGGTGTTCCCGCGGAGCTGTGTGTACGTTGACGCCCGGTTTCAGCAGCAT 47716
QY 815 ----GCCA-----AGG-----GT-----ACAGG-----TG----- 830
Db 47715 GCGGGCCATCTCGGGAGACGGTCAAGCTGAGTTAGCACAGGCACTCGGGGAGCTGCCGC 47656
QY 831 TCCCGTGGGACAAAGGGGACACTG-CA-----G---TGTAAGCTT-CAGAGT-C--- 877
Db 47655 ACCCC--GGGACA--CGTGGGCACTGCCACTTCTGCTCTGAGAGGCTTACAG--GTACTG 47602
QY 878 -----CCTCAGC-AGA-ATTCCAGTGGTA-----CA-----AG----- 904
Db 47601 GATGTTGAAAGCGCT-AGCAAGAGGATTCAGGGGCAAGGCCCACTGTCTAGGGGGGCC 47543
QY 905 --GA-TG-----A-CA--A---AAGACTGATTTGAAG-----AAAG--AAAG- 935
Db 47542 TAGACTGCTCCCATCCCATCAGCATCCCAAGACT-----AGGACAAAAGCCAAAGA 47489
QY 936 -G-GGTGA-----AAGTGGAAAC-----AGACCTTTTCT-----CTCA--AACTCA- 974
Db 47488 TGTGCTGACTGTTTAAAGG-----CTTCTGTCTCTTTCTCTAGTGC-CAACAGAACCCAC 47434
QY 975 TCTTCTT-CAA-----TCTCTCTCAA-CA-----TG-A----- 999
Db 47433 TCTCTTGCAAAGGCTCTCTGGGGCCTGTC-CTGAGACACCCCGCTCCCTGCATCCCTC 47375
QY 1000 -CTATGGGAAC-----TA-----CACTTG--CGTGG-----CCT-- 1025
Db 47374 CTT--GGAAACCTGCAAAAGGTATCACCTCTCCTCTGGGCTTTGGCAATGACATCCCTGG 47318
QY 1026 ----CC-----AACA-----AGC-----TGG-GCCACA-----CCAATG- 1049
Db 47317 CAGAGCTTGGGAACAAGGAGGAGCCTGGCTTTGGAGTCAACAGCTGAGCCCAAGC 47258
QY 1050 CCAG--CA-TCAT-----GCT-----ATT--TG-----GT--CCAGCGC-CGTC 1081
Db 47257 CCAGCTTCACTCATCCAGCTGCTCGCTTGGATGGGTCACTGTAGCATGTGCACTTC 47198
QY 1082 AG-----C-----GA--GG--TG--AG--CA--ACGGCACGT-----C----- 1104
Db 47197 AGGGCTTCTGTGAAGATGGGAATGCAAGTCCCACTCACAGCATGTGATGACATGAT 47138
QY 1105 GA-----GG-AGGC--A-----GGC-----TGC-----GT--C 1123
Db 47137 GACCAACCTACAGGAAGGCGCTGACTCGGTGTCGGCTCTCGATGAGAGTACCC 47078
QY 1124 T--GGCT-GC--TG-CCT--CTTCTGG-----TC-----TTG-----C---AC-CTG 1153
Db 47077 TGAGGCTGGCAGTGGCTCTCTCTGCGCCCATCATATTGAGAAGTAGGCCATGAACTCTG 47018
QY 1154 -----C-TTC-----TCAAAATTTGAT-----GTGAGTG--CCA-----CTTCC--CC 1186
Db 47017 GGGCATCCCATTTCTGTCAAGCTGTGCTTCTGTGTGA-TGAGACCAAGAGGCTCTCATCC 46959
QY 1187 ACCC-----GGGAA-----AG-GCTGCC--GCCA----- 1207
Db 46958 TCCAGGAGGACAGAGCTTAGCTTAGGGGAAGAACTCAGAGGATGCCAGCAGGCTC 46899
QY 1208 -----CCACCACCAACCAACAGCAATGGCAACACCCAGCA 1248
Db 46898 CTTGTGTGAGCTAGGCCCGCCAGCACCACCAC--CA-CCAT--CATCAT--CATCA 46846
QY 1249 --ACCA-ATCA---GAT-----AT-AT-A---CAA-ATGA---AATTAGAAG----- 1280
Db 46845 TCATCATCATCTTGTGATGTTAATATGATGTCACTTGTGATTTGAGT-GAAGGATGT 46787
QY 1281 AAA-----CACAGC-----TCAT-----GGG-----AC--AG--AA-ATTGA 1309
Db 46786 AAGATATTGAC--CCTGGGTGTGTC-TGAGAGGCTGTGCTAAACGAGATTAACTTTGA 46730
QY 1310 G---GGAGGGGAA--CAAAGA-ATA--CTT-----TGGG-GGG-----AA--A----- 1341

Db 46729 GTGAGTGGGGAAGGC--AGACCTACCTTAATCTGGGTGGGCAACCACTAATCAGCTGC 46672
Qy 1342 -AG-----AG-TTTTAAA-----AAGAAT-TGAAA-----TT-GC 1370
Db 46671 CAGACGCCAGATATAGAGCAGCAAGAAATGTGAAGGCTAGACTGGCTTAGC 46612
Qy 1371 CTTCGAG-----ATATTT---AGGTACAAATGGAGTTTCTT---TTCC--CAACGGGA-- 1416
Db 46611 CTCCAGCCTACATCTTCTCCGGTGC--TGGA--TGCTTCCTGCCCTCAAC--ATC 46560
Qy 1417 AGA--ACA-----CAGCACACCGG--CTTGAC-----CCAC-----TGC 1448
Db 46559 AGACTCCAAGTCCTTCAGC--TCTGGGACTTGGACTGGCTTCTCTGCTCAGCTTGC 46503
Qy 1449 AA--GC-----TG--C-----ATCGTG-----C-----AA--CCCTTT 1470
Db 46502 GATGGCCTATTGTGGGACCTTGTGATCTGTGAGTTAATGCTCTTAAATAATCCCTTT 46443
Qy 1471 TGGTGCCAGTGGGCAAG--GGCTCA--GCCTCTCTGCCCA--CA-----GAGTGCC-- 1517
Db 46442 TAG--GCCA-----GGCAGGTGGCTCAGCCTATAATCCAGCACTTTGGGAG--GCCAAG 46390
Qy 1518 -CAGTGCAGTGGGCAAG--GGCTCA--GCCTCTCTGCCCA--CA-----GAGTGCC-- 1557
Db 46389 CAGGAGATCAGCAGG-----TCAGGAGATCGAGACCATCTCTGGCTAACACGGTGAAAC 46335
Qy 1558 -TCAGTC--C-ATAGAGAGCAACAGAAATGAG--ACCT-----T 1589
Db 46334 CTC-GTCTCTACTAAATATC-AAAAAATTAGCCGGGTGTGGCGGGCGCTGTAGT 46277
Qy 1590 CC-----GGC-----CCA--AGCTGGC--G-----CTGGC--GGCA--CTTTG-- 1620
Db 46276 CCGAGTACTCAGGAGGCTGAGCGAGGAGATGGCATGAACCTGGAGGCGAGAGC--TTGC 46218
Qy 1621 -GT-----AGAGTGTGCAC--CA--CGCGGTGTGTGTA--AACGTGA----- 1658
Db 46217 AGTGAAGCAATGTGCACTGCACTCCAGCCTG-G--GGAGAGCGAGACTCCGTC 46161
Qy 1659 --AATAAAGAGCAAA-AAAAA 1679
Db 46160 TCAAAAAAATA--AATAAAAAA 46139

RESULT 6

US-08-475-035-3
; Sequence 3, Application US/08475035
; Patent No. 5985553
; GENERAL INFORMATION:
; APPLICANT: KING, C. R.
; APPLICANT: KRAUS, MATTHIAS H.
; APPLICANT: AARONSON, STUART A.
; TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM
; TITLE OF INVENTION: EGF RECEPTOR GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,035
; FILING DATE: 7 Jun 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Peirymann, David G.
; REGISTRATION NUMBER: 33,438

; REFERENCE/DOCKET NUMBER: 1414.656
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3816
; US-08-475-035-3

Query Match 41.8%; Score 701.1; DB 2; Length 5532;
Best Local Similarity 39.3%; Pred. No. 0.00023;
Matches 1387; Conservative 0; Mismatches 196; Indels 1943; Gaps 374;

Qy 1 GTTGTGTGCC--TTTCAG-----C--AAACACG--TGGA-----TTT----- 29
Db 1395 GTT-TTTGTGATTCAGGCTTGGCTTGAACACAGGACGACCTCCATGCTTTGAGAAC 1453
Qy 30 ---AAATC-T-----CCTTGC-ACA-----AG-----CTTG-AG-----AGC- 55
Db 1454 TAGAATCATACGCGGCGAGCAAGCAACATGCTCAGTTTCTCTTGCAGTCTGACGCC 1513
Qy 56 ---AACACA--ATC-----TA-----TC-AGAAAGAA-----AGA--AA 82
Db 1514 TGAACATAAATCCTTTGGGATTACGCTCCCTCAAGGAGATAGTGATGGAGATGTGATA 1573
Qy 83 -----GAAAAAACCAGCACTG-----A--CAAA-A-AAGAA-----GAAAAAGAA----- 119
Db 1574 TTTTCAGAAACAAA--AATTGTGTATGCAATACATATACATAAATACTGAAAA--AACTGTT 1628
Qy 120 ---GA-----AGAAAA--AAAT-----CA-----TCAAAACCATCCAGC--C 150
Db 1629 TGGGACCTCCGGTCAGAAAAACCAAAATATATAAGCAACAGAGGTGAAAA-----CAGCTGC 1683
Qy 151 AA-----AAATGCACATTTCT--ATCTCTTGGGCAATCTTCAGC--GGGCTGGCTG----- 197
Db 1684 AAGGCCACAGGC-CAGGTCTGCCATGCTTTGTGC--TC-CCCCGAGGGCT--GCTGGGGCC 1738
Qy 198 -----C-----TCTGTGTCTCTT--CCAAGGAGTG-C--CCGTGCGCAGCGGA----- 235
Db 1739 CGGAGCCCGAGGACTGCTCTCTTGCC--GGAATGTGAGCCGAG--GCAG--GGATGGCTG 1794
Qy 236 GA-----TGCCACCTTC-----CCCAA-----AGCTA--TGACAAAC-----GTG--A 269
Db 1795 GACAAGTGCAAGCTTCTGGAGGGTGAGCCCAAGGAGTTTGTGAGAACTCTGAGTGCA 1854
Qy 270 CGGT-----CC--GG-----CAGG--GGGAGAGC 289
Db 1855 CAGTGCCACCCAGAGTGCCTTCCAGGCCATGAACATACCTGTGACAGAGCGG--GACC 1913
Qy 290 -GCCACCOCT-----CAG-GTG--CACT--ATTGA-----CAACCGGGTCA-----CC 325
Db 1914 AGACA-ACTGTATCCAGTGTGCCCACTACATTCAGCGCCCCCTCTGGTCAAGACCTGCC 1972
Qy 326 CGG-----GT-----GG-----CCTGG-CT--AA--ACCGGAG----- 348
Db 1973 CGGAGGAGTCTATGGGAGAAAAACAACACCTGTCTGGAAGTA--CGCAGACCGCGGCCAT 2031
Qy 349 -----CA-----CCATC--CT-----ATG--CTGG-----GAA-- 369
Db 2032 GTGTGCCACCTGTGCCATCAAACTGCACTACGATGCACTGGGCCAGGCTTTGAAGGC 2091
Qy 370 TG-----ACAAAGTGGTGCCT--GGATCC-----TCGC-----GTGG-----TCCT 402
Db 2092 TGTCCACGAATGG--GCCTAAGATCCCGTCCATCGCACTGGGATGTGTGGGGCCCTCCT 2150
Qy 403 -----T-----CTGAGCAAC--ACC-----CA-----AA--CGCAGTACAGCATC 433

Db 2151 CTTGCTGCTGGTGGTGGCCCTGGGATCGGCTCTTTCATCGAAGGCC-----CA-CATC 2205
QY 434 GAGATCCAGA-----AGG-T--GGA--TG-TGATGACAGG-----GCC-CT 469
Db 2206 G---TTGGAAGCGACGCTGCGAGGCTCTGGAAGA-GAGGAGAGCTTGTGAGCGCTCT 2261
QY 470 TACAC-----CT-----GCTC-----GG-----TGAG--ACAGA-- 492
Db 2262 TACACCCAGTGGAGAGCTCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAACCTGAAT 2321
QY 493 CAACACCCAAAGACC--T-CTAGGG-----TC--CAC-----C 521
Db 2322 CAA-----AAAGATCAAAGTGT-GGGCTCCGGTGGCTCGGCACGCTGTATAAGGGAC 2374
QY 522 TC-----AT-----TGTGCAAGT--ATCTCCC-----AA--AATGTAGAG-- 553
Db 2375 TCTGGATCCAGAGGTGAGAAAGTTAAAT-TCCGTCGCTATCAAGGAAT--AAGAGA 2432
QY 554 ----ATTCTTC-----A-GATAT-CTCCATTAA-----TGAAG-- 582
Db 2433 AGCAACATCTCCGAAGCCAAAGAAATCTCGATGAAGCTACGTGATGGCCAGCGT 2492
QY 583 GAACAA-----T-----ATTAGCTCACCCTGCA--TAGCAACTGG 615
Db 2493 GGACAAACCCCAAGTGTGCGGCTGCTGGGCATCTGCTCACTCACCGT-GCAACTCA 2551
QY 616 TAGAC-CAG--A-G--CTTACGGT--TGCT-----TTGTGAGTG-----AAG--ACGAA 685
Db 2552 T-CAGCAGCTCATGCCCTTGGCTTCCCTGGAATGTGCGGA-ACACAAAGACAA 2609
QY 648 TCT--CTCCCAAGCGGT--TGCT-----TTGTGAGTG-----AAG--ACGAA 685
Db 2610 TATTGGCTCCCA-----GTACCT-GCTCAACTGGTGTGTCAGATCGCAAGGGCATGNA 2663
QY 686 -TACTTGA-A-----ATTACGG-GCATCACCCGGA--GCAGTCAGG--GGACT 728
Db 2664 CTACTTGGAGACCTGCGCT--GGTGCA-----CGCGACCTGGCAGCAGGACGTACT 2717
QY 729 ----ACGAGTGAG--TGCTCCA-ATGAC-G--TGSCCG--GCC--C-G-T- 765
Db 2718 GGTGAAGAC-ACCCAGCATG--TCAAGTACAGATTTTG--GCTGGCCAACTGCTG 2772
QY 766 GGTACGG-AGAGTAAGTCAACCGTG-----AA--CTATCCA-----CC 801
Db 2773 GGTGGGAAGAG-AAAGAAATACCATGCAGAGGAGGCAAGTGCTATCAAGTGGATGCG 2831
QY 802 AT--A-CA-TTT--CAGAA-----GCCA-AG-----GG--TACAGGTG 830
Db 2832 ATTGGATCAATTTTACACAGATCTATACCACACAGAGTGTCTGGAGCTAC-GGGG 2890
QY 831 TCCCGG--TGGA-----CAA--A-AGG--GGA--CACTG-CAGTG 861
Db 2891 TGACCGTTGGAGTTGATGACCTTTGGATCCAGCCATATGACGGAATCTCCCTCCAGCG 2950
QY 862 TGAAG--CTC-----AGCAG--TCCCTCAG-----CAGA----- 888
Db 2951 ---AGATCTCTCCATCTGAGAAAGGAGAACGCT--CCCTCAGCCACCATATGTACC 3006
QY 889 ----AT-TC-CA-G--TGGTACAA-----GGATGA-----CA-----AAA 914
Db 3007 ATCGATGCTACATGATCATGCT--CAAGTGTGATGATAGACGACAGATGTCGCCCAA 3065
QY 915 G--AC-TGA-TTGA-A-GGAA-----AGA----- 932
Db 3066 GTTCCGTGAGTTGATCATCGAATTTCCAAATGGCCGAGACCCCGAGCGCTACCTTGT 3125
QY 933 A---AGGG--TGAAG--TGGA-----AA-----ACAGAC-----CTT-----T- 960
Db 3126 CATTCAGGGGATGAAAGATGCAATTTGCCAAGTCTTACAGACTCCAACTTCTACCGTGC 3185
QY 961 CCT-----CTCAA-AA-----CTCAT----- 975

Db 3186 CTGTATGATGAAGAAAGACATGGACGACGCTGGTGGATGCGAGAGTACCTCATCCACA 3245
QY 976 ----CTTCTTCA-----ATGTCCTTGA-----ACATGA--CTATG--GG 1006
Db 3246 GCAGGCTTCTTTCAGCAGCCCTCCAGTCACGACTCCCTCTCTGAGCTCTCTGAGTGC 3305
QY 1007 AACTA-CA-----CTTTC-----G--TGCCCTCCAAACAGCTGGGCC 1040
Db 3306 AACCAAGCAAAATTCACCGTGGCTTGCATTTGATAGAAATGGCTGCA--AAGCTGTCCC 3363
QY 1041 A-CACCA--ATGCAGCATCATG--TATTTGGTC-----CAGCGCCGTGAGC 1084
Db 3364 ATCA--AGGAAGACAGCTTCTTGACAGGATA-CAGCTCAGACCCACACGCGCTTGA 3420
QY 1085 GAGGTGAGCA--ACGGCAC-----GT-----CGAG--G----- 1108
Db 3421 GAGGACAGCATAGACGACACCTTCTCCAGTGCCTGATACATAAACAGTCCGTTC 3480
QY 1109 --AGGCGAGCTGCGTCTG--G--CTG-CT-----GCTCT- 1137
Db 3481 AAAAGGCGCTGGCTCTGTGCAGAATCTGTCTATCAATCAGCTCTGAACCCCGG 3540
QY 1138 -----T-CTGCTTTGCAC-----CTGC--T-----T 1156
Db 3541 CCCAGCAGAGACCCACACTACAGAGCCCCACAGACTGACGTGGGCAACCCCGAGTAT 3600
QY 1157 CTCAA-ATTTT--G--A--TGTC--AGTGCCAC--TTC-----CCAC-- 1188
Db 3601 CTCACACTGTCCAGCCACCTGTGTCAACAG--CACATTGACAGCCCTGCCCTG 3657
QY 1189 -CCGGAAGGCTGCC-----GCC--ACCAC--ACCACAA-- 1222
Db 3658 GCCCAAGGAGGAGCCACCAATTAGCCTGGACACCTGACTACAGCAGACTTCTT 3717
QY 1223 --CAA-----C-AGC--AATGGC-----AA--CACGACAGC--AACCAAT-CAG-A 1258
Db 3718 CCCAAGGAGCCAGCCAAATGGCATCTTAAAGGCTCC-ACAGCTGAA--AATGCAGAA 3774
QY 1259 TA--TA--T-----ACAAA--TGAA--ATTAGA----- 1278
Db 3775 TACCTAAGGTCGCGCCACAAAGCAGTGAAATTTATGGAGCATGACCAAGGAGTAGTA 3834
QY 1279 -----AGA-----AA--CACAG--CCT----- 1291
Db 3835 TGAGCCCTAAATTCAGACTCTTTTCGATACCCAGGACCAAGCCACAGCAGTCTCCAT 3894
QY 1292 -----CATG-----G--ACAGA-----AA--TTT----- 1307
Db 3895 CCCAACAGCCATGCCCGCATAGCTCTTAGACCCACAGACTGGTTTGCACAGTTTACAC 3954
QY 1308 -----G--AGGGAG-----GGGAA----- 1319
Db 3955 CGACTAGCCAGAGTACTTCCACCTCGGCACATTTTGGGAAGTTGCAATTCCTTTGCT 4014
QY 1320 -CAAA-----GAATA-----CTTGGGGGA-- 1339
Db 4015 TCMACTGTGAAGCATTTACAGAAACGATCCAGCAAGAAATTTTGTCCCTTTGACAGAA 4074
QY 1340 -----AAGAG-----TTTTAAAAAGAAATTTGAAA--AT-TGCCTTGACA 1378
Db 4075 ATTTATCTTTCAAGAGGTATATTGAAAAAANA--AAAAAGTATATG--TGAGGA 4128
QY 1379 TATTTA-----GGTA-CAATGGAGTTT-----CCT----- 1403
Db 4129 TTTTATGATTTGGGATC-TTGGAGTTTTCATTTGCTGCTATTTGATTTTACTTCAATG 4187
QY 1404 ----TTCC--CAACGGGAGAA-----CAC----- 1423
Db 4188 GGCTCTTCCAAACA--GGAAGAAAGTGTGCTGAGCACTTGTACCTGAGTTCACTCA 4244
QY 1424 -----AGCACA--CC-C--GGCTT-----GGA--C-----CCA-- 1444
Db 4245 GGCCCAACTGTGAGCAAGGAGCACAGCCACAAGTCTTCCAGAGGATGCTTGTATTCAGT 4304

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QY 1445 ---CTG---CAAGCTGCATC---GTGC---AAC-CT-----CTT---TGGT 1474
Db 4305 GGTCTGCTTCAAG-GCTTCCTCACTCAAAACACTAAGATCCAGAAGGCTTCATGGC 4362
QY 1475 GCCAG-----TGT-----G-----GGCA-----AG---GGCTCAGCTCTC 1502
Db 4363 CCCAGAGCCGGATCGGTACTGTATCAAGTCATGGCAGGTACAGTAGGATAAGCCATC 4422
QY 1503 TG-CCC-----ACAGAG-----1513
Db 4423 TGTCTCTCTCTGGGCAAGAGAAACGGAGGGGATGAATCTCTCTTAGACTTACTTTTG 4482
QY 1514 -----TGCCCCCAG-----TGGAACA-----TTC-----TG---1535
Db 4483 TAAAAATCTCCCAAGGTACTTACTCCCACTGATGGACCAAGTGTTCCTCAGTATGAGC 4542
QY 1536 G-AG-CTG-----G-----CCATCCC-----AAATCA--AT-----CAGT 1562
Db 4543 GTTAGACTGACTGTGTGTTGTTCTTCCATCCATTTGTTTGAACCTCAGTATGCGGCCCTGT 4602
QY 1563 C-----CAT-----AGAGACGA---ACA---GAATGAGAC---TTCCGGC 1594
Db 4603 CTGTGTCATGAATCATGACGAGAGAGATGACACATCAATATATACTCGGATTCAGC 4662
QY 1595 CCAAGCTGGCGCTGC---GGGACTTTGG---TAG---AC-----TGTG---1630
Db 4663 CCA--CAATTG-GATTTCATGACA-TTTGGACCAATAGCCACAGCTGAGATGTGGAATA 4718
QY 1631 CC-----ACCAGCGGTGTGTGT-G---AAAGC-----T 1656
Db 4719 CCTAAGGATACACCGCTTTGTTCTCGCAAAACGTATCTCCPAATTTGAGGCTCAGAT 4778
QY 1657 GAATAT-A-A-----AAAGAGCAAAA-----AAAA 1679
Db 4779 GAATGATCAGTGCCTTTGGGGCATAGATCAGAGACTACAAAA 4824
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RESULT 7

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US-09-676-610B-17
; Sequence 17, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 17
; LENGTH: 5532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (187)....(3819)
US-09-676-610B-17
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Query Match 41.8%; Score 701.1; DB 4; Length 5532;
Best Local Similarity 39.3%; Pred. No. 0.00023;
Matches 1387; Conservative 0; Mismatches 196; Indels 1943; Gaps 374;

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QY 30 ---AAATC-T-----CCTTCG-ACA-----AG-----CTTG-AG-----AGC- 55
Db 1454 TAGAATCATACCGCGCAGACCAAGCAACATGTCAGTCTTTCTCTTCGATCGTCAGCC 1513
QY 56 --AACACA--ATC-----TA-----TC-AGGAAGAA-----AGA-----AA 82
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Db 1514 TGAACATAACATCTCTGGGATTACGCTCCCTCAAGAGATAGTGAATGGAGATGTGATA 1573
QY 83 -----GAAAAAAACCGAACCTG---A--CAAA-A-AAGAA-----GAAAGAA- 119
Db 1574 TTTCAGGAACAAA---AATTTGTGCTATGCAATACATTAATCTGGAATA---A-CTGTT 1628
QY 120 ---GA-----AGAAAA---AAAAAT-----CA-----TGAACACCATCCAGC--C 150
Db 1629 TGGGACCTCCGGTCAGAAAAACAAATATATAAGCAACAGAGGTGAAAA---CAGCTGC 1683
QY 151 AA-----AAATGCACAAATCT---ATCTCTTTGGGCAATCTTTCAG-GGGCTGGCTG 197
Db 1684 AAGCCACAGGC-CAGGCTGCGCATGCTTGTGC--TC-CCCCAGAGGCT-GCTGGGGCC 1738
QY 198 -----C-----CTGTGTCTCTT-CCAAGAGTG-C--CGTGCAGCAGCGA-----235
Db 1739 CGGAGCCAGGAGCTGCTCTTTGCC--GGAATGTAGCGGAG-GCAG-GGAATGCTGTG 1794-
QY 236 GA-----TGCCACCTTC-----CCCAA---AGCTA-TGGACAA-----GTG--A 269
Db 1795 GACAAGTGCAAGCTTCTGGAGGGTGAGCCAGGAGTTTGTGAGAACTCTGAGTGCTATA 1854
QY 270 CGGT-----CC---GG-----CAGG--GGGAGAGC 289
Db 1855 CAGTGCCACCCAGAGTGCTGCTCAGGCCATGAACATCACCTGACAGAGCAGG-GACC 1913
QY 290 -GCCACCTT---OAG-GTG---CACT---ATTGA-----CAACCGGTCA-----CC 325
Db 1914 AGACA-ACTGTATCCAGTGTGCCACTACATTCAGCGGCCCACTGGTCAAGACCTGCC 1972
QY 326 CGG-----GT-----GG-----CCTGG-CT--AA--ACCGAG-----348
Db 1973 CGGAGAGTCACTGGGAGAAAAACAACCCCTGTCTGGAAGTA-CGACAGACCGCGGCAT 2031
QY 349 -----CA-----CCATC---CT---CT---ATG-CTGG-----GAA---369
Db 2032 GTGTGCCACTGTGCCATCAAACTGCACCTAGCGATGCATGGGCCAGCTTTGAAGGC 2091
QY 370 TG-----ACAAGTGTGCTT-GGATCC-----TCGC-----GTGG-----TCCT 402
Db 2092 TGTCCAAACGAATGG-GCCTAAGATCCGTCCTCCATCGCACTGGGATGTGGGGCCCTCT 2150
QY 403 -----T-----CTGAGCAAC-ACC-----CA---AA--CGCAGTACAGATC 433
Db 2151 CTTGCTGTGTGTGTGGCCCTGGGATCGCCCTCTTCATCGAAGCGC---CA-CATC 2205
QY 434 GAGATCCAGA---ACG-T--GGA---TG-TGTATGACGAG--GCG-CT 469
Db 2206 G---TTGGAAGCGACGCTGCGGAGGCTGCTGCAGGA-GAGGGAGCTTGTGGAGCCTCT 2261
QY 470 TACAC-----CT-----GCTC-----GG-----TGCAG--ACAGA---492
Db 2262 TACACCCAGTGGAGAGCTCCCAACCAAGCTCTCTTGAAGATCTTGAAGAACTGAAAT 2321
QY 493 CAACCAACCCAAAGACC---T-CTAGGG-----TC-CAC-----C 521
Db 2322 CAA-----AAAGATCAAAAGTCT-GGGCTCGGTGGCTTGGCACGGTGTATAGGGAC 2374
QY 522 TC---AT-----TGTGCAAGT---ATCTCCC-----AA--AATGTAGAG- 553
Db 2375 TCTGGATCCAGAAGGTGAGAAAGTTAAAT-TCCCGTGTGCTATCAAGAAAT-AGAGA 2432
QY 554 ---ATTCTTC-----A-GATAT-CTCAATTAA-----TGAAG-----582
Db 2433 AGCAACATCTCCGAAAGCCAAACAGAAATCTCGATGAAGCTACGTGATGGCCAGGT 2492
QY 583 GAACAA-----T-----ATTAGCTCACCTGCA---TAGCACTGG 615
Db 2493 GGACAAACCCACGTCGTGCGCGCTGTGGGATCTGCTCCCTCACCTCCACCGT-GCAACTCA 2551
QY 616 TAGAC-CAG---A-G-CCTACGGTT---ACT---T---GGAGACAC-----A 647
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Db 2552 T-CAGCAGCTCATGCCCTTCGGCTGCTCTCTGGACTATGTCGGGA-ACACAAAGACAA 2609
Qy TCT---CTCCAAAGCGGT---TGCT---TTGTGAGTG---AAG---ACGAA 685
Db 2610 TATTGGCTCCCA---GTACCT-GCTCACTGTGTGTGAGATCGCAAAAGGCGATGAA 2663
Qy 686 -TACTTGA-A---ATTGAGG-GCATCACCCGGGA---GCAGTCAGG---GGACT 728
Db 2664 CTACTTGGAGGACCGTCCGCTT---GGTGCA---CCGCGACCTGGCAGCAGCAAGCTACT 2717
Qy 729 ---ACGAGTGAG-TGCCTCCA-ATGAC-G---TGCGCGC-GCC---C-G-T- 765
Db 2718 GGTGAAAC-ACCCAGAGATG-TCAAGATCACAGATTTGG---GCTGGCCAAACTGTG 2772
Qy 766 GGTACGG-AGAGTAAGGTACCCGTG-----AA---CTATCCA-----CC 801
Db 2773 GGTGCGAAGAG-AAAGAATACCATGCAGAGAGGAGCAAGTGCTTATCAAGTGGATGGC 2831
Qy 802 AT---A-CA-TTT---CAGAA-----GCCA-AG-----GG---TACAGGTG 830
Db 2832 ATTGGAATCAATTTTACACAGATCTATPACCCAGCAGAGTGATGCTGGAGCTAC-GGGG 2890
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Qy 862 TGAAG---CCTC-----AGCAG-----TCCCTCTCAG-----CAGA----- 888
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Db 3007 ATCGATGCTACATGATCATGTGT---CAAGTGTGGATGATGACGACAGATGCGCCAAA 3065
Qy 915 G--AC-TGA-TTGA-A-GGAA-----AGA----- 932
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Qy 961 CCT---CTCAA-AA-----CTCAT----- 975
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Qy 976 ---CTTCTTCA-----ATGTCTCTGA-----ACATGA---CTATG---GG 1006
Db 3246 GCAGGGCTTCTTCAGCAGCCCTCCAGTCAAGCTCCCTCTGAGCTCTCTGAGTGC 3305
Qy 1007 AACTA-CA-----CTTGC-----G---TGGCTCCAAAGCTGGGCC 1040
Db 3306 AACCGCAAAATTCACCGTGGCTTGCAATTGATGAGAAATGGGCTGCA--AAGCTGTCCC 3363
Qy 1041 A-CACCA--ATGCCAGCATCATGC---TATTTGGTC-----CAGGCGCGTCAAGC 1084
Db 3364 ATCA--AGNAGACAGCTTCTGACGGATA-CAGCTCAGACCCCAAGCGCGCTTGACT 3420
Qy 1085 GAGGTGAGCA--ACGGCAC-----GT-----CGAG---G----- 1108
Db 3421 GAGGACAGCATAGACACACCTTCTCCAGTGCCTGATACATAAACCGTCCGTTCCC 3480
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Qy 1138 ---T---CTGCTCTGAC-----CTGC-T----- 1156
Db 3541 CCCAGCAGAGACCACTACACAGGACCCCAAGCAGCTGCGAGTGGGCAACCCCGAGTAT 3600
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Db 3775 TACCTAAGGCTCGCGCCACAAAGCAGTGAAATTTATTGAGCATGACCAAGGAGTAGTA 3834
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Db 3835 TGAGCCCTAAATTCAGACTCTTTTCATATCCAGGACCAAGCCACAGCAGGCTCTCCAT 3894
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Db 3955 CGACTAGCAGAGTACTTCCACCTCGGCGCACATTTTGGGAGTTGCTATTCCTTTGCT 4014
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Db 4015 TCAACTGTGAAGCATTTACAGAAAGCATCCAGCAAGAAATATTTGTCCTTTTGAGCAGAA 4074
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Db 4129 TTTTATGATGGGATC-TTGGAGTTTTCATTTGCTGCTATTGATTTTACTTCAATG 4187
Qy 1404 ---TTCC---CAACCGGAGAA-----CAC----- 1423
Db 4188 GGCTCTTCCAA---GGAAGAGCTGTGCTGTAGCACTTGCTACCTGAGTTCAATCA 4244
Qy 1424 ---AGCACA-CC-C-GGCTT---GGA-C-----CCA-- 1444
Db 4245 GGCCCAACTGTGAGCAAGGAGCAGACCAAGCTCTTCCAGAGGATGCTTGATTCAGT 4304
Qy 1445 ---CTG---CAAGCTGCATC---GTGC---AAC-CT-----CTT---TGCT 1474
Db 4305 GGTCTGTCTTCAAG--GCTTCCACTGCAAAACACTAAAGATCCAGAAAGGCTTCAATGGC 4362
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Qy 1503 TG-CCC-----ACAGAG----- 1513
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Qy 1536 G--AG-CTG-----G---CCATCCC-----AAATTC-A-AT-----CAGT 1562
Db 4543 GTTAGACTGCTTGTGTCTTCCATTCATTTGTTTGAATCTAGTATGCGCCCTCTG 4602
Qy 1563 C-----CAT-----AGAGACGA---ACA---GAATGAGACC-----TTCCGCGC 1594
Db 4603 CTGTGTCTCATGAATCAGCAAGAGAGATGACACATCAATAATACTCGATTCAGC 4662
Qy 1595 CCAAGCGTGGCTGC---GGGCACTTTGG---TAG---AC-----TGTC--- 1630
Db 4663 CCA--CATTG-GATTTCATGCA-TTTGGACCAATAGCCCCACAGCTGAGAATGTGAATA 4718

QY 1631 CC-----ACCAGCGGTGTGTGT-G-----AAACG-----T 1656
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RESULT 8
US-09-220-132-30
; Sequence 30, Application US/09220132
; Patent No. 6508607
; GENERAL INFORMATION:
; APPLICANT: SHYJen, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07134-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 14770
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-30

Query Match 41.7%; Score 700.9; DB 4; Length 14770;
Best Local Similarity 35.1%; Pred. No. 0.0016;
Matches 1459; Conservative 0; Mismatches 165; Indels 2531; Gaps 406;
QY 2 TTGTG-----TC-----CTTC-AG-C-AAAAAC-----AGTGGATT-----28
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QY 53 AG--C-----AA-CACAAT--CT-AT-CAG-----GAAAGAAAGAA-----81
Db 173 AGGATCTTTTAAATGCAATATATGGCTCATGAGCTCTCAATTAAGAA--AACAGGAT 231
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Db 350 ACCTTGAAAGCCCTCGACTACATAAAAAATGAGTTGACATCAACATTTGCAATCAGA 409
QY 138 A-----AA-----CCA-----TCCA-----GCCA-----151
Db 410 ATGGGTGNAACCTCTCCACCTTCTTCCAAAGAGGCCATGTAGAGGTGTTTCTGAGC 469
QY 152 -----AA--AATG-----CACA--ATT--CT 166
Db 470 TGCTGAGAGAGAACCAATGTTGATGAGCTACAAAGAAAGAAACACAGCAATGCAAC 528
QY 167 ATC-----TCT-----TGGGCAA-----TCTT-----183
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QY 236 --GATGC-CACC-----TTTC-----CCAA-----A 253
Db 708 TGGCTTTCACACCATTTGGCAGTGGCTTTTGCAACAAGGTACAGCAAGTGGTTTGGCTCT 767
QY 254 GCTATGCAACAGTGAC-----GG-----TCCGGCAG-----GGG-284
Db 768 GCTA--GAGAA--TGACACCAAGGAAAGTGGCTTCC--CAGCTCTTTATATGCGGC 821
QY 285 -----AG-----AG-CGCCACCT-CAGGTGCACTATTGACAA-----316
Db 822 CGCAAGAGACGACACAAAGCGCGCTCTGCTGCA--GAATGACAAATGCAATG 880
QY 317 -----C-----G-GG--TCAC-CGG-----GG-----TG 331
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QY 332 --GCC-----TG--GCTAAACCG-----CA--GC-----AC--CA 353
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QY 354 -TCCT-----ATGACA--AG--TGG-----TGC-CT-----384
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QY 365 G-GGA-----ATGACA--AG--TGG-----TGC-CT-----384
Db 1061 GAGAGCTTAAATCGATGCCAAACAGGATGCTGCACACCACTGCACTGTGGAGCA 1120
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Db 1181 AAACAAGATGGATTATCTCCATTTGCACATGGCCACAAAGGGATCATTTAACTGCG 1240
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Db 1241 TCCAGCTTCTCTCAGCAATATGTACCGTGGATGTCCCAATGACTACCTGACTG 1300
QY 466 CCCTTACAC-----CTGCTC-----GG-----TGC-----AG 487
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QY 573 -----TTA-----ATG-----AAGGG-----583
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QY 687 ACT---TGGAAA---TT---CAG 700
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QY 701 ---G-GCATCACC---C-GGAGCAGTCAGGGGACT---ACGAGTGCA-GTGGC 742
Db 1951 AAAAGTGCAITCCAGATGCTCTGGGA---AG---AGCGGGCTTAACACCACTGCATGTAGC 2006
QY 743 TCCA-ATGAC---GTGGCC---GC---GCCGTGG---T-A 769
Db 2007 TGCACATTACGATAATCAGAAAGTGGCCCTTCTGCTTTTGGACCAAGAGGCTCACCTCA 2066
QY 770 CGGAG---AGTAAAGGT---CACCGTGAACAT---CC---ACCA--- 802
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QY 803 T-AACAT---TTCCAGAGCCAA-G-GGTAC---AG 827
Db 2123 TGGACATAGCCACAACTCTGCTGGAAATGTGTGATGTCACAGCGAGTTACCGGGCAAG 2182
QY 828 G---TG---TCC---CCGT---GGGACA---A-AAGG---GGACA---CTGC 857
Db 2183 GAATGTCTCGTCCATCTCG---CAGCTCAGGAGGCGCAGTGGACATGTGTGCTGCTGC 2239
QY 858 ---AG---TGTGAGCCTCAGCAGT---CCC--- 879
Db 2240 TCCTCGGTAGAAATGCGGAATGTGAA-CCTGAGCAATAAGACGCGCTGACCCCACTCCAT 2298
QY 880 ---CTCA---GCAGATTCAGTGGTA---CAAGG--- 905
Db 2299 TTGCTCTCAGAGATCGAGTGAATGTGGCAGAGTCC-TGTAAACCAAGGGGCTC 2356
QY 906 AT---GACAAA-A-G---ACTG-AT---TG---AAGGAA 929
Db 2357 ATGTGGACGCCAGACAAAGATGGATACACACCACTGCTGATGTGGCTGCCACTATGGAA 2416
QY 930 AGA-AAG-G---G---TG-AAAG---TG-GAAAC-AGA 955
Db 2417 ATATCAAGATTGTAATTTCTGCTCCAGCATCTGCAAAAGTTAATGTCACCAACAAAGA 2476
QY 956 ---CCTTTCTCTCAA---A-ACTCA---TC 976
Db 2477 ATGGGTATACGCCATTAC-ATCAGACAGACAGCAGGGGCATGCGATATAATAAATGTC 2535
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Db 2715 TGAAGTTCTTGATATGTCTGATGATGAAGTTCTGTAAGCCCAATGCCCTGAATGCTCAG 2774

QY 1083 ---GCG---AGTGA---GCAA---CGG---CAC-G- 1102
Db 2775 TGATGGCGAATATATCTCAGATGTTGAAGAAGTGAAGATGCAATGACCGGGGACACAGA 2834
QY 1103 ---TC---G---AGGA---GGG---CAGGCTGC--- 1120
Db 2835 CAAATATCTTGGGCGACAGGACCTTAAGGAATGGGTGATGATTCCTGCTGCGAGGG 2894
QY 1121 ---GTCT-GG---CTG-CTGCTC---TTC---T-G 1141
Db 2895 TTACATGGCTTTAGTCTCGGAGCGGTTCTGCGAGCTCCGCTCTCTCAGTTCGATAG 2954
QY 1142 GTCTTGTCACTT---GCTTCT---CA---A-ATTTGATGTA--- 1173
Db 2955 GTCTTACACCTTGAACAGAGAGCTCTATGCAAGGACAGCATGATGAT-TGAAGAATCC 3013
QY 1174 ---GTGCCACTTCC---C---CACCGGAA--- 1195
Db 3014 TTGTGCCA---TCCAAGAGCAGCATCTAACATTCACAAAGGAATTTGATCAGATTCTCT 3071
QY 1196 ---A---GGCTGCGCCACC---ACCA---CCA-C---CAA---CA- 1222
Db 3072 TAGACATTACAGCTGGGCTGCAGACACCTTAGACAAATGCTCAATCTTGTTCAGCCCAT 3131
QY 1223 -CA---AC---AGCA-ATGG---CAA---CACC-GACAGCAA- 1249
Db 3132 TCATCTGGGTTTCTGTTAGCTTTATGTTGAGCGCGAGGGGGCTCCATGAGGGAAG 3191
QY 1250 CC---AATCA---GAT---AT-AT---A-CAAATG---A---AAT 1274
Db 3192 CCGTCATCAGGATGAGATCATCTCTCCAGCAAGTGTACGGCCCCCTCCTCGAAT 3251
QY 1275 ---TAGAAGA---AA---CACAGCTCATGG-GACAGAA 1303
Db 3252 CACCTGCCGTTTGGTA-AAGAGACATAAACTGGCCAAACCCACCCACATGTTGAAGGA 3310
QY 1304 ---ATT---TG---A-GGG---AGGGGAACAA--- 1322
Db 3311 GAGGATTAGCAGTAGGCTGTGAAATGGTCTCTGACAGGGGCACAAATTTTAGGCCCTG 3370
QY 1323 ---AG---AAT---ACTTTGGG---G-GGAAAAGA---GTT- 1347
Db 3371 TCATAGTGAATATCCCTCACTTTGGTCCATGAGAGGAAAGAGAGAACTCATTTGTC 3430
QY 1348 TT-AA-AAA---GAAA-TTGA---ATTGC-C---TTG-CAG---AT---A 1380
Db 3431 TTGAAAGTGAATATGGTGAACCTTGAAGGA--GCATCAGTTTGACAGCAAAATGAAGA 3488
QY 1381 TTT---AGGTAC---AATGG-A-GTT---TTCTTTTCCCA-AA---CGGGA 1417
Db 3489 TTTAACGGATTACTTAATGGCATGGATGAGAACTTGATAGCCAGAGAGTTAGGGAA 3548
QY 1418 GAA---CAC---AG---CA---CA---CCCC 1433
Db 3549 AAAGCGTATCTGAGGATTAATCAGAAAGATTTCCCCAGATTTTTCAGTGTGTTCCCG 3608
QY 1434 GCTT---GGA---C-CCA---CTGCA---AGTGCATC---GT 1460
Db 3609 GATTAAAGCAGGAAGCAACCAAGATTGGTCTCTGAAGGTGGAATTTCTGAGCAGCACACAGT 3668
QY 1461 G---CAA-CCTCTTT---GTTGCC---AG---T---GTGGG--- 1485
Db 3669 GCCCTTGTTCAGCATCTTTCCAGAGGGTGGCTTAATAAAGAAATTCAGATGGGCT 3728
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Db 3729 CCA---GGCCAGCTGTTCAGATGAATTTGMAAAAGATCTTTGGAAACAAAGCAACT 3786
QY 1514 ---T-GCCC---CCAC-GTGAAC---ATTCTGAGCTGGCCATCCCA-AATTCATCA- 1560
Db 3787 TTTAGCCCAATTTGTCACGTGGGAACCA---GAAGACGGAATTCCTATAACCAATCAC 3842

QY 590 --ATTAGCCTCA-C-----CTG-----CATAGCAACTG-----GTAGACCAG-CCT-- 628
Db 2248 AGAGGAGCTTCATCAGACTCTTTGTGTAC-TAGCAACTGCAAGCACTCCAGAGACTGA 2306
QY 629 -----ACG-GT-TACT-TG-GAG--ACA--CATCT--C-----TCCCAAGCGGT 663
Db 2307 ATGAAGATGTCTGTCTGTATGTGTAGGAAGATTTTCATCTGGGGCTTTTTCACAGA-CAG- 2364
QY 664 TGGCT-----T-----TG--TG--AGTGAAGCGAA--T-ACCTGGAAATTCAGGG 702
Db 2365 --GGCTACCTGTATGAATGAATGATTTGAAG--GAAAGGTCACTTAGAAAAAT--GGC 2419
QY 703 CA-----TCACC-----C-----GGGA----- 714
Db 2420 CACCCTGAGTTATTTCACCAAGCTTATGCTTTTGAAGGGGATCTCAAGGTGTTCTCCAG 2479
QY 715 ---GCAGTC-----AGGGGA-CT-AC-GA-----GT-----GCAG-TGC 741
Db 2480 ACTGCAG-CAGAAAGAGGGGAGCTGACAGACAACCTTGTGGCTATGGCCACAGCAGCTGG 2538
QY 742 CT-CCA-----AT-GAC-GTGGCCGC-----GCC-----C-GTGGT---ACGGA-G 774
Db 2539 CTACCATGTGGCTATGGCTGTGGAAGCTTTTGCCTCAACAGCTGTGTTTCA-GGATC 2597
QY 775 AGTA-----AAGG-----TCACCGTGAACCT--ATCCAC----- 800
Db 2598 AGTATGTCAAGGCTGCTTCTCACC-T--ACTTTCATCCACAAGTGTATGAAGCGGTGG 2654
QY 801 -----CATA-CATTT--CA-GAA-----GCCAAGG----- 821
Db 2655 AGCTGCTCAAGTCAACCATTTTACAGGGAAGCTATTGCGATTTGCCAAGGCCCGCTGC 2714
QY 822 -----GTAC--AGG--TGT-CC-CGG-TGGG-AC-----A-NAAG-G 848
Db 2715 GCCCGGAGACCCAGTCTGTAGGACTTGTACTCAGCTGGGGAACCGCTCTAGAAAGAG 2774
QY 849 --GNACAC--TGCAGT-G-TG--AA-----GCC-----T-CAG 872
Db 2775 ATGSCCACTATGCTGTAGCTGCAAAATGCTATTTAGGGGCCACTTGTCTTATGATGAG 2834
QY 873 C--AGT--CC-----CCTCA-----CCAGAAAT-- 891
Db 2895 CCAAGTTTGGCCAAAAGGGGAGTGGGCATCACTTAGAACGCGCTGACAGTTGGCTG 2894
QY 892 CCAGTGSTA-CA-AGGATGA-----CA-A-----AAGA-CTG 919
Db 2895 CCA-TCGTAGGAGGATGAGTTGCTCTCTTCCCTGGCTCTCAGATGTGCCCAAGAGCTG 2953
QY 920 ATT-----GA-----AGGA-----A-GAAAG-----G 936
Db 2954 CTTCTGGCCACAACACTGGGTGGGAGCCAGGAAGCCCTGCAGCTGCATGAAGTCTACAG 3013
QY 937 GGT--GAAA-----GT-----GGAAGAA-CAG 954
Db 3014 GGTGAGATTTGGTTTGGCTTCTGTGAGCTACTGTCCAGGCACTGTGGAGGAAAGCAG 3073
QY 955 ACCTTTC-----CTCTCAAAA-CTCATCTCTTT--CAATGTCTCT--GAACA----- 996
Db 3074 --CTTTCAGAGGC-----AAAAGCTCTCTCTTACCA-----CACTTGGAAACAGCGGCAC 3123
QY 997 -----TGACT--A-TG-GGAA-----CTTACA--CTTG-- 1017
Db 3124 CGAAGGCGCTTTCTGGAGAGGGTGAAGTGTGAGTGTGGAAGAGCATCTTCAGCCCTTGAC 3183
QY 1018 -CGTG-----GCC--TCCACAAGAGTG-----G-----GC- 1039
Db 3184 CCTGAGCATATCAGAAGCCTTTC--AGAAGCTGCAGAACATCAAGTACCCATCTGCT 3241
QY 1040 -----CACACCAATGC-----CAGCATCATGCT--ATTGGTCCA----- 1072
Db 3242 ACAATAACACACC--TGCCCAACAGC-TCTGCTTCACATTTG--CCATGACTTGACCC 3296

QY 1073 -GGC-----GCCGTGAG-----CGAGG-TGAGCAACGGCAC----- 1101
Db 3297 TGGCAGTGTGAGCCCAACAGATGGCTCTCTGGGACGAGGCTGTGCA--GGCGCTCTCTGG 3354
QY 1102 -----GTC--GAG--GA-----GG-----GCAGG-----CT--GC 1120
Db 3355 GCGGTGGTCCGAGCTTATGACTCAGGGAGCTTCACCATCATGAGGAAGTGTACTCAGC 3414
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Db 3415 CTTTCTCCTGATGCTG-TGACCACCTTAAGAGACAAGTTGGGGAGCAATCATCCCTG 3473
QY 1148 ---CACCTGCTTCTCAAA--TTTTGA-----TG--TGA----- 1173
Db 3474 CCACACCAAGCTT-TCAAAAGTTTGGAGGCGCTTTTCTTTATGGCGCTGTGTATGAATTC 3532
QY 1174 --GTG-----CCA--CTTCCCCA--CC-----C-GGG-AAAGGCTGCCGCCAC- 1208
Db 3533 TGGTGGTCTCTCTCCAGACCTTGCCTCAATTCAGAGTGTGGGTAAAGGGCTG--GTCACA 3590
QY 1209 ---CA-----CCA--CCACCA-----ACAC-AAAGCAATG--GCAAC--ACC 1241
Db 3591 GAACACTCTCTGTGAGCCAAAGCCAGCAGTTAGACACTGCCAGCAGTGAAGAAAGCGACC 3650
QY 1242 --GA-----CAGC--AACCAA-----TCAGA-TATA-----T-ACA----- 1266
Db 3651 CTGAAACTTCTCAGCAGAGCCAAACAGGCGCTTCAGAACTAGACTTGAGACTCAGAGAAG 3710
QY 1267 AA--TGA--AA-----TTA--GA-----AGAAA--CA--CAGCTC- 1292
Db 3711 AAGGTGAGCAATGCTGAGTACTTTTAAAGAGCTCTTTTCAAGAAAGCATCCAGTCTCC 3770
QY 1293 --A-TGGACAGA-AA--TT--TGAGGGAGGGGAAACAAGAAATACTTTGGGGG----- 1337
Db 3771 AAAACT--CACAGAAACTGTTGCTGA--AG-----TCCAG-AGACCTTGGCAGAAATG 3820
QY 1338 ---GA-----AAAGAT--TTTAAA--AAAG-AAAT-----T 1361
Db 3821 ATCCGACAACACCAAAAGAGTCAACTCTGTAAATTCACAGCAAAATGCTCTGATAAGAAT 3880
QY 1362 GAA--AAAT-----G--CCT-TGCAGATATT-T-----AG-GT----- 1387
Db 3881 GAACCGGAGTAGAAGCAGAGCAGCAGCCCTCTGAG--TTCTCAGAGCAGTGTAAAGAA 3937
QY 1388 ---ACATGGAG--TTT-TCT-----TTTCCAAAACGG-----GA----- 1416
Db 3938 GAAAAAAAT-GAGCCACTTCTCTGCTGAGTTAAACCAAAAGGCTTACCAGGCAATCA 3996
QY 1417 -AGAA--CA-----C-----AGCA--CA--CCCAG--CTTGGACCCA-----CTGCA 1449
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QY 1450 -AGTGCATCG--TG-----CA--A--CCTCTT--TGG-----TG--CCAGTG-- 1481
Db 4054 GTGCTGCTCTGCTCTCTCATCAGTCCCACTTCTGCTGCTGTCTGCTGCCCCAG-GAAA 4112
QY 1482 TG-----GG--CAAGGC--TCAG-----C-----CT-----C 1500
Db 4113 TGCAGCAGCAGGCCCCAAGAGCTCTTTCAGAAATACGCAACACGAAAACCTTACAGAAGAC 4172
QY 1501 TCTGCCACAGA-----GTG-----CCCCAC-----G-----TG--GA 1527
Db 4173 ACTGC--CAGACCTTCTGTATGTGAATTTTCACACCTTGAAGAAATTCGCAAAATGA 4229
QY 1528 -----ACAT-----TCTGAGCT-GGCCATC-CCA-A-ATTCAATC-AGTCCA 1565
Db 4230 AATGTTTGACATCTTCCCTCTGAGTATGCCC-TCACCAGACATTCCTCTGCTGCC 4288
QY 1566 TAG-----AG-A--CGAACAGAAAT-----GA-----GA-----CCTT 1589
Db 4289 TAGATGTTTTGCAAGTAATCCAAAAGAAATACAAAAGGATTAAGTTTGAATCAACCTG 4348
QY 1590 CCGGCCCA-AG---C-GTGGCGCTGCGGCGACTTTGTTAGAC-----TGTG-----CC-A 1633

Db 4349 CCTACCCATAGACACCGTGGATCTG-----ACCTT---TAGACTCAATTTGGTCTCTTA 4400
 Qy 1634 C-----CACG---GC-----GTGTGTGT---GAA-----AC-----GTG 1657
 Db 4401 CTGGAGGGAAGATCATGAAAGCCACACAGT-AGTTATTCAGAACTAAACACCTGCAGAGTG 4459
 Qy 1658 -----AAA---TA-----A---AAAGAGCAAAA- 1676
 Db 4460 TTGTCATCTCTACAGCTTAGCGAGGTTTACCCAAAGAGGAGAACTTCTGCTGCAC 4519
 Qy 1677 --AAA 1679
 Db 4520 CCAAA 4524

RESULT 10

US-09-566-921-133

; Sequence 133, Application US/09566921

; Patent No. 6682888

; GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.

; APPLICANT: Tingley, Debora W.

; APPLICANT: Edwards, Carla M.

; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE

; FILE REFERENCE: PA-0024 US

; CURRENT APPLICATION NUMBER: US/09/566,921

; CURRENT FILING DATE: 2000-05-05

; NUMBER OF SEQ ID NOS: 138

; SOFTWARE: PERL Program

; SEQ ID NO 133

; LENGTH: 8734

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6682888 256009.4

; NAME/KEY: unsure

; LOCATION: 500

; OTHER INFORMATION: a, t, c, g, or other

US-09-566-921-133

Query Match 41.6%; Score 698.9; DB 4; Length 8734;
 Best Local Similarity 41.6%; Pred. No. 0.00063;
 Matches 1396; Conservative 0; Mismatches 176; Indels 1785; Gaps 413;

Qy 3 TGTGTC---CTTC-AG--CA-----AAAAGTGGAT-----TT----- 29
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 Qy 30 -----AAATCT-CCTT---GC---A-----CA-AG----- 46
 Db 199 ATGAAGATCCCAAAATTTACCTTCTCTGGCCGTGAGCTGTTGGCAGAGAAATGGGGTG 258
 Qy 47 -----CTTT-----G-AGAG--CAACA--CAATCT-AT-CAGGA----- 72
 Db 259 GATGTCATTCCTTAAGCAGAGCCAGCATCCAGCTGGTGGAGACGGCGAGTGGG 318
 Qy 73 AGGA-----AAG-AAA-GAAAAAACCC--G-----AA-----CCTGA-----CA- 102
 Db 319 AAGAGTCTGAAGTCAAACTGMAAAAGTCCCAAGTTTAAATGCTTTCCTGAGTATTCAT 378
 Qy 103 -----AAA-----A-----A---GAAGAAAA---GAAGAG-----AAA-AAAAAT 132
 Db 379 CTCCCAAGATTCTATGCTGAGCGTGGAGCTAAATTTGA--AAGGTCCCAATTCAGAT 436
 Qy 133 -----CATGA-----AAA-----CCA-----TCCA-GCC-----AAA-----A 154
 Db 437 GCTGACATGATATCAAGCTCCCAAGATCTCCATGCTGATATGACTTAAACTTGAA 496
 Qy 155 ATG-CACAA-----AT-----TTCT-----AT-----CTCTT 173
 Db 497 AGGNCCTAAAGTGAAGGGCGATGGATGTTTCTCTGCCCAAAATGGAAGGTGACCTCAA 556

Qy 174 GGGC---AAATCT---TCACGGGGC---TGG-C-----TGCTC-----TG-TGT 205
 Db 557 GGGCCAGAGAGCTGACATCAAGGGCCCAAGTGGACATTAATGCTCCAGATGTTGATGT 616
 Qy 206 -----CT-----T---CCAAGG---AGTGGCC---GTGC-GCA----- 230
 Db 617 TCAGGGCCAGATGCGCACCTGAAGATGCCCAAGGTGAAATGCCAAGTTCAGCATGCC 676
 Qy 231 --GC-----GGAGATG---CC-----ACCTTCCCAAGCT-----AT- 258
 Db 677 TGGCTTCAAGGAGAGGGCCACAGATGTGGATGTGAACC-TGCCCAAGGCTGACCTTGATG 735
 Qy 259 -----GGA--CAACGT-GAC-----GGTCC-----GGC-----AGGG-- 282
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 Qy 283 -----GG-----AGA-GC-----GCCACC-----CT-CA 299
 Db 796 AGTTGAAGGTCCCAATTCAGATGCTTGAGATGAACATCAAGCCCCCAAGATCTCCA 855
 Qy 300 GGTGCACT--ATTGA-C--AACC-G---GGTCACCC-----GGGTG----- 331
 Db 856 --TGC-CTGACATTTGATCTTAACCTGAAAGG--ACCCAAAGTGAAGGTTGATGATGT 910
 Qy 332 G-C-CTGGCTAAACCG-----CA-GCACCA--TCCTCTATG-CTGGGA-ATGA----- 372
 Db 911 GTCTCTGCAAAAGTGAAGGTGACATGCA--AGTTCC-----TGACTTGGATATTAAGG 964
 Qy 373 --CA-AGTGG-----TGCC-----TGATCTCTCGG-----TGTCCTTCG 406
 Db 965 CCCCAGTGGATATTAATGCCCCCAGATGTGATGTTGAGGCCAGACTGG--CACCTG 1022
 Qy 407 A-----GC-----AACA--CCCAACG--CAGTACA-----GCATC-----GAGA-- 437
 Db 1023 AAGATGCTTAAGATAAAATGCCCCAA--GATCAG--CATGCTGGCTTCAAGGAGAGG 1078
 Qy 438 TCCAGAACGTGATGTGTA--TGACGAGGC--CCTT-AC-----ACC-----TGC 478
 Db 1079 TCCAGAA--GTGGATGTGAACCTGCCCAAGGCTGACCTTGACGTCTCAGGACCCAAAGTGG 1137
 Qy 479 TCGGTG-----CAGA-----CAGA-C-AAC----- 496
 Db 1138 AGTTGATGTTCCAGATGTGAATATTGAAGTTCAGATGCGAAGTGAAGGCCCTTAAT 1197
 Qy 497 -CA-----CC-----CAAGACCTTAG-GGTCCA--CCT-CAATG--TGC 530
 Db 1198 TCAAGATGCCAGAGATGAACATCAAGGCCCAAGATCTCCATGCTGACTTTGATTTGC 1257
 Qy 531 AAGTATCT-----CCCAAAATTGTA--GAGA-----TTTCT-----TCAGAT-- 565
 Db 1258 -----ATCTGAAGGCCCTTAAGTGAAGAGATGTGGATGTTTCTCTCCCTAAGATGAA 1313
 Qy 566 -ATCT-----CCATTA--TG-----AAGGG-----AACA-----ATATT-A-GCCTC 598
 Db 1314 GGTGATCTAAGAGGCCCTTGAAGTTGACATCAAGGCCCAAG--AGTGGACATTTGATGCC 1372
 Qy 599 ACCTG-----CATAG--CA-CTGG--T--AGA--CCA-----GA-----GCCTA- 629
 Db 1373 AGATGTGATGTTGATGCCAGACTGGCACCTGAAGATGCCAAGGTGAAGATGCCCA 1432
 Qy 630 -----C-GGTTACTT--GGAGA-----CA-----CATCTCT-----CCCAA 657
 Db 1433 ATTCAGATGCCAGG--ATTTAAGGAGAGGCCCAAGTGGATGT-TAATTTGCCCAA 1489
 Qy 658 AGCGTTCGCTTTG-TG-----AGTGAAGACGAAT-----ACT--TG-----G 692
 Db 1490 AGC---TGACATGATGCTCAGGACCCCAAGTG--GAC--ATTGACACTCTGATATTG 1542
 Qy 693 AAATTC-----AGGCAATC--A-----CCC-----G-GGA--GCA-G 718
 Db 1543 ATATTGATGTTCCAGAGGGGAACTGAAGGGGCCCAAAATTTAAATGCTGACCTGACC 1602

QY 719 TCAGGGGACTACG-AG-----TGC-----AG-TG-CC-----TCCA---AT 748
Db 1603 TCAGGGCAC--CGAAGATCTCTATGCTGAAGTGAACCTGAATCTGAAGGTCCTCAAGAT 1660
QY 749 -----GACGTGGCCG-----C-GCCC-----GTGCTACGAGA-GTAAAGGTCAACGTGA 791
Db 1661 GAAGGGCGAGTGGAGCTTCTCTGCGCCAAAGTGG--AAGCGACCTCAAGGGC-CC-TGA 1717
QY 792 ACTATCCACCAT-ACATTTCCAGAG--CC-AAGGGTACA--GGTGTCCCGG-TG-GGA 841
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QY 842 C--AAAGG-----GGACAC-----TGC-----AGTGTAA--GCC-----TCAGCA 874
Db 1766 CGTTCAGGCCCAAGCTGG-CACCTTAAATGCCCCAAGTGAATATGCCCAAGTTCAGCA 1824
QY 875 GTCC-----CCTC--AGCAGAAATCC--A-GTG-----GTG--CAAGGTGA-----909
Db 1825 TGCCTGGCTTCAAGAGAGAGGGCCAGATGTGGATGTGAACCTGCCCAAGGCTGACCTTG 1884
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Db 1944 GCGAAACTAAG-GGCCCTAAATTC-A-AGA--TGCCTGAGATGAACATCAAGGCCCA 1998
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QY 1007 A-ACTACACTTGC-----GTGG-----CCTCCAAACAAGCTGGGCC-----ACACC 1045
Db 2059 ATGTTTCCCTTCTTAAAGTGAAGGTGACCT--CAA--GGGCCCAAGAGTTGACATC 2111
QY 1046 AATG--CCA-----G-CATC-ATGC-----TA-----TG-TGCTCCA-----GGC- 1075
Db 2112 AAGGCCCAAGTGAAGTGAATCGATGCCCTGATGTAGATGTTCTATGCGCCAGACTGGCAC 2171
QY 1076 -----GCCGTGACGAGGTGA--GC--AA--CGGCACG-----TC-----GAG 1107
Db 2172 CTGAAGATGCC--CA--AGTGAATGCCCCAATTCAGATGCGAGGATCAAGGA- 2225
QY 1108 GAGGG--CAGGCTGCTGCTGCTGCTCTT-CT--GGTCTTGCACCT--G-GTCTCT 1158
Db 2226 GAGGCCCA-GATG-----TGATGTTTACC-CTTCTAAGG-C-TG-ACATTTGATTTCT 2276
QY 1159 -----CAAAAT--TTGATG--TGAGTGCCACT-TC-----CC-----ACC 1189
Db 2277 GGCCCCAAGTGGACATTTGATGCCCTTGA-TGTGATGCAAGGTCCAGATGCAAACT 2335
QY 1190 C--GGG--AAAG-----GCTGCC-----G-CCACCA--CCACCA-----CCA--- 1219
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Db 2456 CAAAGTGAAGGTGATCTCAAGGCCCTGAAATTTGACATAAAGGCCCAAGTTTGGACAT 2515
QY 1255 -----CA--GAT-----ATAT--A-----C-----AAAT-----G--AAAT--A 1276
Db 2516 TGACACACTGTGATCAATTTGAAGTCCGGAAGGAAATTTGAAGGGCCCAAAATTTAA 2575
QY 1277 GA-----AGA--ACA-C--ACC-----CTC-ATG--G-----GA-----CA--- 1300
Db 2576 GATGCTGATGAACATCAAGACTCCCAAAATCTCTATGCTGACTTTGATTTGACACT 2635
QY 1301 GAAA--T-----TTG-AGGG-----AGG-GGAA-----C- 1320

Db 2636 GAAAGTCCCAAGGTGAAGGTGATGTGATGTTTCACTACTTAAGTGGAAAGTGTCT 2695
QY 1321 --AA-----AGA--ATACCTTTG--GG-----GGGA-----AAAG-----AGTTT- 1348
Db 2696 GAAAGGGCCAGAGGTAGACATTTGAGGTCTCTGAAGGGAAGCTCAAGGTCCCAAGTTTAA 2755
QY 1349 -----TA-A--AAAAG-----AAAT-----TGA-----AAATTTGCCTTTGCAGAT 1379
Db 2756 GATGCTGATGTACATTTCAAAAGGCCCAAAATCTCCATGAGTGACATTTGATTT--GA- 2811
QY 1380 ATTT--AGG-----TACA-----ATCGAGTCTTTCTTTTCCCAAC--GGGA- 1416
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Db 2872 ATCTGAAGGTCCCAAGTGGATGTCAAGGCCCTTAAGTGGCATTTGACATCTCTGATA 2931
QY 1439 --GAC-----CC-----ACTG-----CAA-----G-CTG-----C 1455
Db 2932 TTGACATTTATGTTCCAGAGGGAACCTGAAGGGCCCAAAATTTAAATGCTGACTTAC 2991
QY 1456 A--TC--GTGCA-----ACCTCT-----TTG--G-----TG-----CC--AG 1479
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QY 1480 TGTGGGCAAGGCG-TCA--GCC--TCTCTGCCACACAG-----AGTGCCC 1518
Db 3051 -GTG--AAGGGCGACATGACATTTCTCTGCCCAAGTGAAGGCGACCTCAAGGGCCC 3106
QY 1519 CCAGTGAACATTTCTGGAGTGGCCATCCCAATTT--CAATCA-GTCCATAGA--G 1570
Db 3107 CGAAGTTG-ACA-TC--AG--GG--ACCCCAAGTGAACATTTGATGTCC--CAGATGTG 3156
QY 1571 ACG--AA--CAGAAATGAGACCT--T--CC--G-----GCCCA--AGCG 1601
Db 3157 ACGTTCAAGGCCAGATGTCACCTTAAATGCCCCAAGTGAATGCCCCAAGTTCAGCA 3216
QY 1602 TGGC--GCT-----GCGGGCAC--TTTGG-----T-----AGACTG-- 1628
Db 3217 TGCCTGGCTTCAAGAGGAGAGGGCCAGATGTGATGTGAACCTGCCCAAGCTGACATTG 3276
QY 1629 -TG-C-CA--CCA--CGG-CG-TG-TGT-----TGTA-----AACGT-----1656
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Db 3337 CGAACTAAGGGCCCCCAAGTTCAGATGCTGATGAGATCAAGGCCCAAGCCCCCAAGA 3393

RESULT 11

US-08-619-198-8
; Sequence 8, Application US/08619198
; Patent No. 5885831
; GENERAL INFORMATION:
; APPLICANT: Young, Michael W.
; APPLICANT: Sehgal, Amita
; APPLICANT: Vosshall, Leslie B.
; APPLICANT: Price, Jeffrey L.
; APPLICANT: Myers, Michael
; TITLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED
; TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,198
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-128A CFI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5192 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-619-198-8

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Query Match	41.6%	Score 698.6	DB 2	Length 5192
Best Local Similarity	39.1%	Pred. No. 0.00023		
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QY	2	TTGTGTCCTTCA--GCA-A-AACAG--TGA-TTTAA-----ATCTCT-TGCACAAGC	47	
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Db	166	GGGATAGAAAAAATTTAAATAATTTGTTACAGATACCGCGCAATGCTAAGAAGTACCTC	225	
QY	143	-A---TC-CAGCCAAAAATG-----CACAAAT--TCT-----ATC	169	
Db	226	AATGTTGCGAGTCGACAATGAGCAGAGTTAGGCAGCTCCACAATCACTTGGAAATAATC	285	
QY	170	---TCCTT-----GGGCATC--TTCACGG--GG--CTGGCTGCTC--TGT--	203	
Db	286	AGAACTTTGATAAAGTGAATCGGTT-ATGGACTGGTTACTAGCAACTCCGCAGTTGTAC	344	
QY	204	---G-TCTCTTCC-----AAGG-----A-GTG-----CCCG--TGC--	227	
Db	345	AGCGGTTCTCTCTCTGGGTTGCTGGAGGGCGATACCTATGTGGTCAACCCGGAATGCA	404	
QY	228	--G-CA-----GCGGAGATGCCACTTCCCAAG-----CTAT--GGAC--AAC--	265	
Db	405	TTGGCCATTCTGGAGGAGAT--CAACTAC---AAGCTCACCTATGAGGACCAAAACATG	458	
QY	266	G-----T-GACGGTCC-----GGC-----AGG-----G	282	
Db	459	CGCACCTTTGACCGGGCAATTGGATTTGGCCAGAAATGTGAGTCCAGACTGTATCCGGTGT	518	
QY	283	--GGAGAGCGCCACCCTCAGG--TGC---ACT--ATT--GACAAACGG-----GTC-	322	
Db	519	CTGGAGATGCA--AGGATGATCGGTCCTGGAGTCGGTCACTCCGGATCTACGTCA	573	
QY	323	---AC-----CCGGGTGG-----CC-TGG-C-TAA--ACCGCA-----	347	
Db	574	ATCTGACGGTGCC--GGTGGAGTGCCTCTTCTCCGTGGACGTTGATGTCGACCGGATGTG	632	

QY 771 GGA---GAGTAAAGTACC---GTG---AACT---ATCCA---CCA-T-----803
Db 1706 GGATTCGG-GTTATGG-CACCCAGGTGGAATATCAGGAATCCATTTCACCTCCAGCAAC 1763
QY 804 -AC-AT-T-----TCAGAAGCC-----AAG-----820
Db 1764 GACGATGAGCGCGAGGAGGAGCGAGCAGCAGAGCCTCCGCTGTAACAGCAAGCCA 1823
QY 821 -GG-TA---CA-GG-----TGTCCTCGGTGGCAAAAAGG---GAC-----A 853
Db 1824 CGGAATAAACACCGGACGAGTATGTCGCAATGAGCAAAAAGGAGCTTAGACGCAAAA 1883
QY 854 CTGCACTGAGCCCTCAGCA---GTCC---CCTCAGCA---GAA---TTCCAGTGTACA 902
Db 1884 CTG---GTCAAG-CGCAGCAAAAG---CAGCCTCATCAACATGAAGGGTC---TGGTACA 1933
QY 903 -----AGGATGACA-----AAAGACTGATTAAGGAA---A-----GA---932
Db 1934 GCACACCCCCCGATGATGACATCTCCA---TCTG-CTGAAGGAATTCACCGTGGATTT 1990
QY 933 -----AAGGGTGA---GTGGA---AA---ACA-G-AC---CTTTCTCTCT- 965
Db 1991 CUTCCTCAA-GGGTTACAGCTATCTGTGGAGGAACTGCACATGCACATCTGTTTCCAATG 2049
QY 966 CAAA-----ACTCAT---CTTCTT---C-----AATGT-CT-CTGAA-----994
Db 2050 CAAAGGTGCCCATGACACATCGCACTTCTTTGGCTGTGTAACTTCTCTGAAGTTTG 2109
QY 995 -----CA-T-GA-C---TATGG-----GA-ACTA---CAC-----TTG- 1017
Db 2110 CGCCCAACTGGAGTGTGATATGAGACATCGACACTATTCTCACCTACGATGTTTGA 2169
QY 1018 -----CGTGGCCT-----CC-----AACAGCTGG-----GCC-ACA- 1043
Db 2170 GCTACTTCACCTATGAGGGTGTGTCCTATGTAGCAAA-CTGGAAGTGAAGTCCGACAG 2228
QY 1044 -----CCATG-CC---AGC---ATC-----ATGCTATTGG-----1068
Db 2229 GAGGCACTGACCTGAAGCCCTATCTAAGGCGCAATGC-ACCTTGGTGTGAGCGGCATCCG 2287
QY 1069 -----TCCAGGCGC-----CGT-CAGCGAGGTGAGC-----AAG-CAAG- 1102
Db 2288 GGAGTTCCTCCAGGC-CATTGATAGTACACAAAGTGA-CTCATCTGAACGAGAGCAG 2345
QY 1103 -----TCGAGG-AG---G-GCAG---GC-----TG---CG-TCTG-GCTGC---1130
Db 2346 AAAGCCCATTTGAGCGAGCTTCAGCTGCAGATTAAGCAAAATGTCGATCTGAGTGCCTT 2405
QY 1131 -----TGCTCTCTG-GTC-TTGCA---CCTGC-TTC-T-CAA---ATTTT---GAT 1169
Db 2406 TTTGTGCTCTGCTGAGCGGTTTCAATCCAGCAATTCATTCAGCAGTATCTTCAGGAT 2465
QY 1170 GTGAGTG---C---CACTTCC-CC-AC-----C-----CGG-GAAA-----GG 1198
Db 2466 CTG-GTGGTTACCAATCAGATCTCTCTACTCATCTGACAGTTTCGGCAAACTTGTGTGG 2524
QY 1199 CTG-----C---CGCC-----AC-CA-----CCAC-----CA 1216
Db 2525 ATGTCAAAACCATTCGCTCTCGAGACATAAACAAGTTTTCAGCTGGAGGTGATGCA 2584
QY 1217 C-----C-----CAAC-ACAAC-----AG-----CAATG-----1233
Db 2585 CTACTATGGCATTTCTGTGGAGGACTTCAACAACAACGAGAGTTTCTCAATGACTGCAT 2644
QY 1234 -----GCAACAC-----CGA-----CAG-----CAACC 1251
Db 2645 CTTCCACCATGATGATCAGATCGGTGGGATCTGGCCAGATTTGGGTTTCTATTTCAACC 2704
QY 1252 AATCA---GATA---TATCAAAATGAAT-AGAAG-----A---AAC-----AC 1286
Db 2705 AATTTATTTGAAACCTATTCAA---GAATTTGGAAGCGGACTATGAATGCTGCGATGAC 2762
QY 1287 AG-C---C---TC-----ATGGGA-----CA-----GAA-----1303

Db 2763 TGGTCTGATCTTATCGAGTATGTGATTCACAAGTTTCATGAATCTCTCCGAAGTCGCCA 2822
QY 1304 -----AT-----TTGAGGA---G-----GGGAACA-AA---GA---ATAC- 1329
Db 2823 CTCACCATCTCTACAACTTCCTTTGACGGAATGACCAGGAACACACACAGAGCATACC 2882
QY 1330 -TTTG-----GG-G-GGA-AAA-GA-----GTTTTA-----AAA 1353
Db 2883 GTTTCCTCTTGGTCCGAGGAGGAATGGACACACTTTTATTTGTTATTTGTCAGAGCAAG 2942
QY 1354 AAGAA-----ATT-----GAAA---A-TT---GC-CTTCCAG---ATATTTA-GG-TACAA 1391
Db 2943 AAGAACACAGTATTTGTCGGAAGAGTAGTTAAGCTCTT-CAGCAACA---ACGGCAACAA 2998
QY 1392 -TGGA-----GTTTTCT-TT-TCCCAACGGGAA-----G-AACACAG-CA-----CAC 1430
Db 2999 GCTGAAAACACGAGGATTTCTATTATCC---AAC---AATTTTGCACA-AGACATTTATCAC 3052
QY 1431 CCGGCTTGG---AC-----CC-----A-C-----TGC-----AA---GC 1452
Db 3053 CCTG-TTGGAAATGATGACCTGATGAAGTTTCGAGGATCGGAGTATCAGAGAACTTTGC 3111
QY 1453 TG-CA-T---CGT---GCAAC---C---TCT---TTG-----GTGC-----1476
Db 3112 TGACAACTCCCACTTCCGCAACACAGAGTCTGGAATGAGATTAAAGGAGTGGCCTTACG 3171
QY 1477 -----CAG-----TG-TGGGC-----AAG-----GGCTC 1494
Db 3172 GCAAAACCTCAGATGATGTTTCAGATCTCTGTGGACCTGATCATTTAAGGAAACAAAGCGC 3231
QY 1495 AGCCTCT-----CTGC-----CCACA---GAGTGC-----CCC---1519
Db 3232 AGCATTTGTTATGGCTGCAAGAGATCTCTCATTTGAGTGTCTTCTGTTAAACTGACCTGTC 3291
QY 1520 -----CACG-T-T---GGAA---C-AT---TC-TGGAGC---TGCCCATCCCA---1551
Db 3292 GGAGTGTCTCAAGTTTCCGGAAGCGATCATCATGAGGAGCGGTGCCC-TACCATCTGC 3350
QY 1552 AT-T-CAATC---AGTCAAT-----AGAGACGAACA-GA-----A 1580
Db 3351 ATCTGCAAGCAGAGTCCATTCCTGCTGTCAGTG---GAACAAGCAATCCACTACGA 3408
QY 1581 TG-----AGACCT-----TCCGG-CC-CAAGGTGC-----C-GCT-----1608
Db 3409 TGCTGTACAG-CCTTTTGTCTCTCTCTCCACAAGC-TGGGCAATTCAGCTGCGGCGGA 3466
QY 1609 -GCGGGC---A-CTTTGTTAG-----ACTGTGCCACC-----ACGG---1639
Db 3467 CGCGGGCTCGATCTTCCGCAAGATTCGGGACTACTG-GACACGGAGACAATGTACGGAC 3525
QY 1640 -CG-----TGTC-----TTGTGAACGTGAATAA---AA---AGAGCAAAAAA 1678
Db 3526 TCGCCAAAAAGCTGGGAGCCGCTGGACAAACGTGAGTTAAAGTCAACACAGAAAAAACA 3585
QY 1679 A 1679
Db 3586 A 3586

RESULT 12

US-08-619-198-1
; Sequence 1, Application US/08619198
; Patent No. 5885831
; GENERAL INFORMATION:
; APPLICANT: Young, Michael W.
; APPLICANT: Sehgal, Anita
; APPLICANT: Voshall, Leslie B.
; APPLICANT: Price, Jeffrey L.
; APPLICANT: Myers, Michael
; TITLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED
; TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
; NUMBER OF SEQUENCES: 8

/ CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Klauber & Jackson
 / STREET: 411 Hackensack Avenue
 / CITY: Hackensack
 / STATE: New Jersey
 / COUNTRY: USA
 / ZIP: 07601
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/619,198
 / FILING DATE: 20-MAR-1996
 / CLASSIFICATION: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Jackson Esq., David A.
 / REGISTRATION NUMBER: 26,742
 / REFERENCE/DOCKET NUMBER: 600-1-128A CPl
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 201 487-5800
 / TELEFAX: 201 343-1684
 / TELEX: 133521
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 5198 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: linear
 / MOLECULE TYPE: cDNA
 / DESCRIPTION: tim cDNA sequence wherein R at position 1575
 / HYPOTHEICAL: NO
 / ANTI-SENSE: NO
 / ORIGINAL SOURCE:
 / ORGANISM: Drosophila melanogaster
 / US-08-619-198-1

Query Match 41.6%; Score 698.6; DB 2; Length 5198;
 Best Local Similarity 39.1%; Pred. No. 0.00023;
 Matches 1432; Conservative 0; Mismatches 169; Indels 2060; Gaps 426;
 QY 2 TTGTGCTCTTCA-GCA-A-AACAG---TGGA-TTTAA---ATCTCT-TGCACAGC 47
 Db 1 TT---T-CATCAGTGCATATAACAGCAGCTGAACTATAACAGATCTATCTG---CAA-- 52
 QY 48 TTGAGAGCAACACAA---T-CTATCAGAAAG---AA-----AGAAAGA-AAAAAACC 92
 Db 53 ---AGA--AACCCAAAAGTGC--TCAGAAAAGCTCAATTGCTTAGAAAACATAAACAATC 105
 QY 93 GAACC-----TGA---CA-----AAAA--AGAA-GAARA-AG---AA----- 119
 Db 106 --AGCTTTAATTGTTGATTCGAATTCGGCTAAACTAAACTAAACATAAAATTTGTCT 163
 QY 120 --GA-AGAAAA---AAATCAT---GA-----AA--ACC-- 142
 Db 164 GCGATAGAAAAAATTTAAATAATTGTTACAGATACCGGCAATGCTTAAGAGTACCTC 223
 QY 143 -A---TC-CAGCAAAAATG-----CACAAAT---TCT-----ATC 169
 Db 224 AATGTTCCAGTGCACAAATGAGCAGAGTTAGCAGCTCCACAATCACATCTGGAATAATC 283
 QY 170 ---TCTT-----GGGCAATC--TTACCGG---GG-----A-GTG-----CCCG-TGC- 227
 Db 284 AGAATTTTGATAAAGTGAATCGGTT-ATGAGTGGTGTCTTGGAGGCGGATACCTATGTGTCACCCGATGCA 402
 QY 204 -----G-TCTCTTCC-----AAGG-----A-GTG-----CCCG-TGC- 227
 Db 343 ACGCGGTTCTCTCTCTCTGTTGTTGAGGCGGATACCTATGTGTCACCCGATGCA 402
 QY 228 ---G-CA-----GCGAGATGCACCTTCCCCAAG-----CTAT--GGAC--AAC----- 265
 Db 403 TTGGCCATCTGGAGAGAT--CAACTAC-----AAGCTCACTATGAGGACCAACAACACTG 456

QY 266 -G-----T-GACGGTCC-----GGC-----AGG-----G 282
 Db 457 CGCACCTTTTCAGCGGCCAATTGGATTTCGCAGAAATGTGAGGTTCAGACCTGATACCGCTG 516
 QY 283 ---GGAGAGCGCCACCTCAGG---TGC---ACT---ATT---GACAAACGG---GTC- 322
 Db 517 CTGGAGAAATGCCA---AGGATGATCGGTCTCGGAGTCGGTCACTCGGATACTCGTCA 571
 QY 323 ---AC---CCGGGTGG---CC-TGG-C-TAA---ACCGCA----- 347
 Db 572 ATCTGACGGTGCC-GGTGGAGTGCTCTTCTCGGTGACGCTGATGATACCGCAGGATGTG 630
 QY 348 ---G---CACCATCTCT---TA---TGCCTG-----GMAA-----T--- 370
 Db 631 GGTGCGCACACCATCTTCGAGCTGAATAAGCTCTGTACACACAGGAAGCAATTTACC 690
 QY 371 ---GA---CAA---GTGGTG---C---CTGGA-TC----- 389
 Db 691 GAGGCCAGGAGCACCAAGACGCTGGTGGAGTACATGAACACATATCTGGAGTCGGACCT 750
 QY 390 ---C---TCG-CG---TG-----GTC-----CTTCTGAGCAA--- 411
 Db 751 AAGCTGTGCGCGCACAAATGCGATCAAAATCAACAATGCTGCTGCTGCTGCTGAGAAATATC 810
 QY 412 ---CAC---CCA-A-ACGCA---GT-A---CA---GCA-TCGA----- 435
 Db 811 CTGCACATTCAGAGACGATGCCCATTCGCTGATGCCATGATGATGATGATGATGATGATGAT 870
 QY 436 -G-ATC-----CAGAAC-----GTGGA----- 450
 Db 871 GGCATCTCCATGCAGAACACGATCTGTGGAATCTCTTCATCCAGAGCATCGACAGTTA 930
 QY 451 ---TGTGT---ATGAC-----GAGGGCC--CT-----TACACCTG 477
 Db 931 CTCCTGTATCTGATGACTGTCCGACAGAGCCTCTTCGGGAGTGACCATGTGCAACTG 990
 QY 478 ---CT-C-GG-T-GCA-GACA-GACAA---CCA---CCCA---AAGACCTCT 511
 Db 991 ATTGCTTTGATCTACAGGATCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1050
 QY 512 AGGGT-CACCTCT-ATT-----G-TGCAA---GT---AT---C---TCCCA 542
 Db 1051 ---GATCCCACTCCGATTCCTCGGACAAACGCGCAGCAATGCGCTGGCATGGCGGTGGCA 1108
 QY 543 -----AA-----A-TTGTAGAGATTTC-----TTCA-GA-TAT--- 567
 Db 1109 TCGGGAGGAACACGCGGCCACTTTTCAG-GAGGT-CAGCCGCAAGGGTCAGAGTATCAG 1167
 QY 568 ---CTCCAT-----TAA-----T-GAAG-GG--AACAAATAT- 591
 Db 1168 AACGCCATGGCCAGAGTCCAGCGGATAGCCCGATGCTCGAAGAGCCAGCGATATG 1227
 QY 592 -----TAGC-CTCA-CTTGCAT-----AGCAA-----C 612
 Db -228 ACGGGGAACGACAGCAGCAGCAGCTGGATTCGCGGAGCAATCGCAGCCGCGCGGATGCC 1287
 QY 613 ---TGG---TA---GACCAGA---GC-CT----- 628
 Db 1288 ATGATGATGAGATTACAGGACCAAGACACAGGCAACTGAACGAGCATGGCGAAGAG 1347
 QY 629 -----ACG-----GT---TAC---TT-----GGAG 642
 Db 1348 GATGAAGATGAGGACGAAGTGGAGGAGGAGAGTACCTACATTTGGGCCCGCCGCTCGAG 1407
 QY 643 -----ACACA-----T-----CTCT-----CCCAA----- 657
 Db 1408 CCCCTTAACCTTAACACCAACACAGCTGACAAAGTCAACAACTTACCAACCCACCTCC 1467
 QY 658 A--GCG-----GTGCTTTG---TGAG---TGAAG--ACGA-ATACT-TG---GAA 694
 Db 1468 AGTGGCCACNAGGCTGCTGGGCAATGAGCCATTCAGGCCAACCCACTCTCTCCAG-- 1525

QY 695 ATTGAGGAT-CACC-CGGG-----GCAG-----TCAGGGA-----CTACGA 732
Db 1526 --TCAGAGCTCCACCTCGGCACACGCTCAATGTCAGAGTTTCAACGAATCTCTACGC 1583
QY 733 GT-----GC-----AGT-----GC-----CTCCA-AT 748
Db 1584 GTCCACGATCTGCGGTCAATGCGCCCAAAAGTCCCCACATGCGCGGCGAGCTCCAGCT 1643
QY 749 GAC-----GTG--G--CC-----GGG-----CCC-----AAG-----820
Db 1644 GACCAAGGCAAGTGTGTCCAGAGCGGGAATGCTCCCTCCGCACTCGAGGTATC 1703
QY 771 GGA-----GAGTAAGTCAAC-----GTG--AACT-----ATCCA-----CCA--T-----803
Db 1704 GATTCGG--GTTATGG--CACCCAGGTGAAATCAGAAATCCATTTCCACCTCCAGCAAC 1761
QY 804 -AC-AT--T-----TCAGAGCC-----AAG-----820
Db 1762 GACGATGATGGCGCGAGCGGAGCGGACGACCGAGAGCTCCGTTAACAAGCA 1821
QY 821 -GG--TA--CA--GG-----TGTCCTCGTGGGCAAAAGG-----GAC-----A 853
Db 1822 CGGAATAAACACGACGACGATTTATGTCGCAATGGACAAAGAGCTTAGACGCAAAA 1881
QY 854 CTGCAAGTGAAGCTCAGCA-----GTCC--CCTCAGCA-----GAA--TTCCAGTGTATCA 902
Db 1882 CTG-----GTCAAG--CGCAGCAAAAG--CAGCCCTCATCAACATGAAGGCTC--TGGTACA 1931
QY 903 -----AGGATGACA-----AAAGACTGATTTGAAGGAA--A-----GA-----932
Db 1932 GCACACCCCGGATGATGATCTCCAA--TCTG--CTGAGGAATTCACCGGTGATTT 1988
QY 933 -----AAGGGGTGAAA-----GTGGA--AA-----ACA-G--AC--CTTTCCTCT- 965
Db 1989 CCTCCTCAA--GGGTACAGTATCTGTGGAGGAACTGCACATGCAACTGCTTTCCAA 2047
QY 966 CAAA-----ACTCAT-----CTTCTT-----C-----AATGT-CT--CTGAA-----994
Db 2048 CGAAGGTGCCATGACATCGGCATCTTTTGGCTGGTAACCTACTTCTCTGAAAGTTG 2107
QY 995 -----CA--T--GA--C-----TATGG-----GA-ACTA-----CAC-----TTG- 1017
Db 2108 CCGCCCACTGAGCTGGATGATGAGCAGCATCGACATCTTCTCACCTACGATGTTTGA 2167
QY 1018 -----CGTGGCT-----CC-----AACAGCTGG-----GCC--ACA--1043
Db 2168 GCTACTTGACCTATGAGGCTGTGTCTCTATGTAGCAA--CTGGAACGTAATGCCGACAG 2226
QY 1044 -----CCAATG--CC-----AGC--ATC-----ATGCTATTGG-----1068
Db 2227 GAGGCGAGTCACTGAAGCCCTATCTAAGCGGAATGC--ACTTGGTGGTGAAGCCATCCG 2285
QY 1069 -----TCCAGCGC-----CGT--CAGCGAGGTGAGC-----AACG--GCAG--1102
Db 2286 GGAATTCCTCCAGC--CAITGATACGTACAAAGTGA--CTCATCTGAACGAGGAGCAG 2343
QY 1103 -----TCGAGG--AG-----G--GCAG-----GC-----TG--CG--TCTG--GCTG--1130
Db 2344 AAGGCCATTTGAGGAGCTTACGCTGCAGATTAGCGGAATGTCGATCTGAGGTGCTT 2403
QY 1131 -----TGCCTCTCTG--GTC--TTGCA-----CCTGC--TTC--T--CAA-----ATTTT--GAT 1169
Db 2404 TTTGTGCTTCTGCTGAGGCTTTCAATCCAGCATTCATTTCCAAAGCATCTCTCAGGAT 2463
QY 1170 GTGAGTG-----C-----CACTTCC--CC--AC-----C-----CGG--GAAA-----GG 1198
Db 2464 CTG--GTGGTTTACCAATCACATCTCTCTACTCTCTGACAGTTTGGCCAAACTTGGTGG 2522
QY 1199 CTG-----C-----CGCC-----AC--CA-----CCAC-----CA 1216
Db 2523 ATGTCAACCATTCGCTCTGCGAGCAGACATAACACAGATTTGGCACGCTGAGGTGATCA 2582
QY 1217 C-----CAAC--ACAA-----AG-----CAATG-----1233

Db 2583 CTACTATGGCATTTCTGTTGGAGGACTTCAACAAACGAGAGATTGTCTCAATGACTGCAT 2642
QY 1234 -----GCAACAC-----CGA-----CAG-----CAAC 1251
Db 2643 CTTTCACTGATGATCATCATCGGTGGCATCTGGCCAGATTGGGTTCTATTTCACCC 2702
QY 1252 AATCA-----GATA-----TATACAAATGAAT--AGAAG-----A--AAC-----AC 1286
Db 2703 AATTATTTTGAACCTATTCAA--GAATTTGGGAAGCGGATCATGAATCTGTGCGATGAC 2760
QY 1287 AG--C--C--TC-----ATGGGA-----CA-----GAA-----1303
Db 2761 TGGTCTGATCTTATCGAGTATGTGATTCAAGATTCAATGATCTCTCCGAAGTCGCCA 2820
QY 1304 -----AT-----TTGAGGA--G-----GGGAACA--AA--GA--ATAC--1329
Db 2821 CTCACCATTCCTACAACTTCTTGGCGGAATGACCAAGGAACAACACAGAGCATACC 2880
QY 1330 -TTTG-----GG--G--GGA--AAA--GA-----GTTTTA-----AAA 1353
Db 2881 GTTTGCTCTTGGTCCGAGGAGGAATGACACACTTTTATTGTTATGTCAGAGCAAG 2940
QY 1354 AAGAA-----AAT-----GAAA--A--TT--GC--CTTGCAG--ATATTTA--GG--TACAA 1391
Db 2941 AAGAACACGATATTGTTGGGAAGATAGTTAAGCTCTT--CAGCAACA--ACGGCAACA 2996
QY 1392 --TGGAA-----GTTTTCT--TT--TCCAAACGGAA-----G--AACACAG--CA-----CAC 1430
Db 2997 GCTGAAAACACGAGATTCTATTATCC--AAC--AACTTTTGAACA--AGACATATTAC 3050
QY 1431 CCGGCTTGG--AC-----CC-----A--C-----TGC-----AA--GC 1452
Db 3051 CCTG--TTGGAATACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3109
QY 1453 TG--CA--T-----CGT--GCAAC--C-----TCT-----TTG-----GTGC-----1476
Db 3110 TGACAACTCCACTTCCGCAACACAGAGTCTGGAATTGAGATTAGGAGTGGCTTACG 3169
QY 1477 -----CAG-----TG--TGGGC-----AAG-----GGCTC 1494
Db 3170 GCAAAACCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3229
QY 1495 AGCTCTC-----CTGC-----CCACA--GAGTGC-----CCC-----1519
Db 3230 AGCATTTGTTATGGCTGCAAGGATCTCTCATTTGAGTCTGCTTCTGTTAAACTGACCTGC 3289
QY 1520 -----CAG--T--GGA--C--AT-----TC--TGGAGC-----TGGCATCCCAA--1551
Db 3290 GGAGTGGTCTCAAGTTCCGGAAGGATCATCATGAGGCGGTGGGC--TACCACTGC 3348
QY 1552 AT--T--CAATC-----AGTCCAT-----AGAGCAACA--GA-----A 1580
Db 3349 ATCTGCAAGCAGAGTCCATTCGGTGGTGCAGTG--GAACACGAGCAATCCACTACGA 3406
QY 1581 TG-----AGACCT-----TCCGG--CC--CAGCGTGG-----C--GCT-----1608
Db 3407 TGTGTACAG--CCTTTTGTCTCTGCTCCACAAG--TGGGCAATTCAGCTGCGGCGGA 3464
QY 1609 -CGGCGC-----A--CTTTGGTAG-----ACTGTGCCAC-----ACGG--1639
Db 3465 CGCGGCTCGATCTTCGCCGAATTCGGGACTACTG--GACACCGGAGCAATGTACGGAC 3523
QY 1640 -CG-----TGTG-----TTGTGAACGTGAATAA-----AA--AGAGCAAAAAA 1678
Db 3524 TCGCCAAAAGCTGGGACCGCTGGCAACAACTGAGTTAAAGTCAACCAAGAAAAACA 3583
QY 1679 A 1679
Db 3584 A 3584

RESULT 13

US-09-566-921-109
 ; Sequence 109, Application US/09566921
 ; Patent No. 6682888
 ; GENERAL INFORMATION:
 ; APPLICANT: Loring, Jeanne F.
 ; APPLICANT: Tingley, Debora W.
 ; APPLICANT: Edwards, Carla M.
 ; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
 ; FILE REFERENCE: PA-0024 US
 ; CURRENT APPLICATION NUMBER: US/09/566,921
 ; CURRENT FILING DATE: 2000-05-05
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 109
 ; LENGTH: 4792
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6682888 369213.15
 US-09-566-921-109

Query Match 41.6%; Score 698.4; DB 4; Length 4792;
 Best Local Similarity 40.1%; Pred No. 0.0002;
 Matches 1399; Conservative 0; Mismatches 194; Indels 1892; Gaps 395;
 QY 1 GTTGTGTCCTTC-AGC-----AA-A-ACAGTGGATTAAAT-C-TCCTTG-----40
 Db 378 GCTGTGTCCTTCAGCTACCTGAATGAGACAGTGAAGTCTTCTTGGAGTCTG 437
 QY 41 -C-----ACA-AGC---T---TGA---GA-GC---AA-----CAC-----60
 Db 438 TCAGGGGAACAGAGCCTTCACTGACCTGGAGCGGAGATGACGTACTCCACTGTG 497
 QY 61 -----AA-TCT-ATC-----AGGAAGAAAG-----A-----AAG 83
 Db 498 TCGCCTTCGTGTCCTCCAAAGTCTTCATCCATGAGGAAGTATGTTCCCTCACTGTCCNAG 557
 QY 84 -AAAAAACGACCTGACAA-AA---AAGAAG-----AAA-----AAGAA-119
 Db 558 TGAAGGAGCC-AACC---CAAGAATTAAGAGCGGACACAGTATGTTAAGACGAG 613
 QY 120 GA-----AGA-AAAAAATCA---TGAACACCA-TCAGACCA-AAAA 155
 Db 614 GACAGTCTGCTTTGTTCAGACAGACAAATCAATCTACAAACCGAGGACAGAGTGA 673
 QY 156 TGCACAAATTC-----TATCT-CTTGG--GCAATC-TTCAC-----G---GGGCTGGTGT 199
 Db 674 T-----TTCGTGTGCTCTCCATGGATGAABACTTTCACCCCTGATGATGATTTCA 727
 QY 200 CT-CTGT-C-TC-----TTCC-AAGGAGTCCCGTGCAG-----GCGGAGATGCCA---242
 Db 728 CTAGTATACATTCAGATCCCAAGGAATCGCAT-CGCACAATGSCAGAGTTTCCAGTT 786
 QY 243 -----CC-----TTCCC-----CAAGC-----T-ATGG-----260
 Db 787 AGAGGTGGCCTCAGCAATTTTCTTTTCCCTCTCATCAGAGCCCTTCCAGGCTCT 846
 QY 261 ACAAGTGAAGTCCCGG-----CAGGGG-----AGAGCGCACCTC-----C-----298
 Db 847 ACAAGTGGTGTGACAGAAATCAGTGGAGGACAGAG---CACCTTTTCCACCGTGG 903
 QY 299 AGG-----TG-----CACTA-TTG---AC-----AACCGG-----TCACC--C-326
 Db 904 AGGAATTTGTTCTTCCCAAGTTTGAAGTACAAATGACAGTGAAGTGAAGTAAATCACTCT 963
 QY 327 -GG-----GNG-GCCTGG-CTAAC-C-----GACGACCATCC 356
 Db 964 TGAAGAGAGATGAATGTATCAGTGTG---TGGCCTATACATATATGGGAAGC-CTGTCC 1020
 QY 357 TCT-----ATG-----CTGGGA--AT-----GACAAG--TGGTG-----CCTGGA-T-CCTC 392
 Db 1021 -CTGACATGTGACGTGTGAGCATTTGACAG--AAGTATAGTACCGTTCC--GACTGCCAC 1076

QY 393 GCGTG--G--TC-----C-TTC--TGAG-----CA-----ACACCAAAAC-----GCAG 424
 Db 1077 G-GTGAAGATTTCAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCATGCTG 1135
 QY 425 -----TA-CAGCA-T-----CGAG---ATCCA---GAAGTGG-ATGTGTATG-----458
 Db 1136 CTTCTATCAGCAAGTAAACCAAGGTCTTCCAGCTGAA-GAGGAAGGAGTATCAATGA 1194
 QY 459 -----AC-GAGGGCCCTTACA-CC-----TG-----CT-----479
 Db 1195 AACTTCACACTGA-GGCCC---AGATCAAGAAGAAGACAGTGGTGGAAATTCAGTGGAA 1251
 QY 480 --CGGTGCGAG-----ACAGACAAC--ACCCAAA-----GAC---507
 Db 1252 GGCAGTCCAGTGAATCACA-AGAACCATAACCAAACTCTCTATTGTGAAAGTGGACTCA 1310
 QY 508 --CTCT---AGGG---TCCACCTCATTGCGA-----AGTA-----T 536
 Db 1311 CACTTTCGACAGGGAATTC-CTTCTTTGGGCGAGGTGCGCCTAGTAGATGGGAAGCGCT 1369
 QY 537 C-----TCCAAAATTTGTAGAG--AT-TTCTTTCAGA-----TAT--CTCC-571
 Db 1370 CCTATACCAAA---TAAAGTCATATTCTCAGAGGAATGAGCAAACTATTACTCA 1425
 QY 572 AT--TA-----ATGA--AGGG-----AA-----CAATATTA-----593
 Db 1426 ATGCTACCACGATGAGCATGCGCTTGTACAGTCTCTATCAACACCAACCAATGTTATGG 1485
 QY 594 G--CCTCAC--CTGCATAG---CAACTGGTAGACAG---AG--CC--TAGCGTT 634
 Db 1486 GTACCTCTTCTACTG-TTAGGGTCAATT-----ACAAGATCGTAGTCCCTGTTAGCGCT 1539
 QY 635 AC--T---TG-----GAGACACATC-----TCTCC 655
 Db 1540 ACCAGTGGGTGTGAGAGAAACAGAGAGGACATCACTGCTTATCTTGTGTTCTCC 1599
 QY 656 AAGC--GGTGGCTTTG-----TGAG-----TGAAGACGA-----A 685
 Db 1600 CAAAG--AGCTTTGTCCACCTTGAGCCCATGTCTCATGA--ACTACCTGTGGCA 1654
 QY 686 TACT-----T--GG-----AAATTCAG-----GSCA-----704
 Db 1655 TACTCAGACAGTCCAGGACATATATTTCTGAATGAGAGCACCTGCTGGGCTGAAGAA 1714
 QY 705 --TCACC-----C---GGGA-GCA--GTGAG---GGGACTAC---730
 Db 715 GCTCTCTCTTATTATCTGATAATGCGCAAGGGAGGCATTGTCCGAACCTGGGACT-CATG 1773
 QY 731 GA-----GT---GCAG-----TG-----CC-TC-CAAT-----748
 Db 1774 GACTGCTGTGAGCAGGAGACATGAAGGGCCATTTTCCATCTCAATCCCTGTGAAGT 1833
 QY 749 --GAGTGGC-----CGC-----GC-----CCGTGGTAC---770
 Db 1834 CAGACATTTGCTCCGTGCTCGTGTCTCATCTATGTGTTTACCTACCG-GGAGCTG 1892
 QY 771 -----GGA-----GA-GT---AAA-----GGTCACC---GTGAAT--A--795
 Db 1893 ATTGGGATTTCTGCAAAATATGATGTTGAAATTTGTCTGGCCAAACAGGTGATTTGAGC 1952
 QY 796 TCCA--CCAT-ACA---T-T-----TCAGAACCAA-----GGGT-ACAG-----827
 Db 1953 TTGAGCCCATCAAAAGTCTCCAGCCCTCACAGCCACCTGCGAGTCAAGCGGCTCT 2012
 QY 828 --GT--GT-----CC-CCGTG---GGCAAAAG-GGGACACTGC-----AGTGA-864
 Db 2013 CAGTCCCTCTGGCCCTCTCCGTGCTGTGTGACCAAGCGTG---CTGCTCATGAAGCCTGAT 2069
 QY 865 ---AGC-CTCAGCAGTCC-----CCT-C-AGCAGAA-----TT 891
 Db 2070 GCTGAGCTCTCGCG-GTCCCTCGGTTTACAACTGCTACCAAGAAAGGACCTCACTGCTT 2128

QY	892	CCAGTGG	-----T-AACAAG-----GATGACAAAGACTG-----AT--TG--	923
DB	2129	CC-CTGGCCCTTTGAATGACCAGGACGATG	-----AAGACTGCATCAATCGTCAATAATGTC	2183
QY	924	-----AA-GGA-----	-----AAG-----AAAGGGGTGAAGTGGAAA	950
DB	2184	TATATTAAATGAATCACATATACTCCAGTATCAAGTACAA	-----TGAAAA--GGATATGT	2238
QY	951	ACAGACCTTTTCCT	-----CTCAAA--ACTCA-----TC-----TTCTTT	981
DB	2239	ACAG-C-TTCCTAGAGACATGGCTTAAGGCAATTCACCACTCAAGATTCGTAAC	-----AC-----	2295
QY	982	-CAA-----TGTC-----TC-----TGAA-----CATG-----	-----AC-----	1000
DB	2296	CCAAAATGTGTCCACAGCTTCAACAGATGAATAATGTCATGGACCTGAAGGCTACGTGTAG	-----	2355
QY	1001	-----T-ATGGGAA-----	-----C-TACA-----CT--TGCGTG-----GC	1023
DB	2356	GTTTTATAGTCAAGTGAATGGGAAGAGGCCATGCACGCTGGTGCATGTTGAAGAGC	-----	2415
QY	1024	CTCCAACAAGCTG-GGGCCACACCAA	-----TGCC--AGCATCATG--CT--ATTGTG	1068
DB	2416	CTC-ACA--CGGAGACCGTACGAAAGTACTTCCCTGAG-A-CATGATCTGGGATTTGG	-----	2469
QY	1069	TCCAGGCGCCG-----TCAGC-----GAGGT--GAGCAACGG-----	-----	1098
DB	2470	T-----GGTG--GTAAACTCAGCAGGTGTGGCTGAGTAGGAGTAACAGTCCCTGCACCAT	-----	2524
QY	1099	CACGTCCA--GGAGGGCAGG-----CTGC--GTCTG--GCTG-----	-----	1129
DB	2525	CAC--CGAGTGGAGGCAAGGGCCCTTCTGCTGTCTGAAGATGTGGACTTGGATATCTCT	-----	2582
QY	1130	-----CTGCCTCT-TCGT-GTCTTGCA--CCTGTCTT-----CTCA-AAAT--TT-----	-----	1165
DB	2583	TCCACTGCCTCTCTCCGAGCCTTCCAGCCCTCTTTGTGGAGTCTCAATATGCTTACTCT	-----	2642
QY	1166	TGAT--GT--GAG-----T-----GCCA-----CTTCCC-----C	1186	
DB	2643	GTGAATCTGGAGAGGCCTTCACTCAAGGCCACCGTCTCTAAACTACCTTCCCAATGC	2702	
QY	1187	ACCCGGGAAAG-----GCTG-----CCGCC-ACC-A-----CC-----AC	1214	
DB	2703	ATCCGGGTCAAGTGTGCAGCTGGAGCCTCTCCCGCCTTCTTAGCTGTCCAGTGGAGAG	2762	
QY	1215	CACCAA-----CACACA-----GCAA-----TGGCAACA-----CC--GACACCAA-	1249	
DB	2763	GAAACAAGCCCTCACTGCATCTGTGCAACGGCGGCAA-ACTGTGTCTCTGGSCATTAAC	2821	
QY	1250	-CCAATCAGATATATA-CAAA--TGAATTT-A-----GA-----AGAAACAC--AGCCTCA	1293	
DB	2822	CCCAA--AGTCAT-TAGGAAATGTGAATTTCACTGTGAGCGCAGAGGCCTAGAGTCTCA	2878	
QY	1294	-----TGGACACA-----AATTT--TGA-----GGGAG-----	1314	
DB	2879	AGAGCTGTGTGGGACTGTAGGTGCCTTCAGTTCTCTGAACCGGAAGGAAAGACACATCAT	2938	
QY	1315	-----GG--GAAC--AA-----AGAA-----TACT	1330	
DB	2939	CAAGCCTCTGTGTGTTGAACCTCAAGGACTAGAGAAGGAAACAACTTCAATCCCTACT	2998	
QY	1331	TTG-----GG-GG-GA-----AAAGAGTT-T--TAAAA-----AAGAAAT--T	1361	
DB	2999	TTGTCCATCAGGTGGTGAAGGTTTCTGAAGAAATATATCCCTGAAACTGCCACCAATGTGT	3058	
QY	1362	-GAA-AAT-TGCC-----TT-GCAGATAT-TTAGG-----T-----	1387	
DB	3059	AGAAGAATCTGCCCGAGCTTCTGTCTCAGTTTGGGAGACATATTAGGCTCTGCCATGCA	3118	
QY	1388	-----ACAA-----TGAG-----TTT-----TCTT	1403	
DB	3119	AAACACACAAAATCTTCTCCAGATGCCCTATGCTGTGGAGAGCAGATATGCTCTCT	3178	
QY	1404	T--TCCCAA-----ACGGG-----AA-G-AACACAGCA-----CA-----	1429	

RESULT 14
 US-09-911-842A-3
 ; Sequence 3, Application US/09911842A
 ; Patent No. 6656707
 ; GENERAL INFORMATION:
 ; APPLICANT: Amgen Inc.
 ; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
 ; FILE REFERENCE: 0101/737592
 ; CURRENT APPLICATION NUMBER: US/09/911,842A
 ; CURRENT FILING DATE: 2001-07-24
 ; PRIOR APPLICATION NUMBER: US 60/222,438
 ; PRIOR FILING DATE: 2000-08-01
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 11230
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-911-842A-3

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Query Match      41.6%; Score 698.3; DB 4; Length 11230;
Best Local Similarity 37.7%; Pred. No. 0.0011;
Matches 421; Conservative 0; Mismatches 152; Indels 2195; Gaps 412;

Qy 2 TTGTGCTCT--TCA-----G--CA--AAACA-----GTG-----24
Db 2806 TTAT-TCCTACGATCACTTCCTGGATGTTGTACAGGAACACCCCGATGTGGCAAG 2864
Qy 25 ---GAT-----TTAAA-----TCTCC--TTG-----CACAAGCTTGAGAC--55

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Db 2865 CCAGATCGTCACGGAATTAAGAACTGTCCTCAATGTCCTGACCCCAAAAT--CAGCTAAT 2922
QY 56 ---AACA-CA-ATCTA---TC---AGGAAGAA---GAA---A 82
Db 2923 TTTTAAACATCACAGTACGAGGTCACCTCCACAGAGAAAGAACGATACCCCTTGAATGGA 2982
QY 83 GAA---AA---AAAC---CGAA---CCTGA---CA--- 102
Db 2983 GAATCAGCAGGACTCATTAAGACATTTGGAACAATCACCAATCGCCTGMAAGCACCTT 3042
QY 103 AA-AAAGA-----A-----GAAAA-----GA-AG-AA 122
Db 3043 GAATAAGAGCCCAATGTAATTTTCCAGCTCGCCTCGAACAACAGTGGTGGCTGACAGCA 3102
QY 123 -----GAAA-A-AAAA-----TCATGAACCA---TC----- 145
Db 3103 TTCCCTCGAAACAGAAAGGCTTTCTCTTC-TGACACACAGGCTCTGTGTGAGGGGGC 3161
QY 146 CA---GCCAA---AA---A---TG-----CAC-----AA 162
Db 3162 GCATGTGTCAACTGCCCCCTGGGAACCTTACTCTCTGGAGCAATTCACCTGTGAAA 3221
QY 163 -T---TC-T---ATCTCT-----TG---GCAA---TCT----- 182
Db 3222 GCTGCCTCATGGGATC-CTACCAAGATGAAGAGGCGAGCTGGAATCGAAGCTCTGTCCC 3280
QY 183 -----TCACGGGG-----CTG---GC---TGCTCTGTGT 205
Db 3281 CCRAAGACTCAGCGGAATACCTCCATTCAGAGAGCTCTCTGNAATCAAGCTCAGTGT 3340
QY 206 -----CTCTTCCA-----AGAG---TGC---CGTG---CGCAG--- 231
Db 3341 AAGCAAGGCACCTACTCTCTCAGTGGGCTGAGACCTGCGAATCGTGTGGGTACT 3400
QY 232 -----CGAGATGCCACT-T-CGC-----CAA----- 252
Db 3401 TATCAACCGGAATTTGATCCCGAGCTGCTCTCTATGCCCGAAGAACCAACCAAGGTG 3460
QY 253 -----AGCTATGGACAAC-----GTGACG-GT---CCGG---CAGGGGAGA--- 287
Db 3461 AAAAGAGGAGCGGTGACATCTCTGCTGTG--GAGTGCCTTCCCAAGTAGGAGATCT 3518
QY 288 -----GGCG---CACCTCAGG-----TGC-----ACTATTGACAACC----- 317
Db 3519 CCGCTTCTGGGCTAACACCTT---GCTACCTTTGCTCTGAGACTATTACCAACCAATG 3575
QY 318 ---GGG---TC-ACC-CGGGTGGCC-----TGG--CTA-AACC-----GCAGCA 350
Db 3576 CAGGGAAGTCTTCTGCTCTGCTTGTCTCTTTATGGAATACACCATCACTGGGGCCA 3635
QY 351 ---CCATC-----CTCTA--TGCT--G--GAATGACAAG--T 377
Db 3636 CGTCCATCAGAGCTGCTCAAGTTTAACTTAACTTCTCTCAGCAGCAGAA-GA-AAGCAT 3693
QY 378 GGTGCTGGATCTCTCGGTGCTCTCTGAGCACA---CCCA-AAC-----G 421
Db 3694 AGTGCC-----CCT--CGTGGCCC--CTG-G--ACATTCGACAGAACAGTACGAAGTCAG 3741
QY 422 CAGTACAG-----CATCGAGAT-----CCAGAAC-GTGA----- 450
Db 3742 CAGT-CAGGCTTTTCA-CGA-ATGCTTTTAAACCCCTGCGACACACAGTGGACCTGCCA 3798
QY 451 -----T-----GTG--TATGACGAGG-----GC---CCT---TACACCTGCT---CG-GT 483
Db 3799 ACAGCTTTGGGCGTGTGTATGTC--TGCTCTGCGCCACCTGGATACACAGGCTTAAAGTGT 3856
QY 484 G---CAGACA-----GA---CAAC-CAC---CC-----AA-----AGAC 507
Db 3857 GAACAGATATGATGAATGACGCTCTCTGCTTTCCTTTCCTCAATGGTGGAAATTTGTAGAG 3916
QY 508 C---TCTAGGG--TCCAC---C-----TCATTGTGCAAGTATCTC---CCAAA-AT-TG 548

Db 3917 CAAGT-TGGGGGATTACGCTGCGAATGTTTCATTGGGC---TAT-TCAGGTCAAATATGTG 3971
QY 549 TAGAGATTTCTTCA--GA---TATCTCCA-----TTHATGAAGGGAA---CAAT-A 590
Db 3972 AAGAAAAT--ATAAATGAGTGTATCTCCAGCCCTTGTCTTAATAAAGAAACCTGCACTGA 4029
QY 591 ---TT---AGC---CT-CACCT-----GCATAGCA-----ACTG----- 614
Db 4030 CGGCTTGGCAGCTACCGCTGTACCTGTGTGAAGGATA-CATGGGTGTGCTCTGTGAAA 4088
QY 615 -----GT-A-GA---CCAG---AGCC---T-----ACG--GTTACTTG--GAGACA 645
Db 4089 CAGACGTCAATGAATGCCAGTCAAGCCCTGCTTAAACAACGCACT---TTGTAAGAC- 4144
QY 646 CA-----TCTC-TCCCAAAG---CGG---TTGG---CT----- 668
Db 4145 CAAGTTGGGGGGTTCCTGTCGAATGCCACCCCGAATTTTGGGTACTCGGTGTGAAAA 4204
QY 669 --T-TG--TGAGTG--A--AG--ACG---AAT-----ACTT-----GGA--- 693
Db 4205 AATGTGATGAGTGTCTCAGTCAGCCATGCCAAATGGAGCCACTTCTAAGGATGGTGCC 4264
QY 694 AA---TTTACG--GCATCA---CCCGGAGCAG--TCA-GGGGACTAGA--GTGACAG 738
Db 4265 AACAGCTTCAGGTG--TCAATGTCC---AGCAGGCTTCACAGGAC-AC-ACTGTGAAC 4316
QY 739 TG--CCTCAAATGACGTGGCG--C-GCCGCTGGTACGAGAGATA--AGGTCAACC--- 787
Db 4317 TGAACAT-CAACGA-GTGTGAGTCCAAACCGT-GTA-GG-----AACGAGGCCACCTGTG 4367
QY 788 --G-TGAACATATCCAC-CATACA-TT-----TCAGAAAGCCA-----AGGGTACAG 827
Db 4368 TGGATGAACATA--AACTCATACAGTTGTAATGTC--AGCCAGGATTTTCAGGCCACAG 4422
QY 828 GTGT-----CC-CGG-----TGG---GA-----CA--AAAGS 848
Db 4423 GTGTGAGACAGACAGCCCTTCCGGTTTAACTGGATTTTGAAGTTTCTGGCATCTACGG 4482
QY 849 GAGC--ACTGTC-----AGTG-TG--AAGCCT-CA-GCAGTCCCTCAGCA----- 886
Db 4483 GTACGTCTCTGATAGTGGAGTGTCTGCCAACCCTCCATGCCGTAACTCGCATCTGGAT 4542
QY 887 GAATTC---A-GT-----GG-----TA--CA---AGSATGACAA 912
Db 4543 GAAATCTCTGATGTATCAACTACGAGAGCGCCATCTCTATGCACTTGAGGATGACAA 4602
QY 913 A-----A-----GACTGATTTGAAGGAAGAGGG-----GTGAAATGGA 948
Db 4603 AGAACACACCTTCTCTGACTGAT--A-CAACGGCTGGGTCTTTATGTGAA--TGGA 4657
QY 949 A---AACAG--ACC-TTTCTCTC---AAA-----ACT---CATCTTCTT-CAATG 986
Db 4658 AAGGAAAAGATCACCACCTGCCCCTCGTAATGATGGCATTTGGCATATATGCA-- 4715
QY 987 TCTC-TGAACA-----T-GA---CTAT-----GGGAACATA-CACTTG 1017
Db 4716 TCATATGACACAGTATTGGTGGAGCCTGGAGGCTCTATATAGATGGGAATATC---TG 4772
QY 1018 -CG-----TGGCCTC-----CAA-----CA--AG--C-TG 1036
Db 4773 ACAGTGTACTGGCCTCTCCATTGGCAAGACCATCTGGTGGCGGTGCTAGTTCTTG 4832
QY 1037 GGC-----CA-----CA-----CCA 1046
Db 4833 GGCAAGACGACGACAAAGAGAGGGGTTCACCCGGCTGAGTCTTTTGTGGGTCCA 4892
QY 1047 -ATGCCAGATCA---TG---CTATTT--GGTC-----CAGGCGCGCT-----C 1081
Db 4893 TAAGCCAGC-TCAACCTCTGGGACTATGTCTCTCCACAGCAGGTGAATGCTGGCC 4951
QY 1082 AGC-----GAGG---TGAG-C-----AAGC-----GCA-----C-GTCG 1105
Db 4952 AGCTCTGCCAGAGGAACCTGAGTCGGGGAACGTTAGTGGCCCGATTTCTGTCTCG 5011

QY	1106	----	AGG	----	AGS	----	GCAG	----	GC	----	TG	CGTCT	1124
DB	5012	GGAAATCAGGGAGAGTGAAGTGTGATTTCCAGCAGCATGTTCTCTCTGATTTGTCCTGCT										5071	
QY	1125	----	GG	----	CTG	----	CTGC	----	CTC	----	CTC	1136	
DB	5072	TTAGAAGGATCOGTGCCTCACCTGAGACCTGCATCAGGAATCGAAGCAGCGCTCCAAA										5131	
QY	1137	T---TCTGCTCTTGCACC-TGCTTCTCAAAT---TTTG-A---TGTG										1172	
DB	5132	GTCAGTCTGTTCTGTGTGATCCGGGCTTC-CAGATGTTGGGAATCCTGTGCAGTATTGTCT										5190	
QY	1173	----	AGTG	----	CACTTCCCA	----	CACTTCCCA	----	CACTTCCCA	----	CACTTCCCA	1187	
DB	5191	GAAACCAAGGCGAGTGGACACAACTACCTCCCACTGTGAACGCATTGCTGTGGGCTGCC										5250	
QY	1188	-----CCCG---GGA-AA-GGCT-----GCCG-----CCA-C---CACCAAC										1214	
DB	5251	TCCCGCCTTGGAGAATGGCTTCTACTCAGCCGAGGACTTCATCGCGGCGACACGGTGAC										5310	
QY	1215	-----CACCA-----AC-----AC-----ACAA										1225	
DB	5311	CTATCAGTGACCACTGCTACTACCTGCTGGGTGATTCGGAATGTTCTGCRACAGAA										5370	
QY	1226	C---AGC---AATGGCA-AACACC-----										1241	
DB	5371	CGGAGCTGGAAAGCATTTACCATCTCTGTCGATGTCGATGAGTGTGCAGTCGGCTC										5430	
QY	1242	GAC-----AGCA-----ACCAATCAGA-----TAT-----										1261	
DB	5431	GGACTGTAGTGAGCAGCGCTCTCGCTTGAACACCAA-CGGATCCTAGTATGCTCTGTA										5489	
QY	1262	-----ATACA---A-ATG---AAATT---AGA-----										1280	
DB	5490	ACCCACATACCGGAGATGGGAAACCTGTGCAAACTGTGAAGCTTGAAGCTCCAG										5549	
QY	1281	AAA---CACA---GCC---TC-----A---TGGG-A---CAG-AAAT										1305	
DB	5550	AAAATCAGAAAATGGCGCTCTCTGGCGAGATTACACCGTGGGTACTGCACTCACAT										5609	
QY	1306	T---TGA---GG---GAG---GGGA-----ACAA-----AGA-----										1325	
DB	5610	TTTCTGTGCGAAGGCGACGAGCTGTGGGAGTGAGCACCATCACGTGTTGGAGACTG										5669	
QY	1326	-----AT-----A-----CTTTGGG-----G-----										1337	
DB	5670	GCGAGTGGATCGCTCAGCGCTCTGTGAAGCCATTTCTGTGTGTGCCACCTGTTTC										5729	
QY	1338	-----GAAA-----GA---GT---TT-----TAA-----										1351	
DB	5730	CTGAAATGGTGTGTGACGGTGGCAATTCACATATGCGAGTAAAGTGGTGTACAGT										5789	
QY	1352	-----AAAAGAAAT-----TGAA-AAAT-----TGCCTTGC-AG-----										1377	
DB	5790	GTGATAAGGATATACTTTGTCTGGGGATGAAGAGTCAGCATGCTTGTAGTGGTTCT										5849	
QY	1378	-A-T-ATT-----TAG-----GT-----AC---AAT-1392										1392	
DB	5850	GGAGTCATTCCTCTCTGTGTGGGGCTAGTGAAGTGTTCACGAGTGGAGGACATAAATA										5909	
QY	1393	-----GG-----AGT-----TTTTCT-TT---TC-----CC---A-A1410										1410	
DB	5910	ACGGCAAAATACATCTTAAAGTGGGCTCACCTACCTTTCTATTGATCGTACTCCTGTGAG										5969	
QY	1411	ACGGGA---AG-AACA-----CA-----GCACA-C---CCG---GCTTGGAC										1441	
DB	5970	AC-GGATACAGTTTACAGGGCCCATCCCTCTTTGAATGCACAGCTTCGCGCAGCTGGAC										6028	
QY	1442	-----CCA-----CTG											

QY	1451	-----GCAACCTC--TTTGGTG--C-CAGTGTG-----GGCA--AGG	1499
Db	6089	GTCACTCACTGGGAGCAACTTCACTTTTGG-GAACACAGT-TGCTTACACATGCAAGAGG	6146
QY	1491	GCT-CAGCCT--CT-----CTG-C-CCA-CAGAGTGCC---CCCACG-----TGGAA-----	1528
Db	6147	GCTACACCCCTGTGTGGCCCTGACACCAATCAT-TGCCAGGCCAACGGCAAAATGGAATTCA	6205
QY	1529	-----CA-----TTCTG-----GAGC-----TGG-CCA-----TC-	1547
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QY	1548	CCA---AAT--TCAATCAG--TCCATAGAC-----GA-----	1574
Db	6266	CCAGAGCTGCTCA--CAGGCTCTTTGGAGACACCGGTTTACTACTGTGGGATGGCT	6323
QY	1575	ACAG-----AAATG--AG-----AC-----CTTC-----	1590
Db	6324	ACAGCCTGGCTGATAATTCCAGCTCATCTGCAATGCCAGGGGAACTGGGTTCCCCCG	6383
QY	1591	CGGCCCAAGC-GTG--GCGGTGC---GGGCACTTTGGTAGACTGTG-----CCA-----	1633
Db	6384	CGGCCCAAGGCTGTGCGCGCTGTGATAGCTCACTT-----CTGTGAAAAACCCCATCT	6436
QY	1634	----CC-ACGGCGTGTGTTCTGAAAC-GTGA--AATAAAAAAGAGCAAA	1673
Db	6437	GTTCCTCAAGC-AATCTTG-GAATCTGTGAGCAA-----AGCAAA	6474
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; Sequence 3, Application US/08841349B			
; Patent No. 5955594			
; GENERAL INFORMATION:			
; APPLICANT: MISHRA, LOPA			
; TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT. . .			
; FILE REFERENCE: XX/P04470US0			
; CURRENT APPLICATION NUMBER: US/08/841,349B			
; NUMBER FILING DATE: 1997-04-30			
; NUMBER OF SEQ ID NOS: 18			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 3			
; LENGTH: 6960			
; TYPE: DNA			
; ORGANISM: Mus musculus			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (333)..(6794)			
US-08-841-349-3			

Query Match 41.5%; Score 697; DB 2; Length 6960;

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1202 GATTGAGAGTACAGACACTTGTCTTGACCTTCTGGAGTGGATTGAACAACATCAT 1261
146 CAGCC-AAA-AA-TGCACAAAT--CTA--TCTC--TTGGG--CAA--TC-- 181
1262 CATCTAAACAAACCGCA-AAATTTGCTAATTCACCTGTTGGGTCCTCAACAGAGCTCCAG 1320
182 --TTCA--CG--GG--G--CTG-- 193
1321 CATTTACACGTCACCGCACAGTGGAGAAACACACTAAGTTTACTGAGAAGGGAAATTTGG 1380
194 -GCTGCTCTGTCTC--TTC--CAAG--CAG-- 194
1381 AGGTGCTCTCTTTTCGCGATTTCAGAGCAAGATGCGAGCGAATATCAGAAAGTCTACATGC 1440
222 CCGTGGCAGGGAGATGC--CACTT--TC--C--CC--AAAG--CT-- 256
1441 CC--CGC--GAGGGGAAGCTCATCTCTGACATCAACAAGGCTTGGGAAAGACTTGGAAAA 1496
257 --ATG--GACAAC--G--TGACGG--TC--CGCAGG-- 281
1497 GCAGACATGAGAGAACTTGGCTCTG--CGAATGAGCTCATACGGCAGGAAAAAATCTGGA 1555
282 --GAGAGA--GC--G-- 290
1556 ACAACTCGCCCGAAGATTTGATCGCAAGCGAGCTATGAGGGAGACATGGCTGAGTGAATA 1615
291 CCACC--CTCAGG--TG--CACTATTGA-- 312
1616 CCAGCGCTTTGTCTCAGGACAACTTTGGATTGACCTTCCCGCTGTTGAGGCTGCTAC 1675
313 C--AAC-CG-GG--TC--AC-- 327
1676 CAAAAACACAGGCGCATTTGAGACAGACATCGCTGCATATGAAGAAGGATTGAGCGCT 1735
328 GGTGGC-CTGGC--T-AAACCGCAG--C-ACCAT--CCTC--TAT--G 362
1736 GGTGGCTGTGGCCAGGGAACCTTGAAGCG-AGAATACCATGACATCAAGCGCATCACAG 1794
363 CTGGGAATGAAA-GTGGT--GC-CTGG--ATCCTCGGTGCTCTCT-- 406
1795 CGAGGAGGACAAATGTCATCCGCTCTTGGGAATACTTGC-TGGAATCTGCTCAGGGCCAGG 1853
407 A-GCAAC--ACC--CAAACG--CAGTACA-GC-- 430
1854 AGSCAGGCTTTGAGATGAACCTGGGATTCGAAGAAGATATTCAGGAATGCTTTATATT 1913
431 ATCGA--GATCCA--GAACGTG--GATGTGT-ATGACGAGGC--C-CTTA 471
1914 ATGGACTGGATGATGAATGAAGGTGCTATTGCTGTCTCAAGACTATGGCAAACTTA 1973
472 C--ACCTG--CTCGGT--GCAGACA--GACAA-CC 497
1974 CTTGGTTTGAAGACCTGTTACAGAAGCATGCCCT--GGTTGAAGCAGACATTG-CAATCC 2031
498 ACCCA--AAG--CCTCT--AG-GGT--CCAC-- 520
2032 AAGCAGAGCGGTGAAGAGGTGTGAATGCTCTGCCAGAAAGTTTGAACAGATGGGAAG 2091
521 -CT--CATTTG--CHAFTA--TC--T-CCA-A--AATGT-- 549
2092 GCTACAAAGCCA-TGTGACCCCAAGGTAAATTCGAGACCGGTGTTGCCACATGAGGTCTGCG 2150
550 ----AGAGATTCTTCAGATATCT--CCATTATGA--AGGGAAC--ATA-T- 591
2151 TATCAGAGCTTT-GTCAGTGTCTGCC-----GAGCGTAGGCTCGCCTGGAAGATC 2203
592 --TAGCCTC--A--C--CT--ATAGCAA--CTGGTAGACACAGAG- 625
2204 CCGTCGCTCTGGAAGTCTTCTCTGGGAGATGGCAGAAGGAAGGCTGG-ATACGAGAGA 2262

QY 626 -----CCT--ACGTTACTTGG--AGA-----CA-----CAT-----CT 650
Db 2263 AGGAAAAGATCCTGTCTCTCTGATGATTAC--GGGAAAAGACTTCACCACTGTCTATGGCGCT 2320
QY 651 -CT-----CC--CA-----A-A--GCGGT--TGGC--TTTG-- 671
Db 2321 GCTGCAAGACACCGGCACTTTGAGGATGAGATGAGTGGCGGTAGTGGCCATTTTGAGCA 2380
QY 672 -----T--GA--GTGAAGAC-----GAATACTT-----GGAA--AT-- 696
Db 2381 GGCATTAAAGAGGTGAAGACATGATTGCAGAGGAACACTTTTGGATCGGAAAAGATCCG 2440
QY 697 TCAGGCGATC-----ACCGGAGCAG-----TCAG-----G 723
Db 2441 TGAGAGATCATTTATATCCGGAGCAGTGGGCAACCTTGGAAACAGCTCTCAGCCATTAG 2500
QY 724 G--GA--CTACGAG-----TG-----CAG----- 738
Db 2501 GAAGAAGCGCTA-GAGGAAGCCTCATTACTGCACCAGTTCCAGGCTGATGCTGATGATA 2559
QY 739 ---TGC-----CTC-----CAATGACGT-GGCC----- 757
Db 2560 TTGATGCTTTGGATTGTAGATATATACTCAAGATTGTCTCCAGCAATGATGTGGGCCATGATG 2619
QY 758 -G--CGCC-CG-----TGCT-ACG--G--AGA-CTA--AAG-G-TCACC--CT 789
Db 2620 AGTACTCCACGAGTCTCTGGTCAAGACNTAAGATGTAGCAGAAGAGATCACCACCT 2679
QY 790 G-A-----ACTAT--C-CAC-CAT--A--CA-----TTTCAGAAGC-CA--AG 820
Db 2680 GCAGGCCCACTATTGACACACTGATGACCAAGCAGTCCCTTCCACAAGCAGATGCAG 2739
QY 821 GG--TACAGTCT--CC-----CG-----TG-GGA-----CAA----- 844
Db 2740 AGTCTCAGATGTGAAGGCGCGCTGGCAGGAATTTGAGGAGCGCTGCAAGAGATGGCAG 2799
QY 845 -----AAGG-----GCACAC-----TG--CA 858
Db 2800 AGTTAACCGCTAAGGAGCAGGCTCTGCAGGACACCTTGCCCTGTACAGATGTTCA 2859
QY 859 GTG-----TGA-----AGC-----CTCA-----GC 873
Db 2860 GTGAGGCTGATGCTGTGAGCTCTGATTTGACGAGAAGGAGCAGTGGCTCAACAACATGC 2919
QY 874 AG-TCC-----CCT-----CAG----- 884
Db 2920 AGATCCGAGAGCTGGAGGACCTTGAAGTCAATCCAGCAGATTTGAGAGCCTTAGAAC 2979
QY 885 CAGAA-----TTC-----CAGTGGT--ACAAG-----GA 906
Db 2980 CAGAAATGAACAACACGAGCTTCCCGGTTGCTGTGTGAACAGATTTGCACGGCAGCTGA 3039
QY 907 TG-ACAAAG--AC--TGATTGAAGAA--AGA-----AAG----- 935
Db 3040 TGCACAATGGCCACCCAGTGA--AAAGGAAATCAGAGCTCAGCAAGACAAACTCAACAC 3097
QY 936 G-GGTGA--AGT-----GGAAAA----- 951
Db 3098 GAGGTGGATCAGTTTCAGAGAACTGGTGCACAGGAAAAGATGCTCTTGTGTGCGCCT 3157
QY 952 -----CAG-----ACCT-----T-----TCCT--C-TC-----AAAA 971
Db 3158 GAGCATCCAGAACTACCACTCGAGTGCATGAACAAATCCTGATCCCGGAGAGAC 3217
QY 972 -----TCATC--T--CTT--CAA-----TGTC-T-----CTGAA 994
Db 3218 CAAGGTCTATCGAGTCTACCAAGACCTTGGCAATGACCTGGCAGGTGTCTATGGCCCTGCA 3277
QY 995 ---CA--TGACT--ATGGGAACCTACACTT-----GC-----GTGGCC 1024
Db 3278 GTGCAAGCTGACTGGCAT-GGAAACAGACTTTGGTAGCCATTTGAGGCGAAGCTGATGACC 3336
QY 1025 TCCA-----ACAGCTGG-G-CC-A-CACCAATG-CCAGCATCATGCTAT--TT 1066

Db 3337 TCAGAAAGAGCTGAGAGCTGGAGTCGAGCACC-CTGACCAAGGCTCAAGCTATCT- 3394
QY 1067 GGTCCAGGC-GCCG--TCAGCAGAGTG-----AG-CAAC--G-GCAGC 1102
Db 3395 -GTCTCGGCTGCCCGAGATCACTGATGTGTGGGAGAAATGAAGCAACCCCTGAAGAAC- 3452
QY 1103 TCGAG--GAGG--GCAGGCTGC--G-TCT--GG-CT--G- 1129
Db 3453 -CGAGAGCCTCCCTGGGAGAGCCAGCAGCTGAGCAGATTTCTGGGAGCTTGGACGA 3511
QY 1130 CTGCC--TCCT--CTG-----GTCT-----TGC-----AC 1150
Db 3512 CTTCAGCTCTTGCTCTCCAGGACCCAGACTCTATCGCTCAGAGGACATGCCCAATAC 3571
QY 1151 --CT-----GCTCTCA-----AATTT-----TGA----- 1169
Db 3572 CTTACTGAGGAGAGAGCTTCTCACAGCAGCAGAAATATCAAAATGAGATCGACAA 3631
QY 1169 -TGTGAG--TGC--CA--C--T-TC-CCCA----- 1187
Db 3632 TTATGAGGAAGACTACAGAGATCGGGACATGGCGGAGATGGTCAACCCAGGGCAGAC 3691
QY 1188 --CC-----CGGAAAGGCTGC-CGCC-----ACCAAC----- 1211
Db 3692 TGATGCCAGTATATGTCTTCTCGCGCAGCGCTGCAGGCCTTAGA-CACTGGCTGAATG 3750
QY 1212 -CACCAC--CAACA-CAA-----CAG--CAATG-----GC 1235
Db 3751 AGCTCCAAATGTGGGAGAGACAGGCAAACTCTCTCCAGCTGCCATCTACCAGC 3810
QY 1236 A-----ACACC-GAC-AGC--AACC-----AAT--CA-GA-TAT----- 1261
Db 3811 AGTTCTTTAGGACACCAACAAAGCTGAAGCTTTCTTAATACCAAGAGTATGTTTGG 3870
QY 1262 --ATAC--AAATG--A--AATTA--GAAG-----AAACA-CAG----- 1288
Db 3871 CTCATACTGAATGCCACCACCTCGGAAGAGCTGAAGAGCCCATTAATAAGCAGGAGG 3930
QY 1289 -CTCATG--GGA--CA-----GA-----AAT--TTGAGG----- 1311
Db 3931 ACTTCATGACCATGATGCCACAGGAGAGATCAATGCTGTGTGGAGAGTGGCC 3990
QY 1312 --GAG--GGGAACA-----A-AGAA--T-ACT-- 1330
Db 3991 GAAGACTGGTGAGCGATGGGAACATCACTCCGACCGCATCCAGGAGAGTGCACCTA 4050
QY 1331 TTG--G--G--GAA--AAG--AGT-----T-----TTAAA-- 1352
Db 4051 TTGACGACAGACACAGGAAGATCGAAGAGCAGCCAGTGAACCTTCTGATGAGGTTAAAG 4110
QY 1353 --AA-----AGAA-----ATTG--AA-----AAT- 1367
Db 4111 ACAACCGTATCTACAGAGTTCTGCGAGATTTGTCAGAGCTGTCCCTCTGGATCAATG 4170
QY 1368 --TGCCTT--GC--AGATAT--TTA-----G-----GTACA 1390
Db 4171 AAAAGATG-CTTACAGCTCAAGACATGTCTTATGATGAAGCCAGAAATCTGCACAGTA-A 4228
QY 1391 ATGG-----AG--TTT-T-----CTT--TTCC-CAA-----AC-- 1412
Db 4229 ATGTTAAAGCATCAAGCAITTTATGGGGAACCTTGCATCCAAAGAAATGGCTTGACAA 4288
QY 1413 --G--GGAA-GAA-CA-----CAGCACACC-----G-GCT-TGG----- 1439
Db 4289 AATTGAGAGGAAGATGACGCTTATTTGAGAAAGCCAGAAACAGAGCTGTGGTAA 4348
QY 1440 --ACCACTG--C-----AAG--C-TGCATC-----GTGCAA 1464
Db 4349 GGAATAACTCACTGGTTTACATAAAATGTGGGAAGTCTTGATTCACACCCAGACAA 4408
QY 1465 --C-CTCTTTGGTGCA-----G-TG-----TGGGC----- 1486

Db 4409 GGCCAGCGGCTCTTTGATGCAATAAGGCTGAGCTTTTCACAAAGCTGCGAGATCT 4468
QY 1487 -----AAGGGCT-----C-----AGCC-----TC--TCTGCC-----CACAGAGTG 1515
Db 4469 TGACAAATGGCTACATGGCTGGAGAGCCAGATTCAATCTGACGACTATGGCAAGA--- 4525
QY 1516 CCC--CCACGTG-GAACATTTCT-----G-----GA-GCTGG-CCATCCCCA---AA 1552
Db 4526 -CCTTACCA-GTGTCAATATTTCTTTGAAAAAGCAACAGATGCTGGAGAAATCAGATGAA 4583
QY 1553 -TTC-----A-ATC-----AGTCCA-----T-A-GA---G 1570
Db 4584 GTTGGGAAGAAGATCGAGAACTGCAGAGCCAGCCAGGCGCTGAGTCAGAGGGG 4643
QY 1571 ACGA--ACAGAAATGAG-----A--CCTT-CCG-GC--CCAG--CGTGGCGCT 1608
Db 4644 AAGAGCAG-ATGAGGTGGAGCAAGAACGCTTACTGTGCAGACCAAGTTTCATGGAGCT 4702
QY 1609 GC-GG-GCAGTTTGGT-AGA-----CTGT--G--CCA-----CC----- 1635
Db 4703 TCTGGAGCCCTTGAGTGAGGAGAGCATAACTCTGTAGCTTCCAGGAGATCCATCAGTT 4762
QY 1636 --AC-----GG-CG-----TGTGTTG-----T-GAAACGT- 1656
Db 4763 CAACAGGATGTGGAGGACGAAATCCTATGGGTTGGCGAGGATGCCCTTGGCAACTTC 4822
QY 1657 --GA--A-----ATTA-----AAA-----G-AGC-----AAAAAAA 1679
Db 4823 CACAGATATGGCCATCACTTCAAACTGTGCAGCTGTTAATAAGAAAA 4873

RESULT 16
US-09-431-184A-3
; Sequence 3, Application US/09431184A
; Patent No. 6642362
; GENERAL INFORMATION:
; APPLICANT: MISHRA, LOPA
; TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
; FILE REFERENCE: P04470051/BAS
; CURRENT APPLICATION NUMBER: US/09/431,184A
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US98/08656
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 08/841,349
; PRIOR FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 6960
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (333)..(6794)
US-09-431-184A-3

Query Match 41.58; Score 697; DB 4; Length 6960;
Best Local Similarity 36.74; Pred. No. 0.00044;
Matches 1471; Conservative 0; Mismatches 168; Indels 2372; Gaps 436;
QY 1 GTTG---TGTCCTTCA--GCA-----AAACA-----G--TG---GATTT--- 29
Db 903 GATGGCATGGCTTCAATGCTGATACATACATGCGCTGACCTGATAGATTGAT 962
QY 30 -----AAATCT-----C-CT-----TGCACAA-GC--TT-----G-AGAGCAA 57
Db 963 AAATGAAGAAATCTAATGCACTACACTCACTCACTGAGATGCTTAACCTGGCAGAGCAG 1022
QY 58 CAC-----AATCT-----ATCT-----ATCA-----GGA-----A--AG 75
Db 1023 CACCTTGGCCTCACTAAACTGTTAGACCTGGAAGATATCAGTGTGGACCACTGATGAG 1082
QY 76 AA-----A-----GA-----AA-----GAA----- 85

Db	2151	TATCAAGAGCTTT--GTCACTGGCGCTGCC-----GAGCGTAGGCGCTCGCCTGGAAGATC	2200
QY	592	---TAGCCCTC---A---C---CT-----GC---ATAGCAA---CTGGTAGACCAGAG--	625
Db	2204	CGTCGCCCTCTGGAAGTCTTCTCGGAGATGSCAAGAGAGGAGGCTGG--ATACGAGAGA	2262
QY	626	-----CCT---ACGTTACTTGG---AGA-----CA-----CAT-----CT	650
Db	2263	AGGAAAAGATCCTGTCTCTGTGATGATTAC--GGGAAAGACTTGACCAAGTGTCTATGGCCCT	2320
QY	651	-----CC---CA-----A---A---GCGGT---TGCGC---TTTG-----	671
Db	2321	GCTGAGCAAGCACCGGCAATTGAGGATGAGATGAGTCAGTCGGCGTAGTGGCCATTTTGACGA	2380
QY	672	-----T---GA---GTGAAGAC-----GAATACTT-----GGAA---AT-----	696
Db	2381	GGCCATTAAAGAAGGTGAAGACATGATTGCAGAGGAACACTTTTGGATCGGAAAAGATCCG	2440
QY	697	TCAGGGCATC---ACCCGGGAGCAG-----TCAG-----G	723
Db	2441	TGAGAGATCATTTATATCCGGAGCAGTGGGCCAACCTGGAACAGCTCTTCAGCCATTAG	2500
QY	724	G--GA---CTACGAG-----TG-----CAG-----	738
Db	2501	GAAGAAGCGCTA--GAGGAAGCCTCATTTACTGCACCAGTTCACAGGCTGATGCTGATGATA	2559
QY	739	---TGC-----CTC---CAATGACGT--GGCC-----	757
Db	2560	TTGATGCTTGGATGTTAGATATATCTCAAGATTGTCTCCAGCAATGATGGGCGATGATG	2619
QY	758	G--CGCC--CG-----TGGT--ACG--G---AGA-GTA-----AAG-G-TCACC--GT	789
Db	2620	AGTACTCCAGCAGTCTCTGGTCAAGAAGCATAAAGATGTAGCAGAAGAGATCACCACCT	2679
QY	790	G-A-----ACTAT---C-CAC--CAT---A-CA-----TTTCAGAGC-CA---AG	820
Db	2680	CGAGCCCACTATTGACACACTGATGAGCAAGCCAGTGCCTTCCACAGCACATGCAG	2739
QY	821	GG--TACAGGTGT-----CC-----CCG---TG--GGA-----CAA-----	844
Db	2740	AGTCTCCAGATGTGAAGGCGCGGTGGCAGGATTTGAGGAGCGCTCAGAGGATGGCAG	2799
QY	845	-----AAG-----GACAC-----TG--CA	858
Db	2800	AGTTAACACGCTAAAGGAAGCAGGCTGTGCAGACACACCTCTGGCGCTGTCAAGATGTTCA	2859
QY	859	GTG-----TGA-----AGC-----CTCA-----GC	873
Db	2860	GTGAGGCTGATCCTGTGAGCTCTGGATTGACGAGAGGAGCTGCTCAACATGC	2919
QY	874	AG-TCC-----CCT-----CAG-----	884
Db	2920	AGATCCCAGAGAAGCTGGAGGACCTGGAAGTCAATCCAGCACAGATTTGAGAGCTAGAAC	2979
QY	885	CAGAA-----TTC-----CAGTGTGT--ACAAG-----GA	906
Db	2980	CAGAAATGAACAACCAAGGCTTCCCGGGTGTCTGTGTGAAACAGATTGCAAGCGGACGTGA	3039
QY	907	TG-ACAAAAG--AC-----TGATTGAAGGAA---AGA-----AAG-----	935
Db	3040	TGCACATGGCCACCCAGTGA--AAAGGAATTCAGAGCTCAGCAAGACAAACTCAACAC	3097
QY	936	G-GGTGAA--AGT-----GGRAAA-----	951
Db	3098	GAGTGGAGTCAGTTTCAGAGAACTGGTGGACAGGAAAAAGGATGCTTTCTGTCTGCCCT	3157
QY	952	-----CAG-----ACCT-----T-----TCTCT-C-TC-----AAAA	971
Db	3158	GAGCATCCGAACCTACCACTTCGAGTGCATGAACCAATCTCGATCCGGGAGAGAC	3217
QY	972	-----TCATC--T-T-----CTT--CAA-----TGTC--T-----CTGAA	994
Db	3218	CAAGGTTCATCGAGTCTACCCAAGACCTTGGCAATGACCTGGCAGGTGTTCATGGCCCTGCA	3277

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QY 995 --CA--TGACT--ATGGAACTACACTT-----GC-----GTGGCC 1024
Db 3278 GTCAAGCTGACTGGCAT--GNAAGAGACTTGTAGCCATTGAGGCGAAGCTGAGTGACC 3336
QY 1025 TTCA-----ACAAGTGG-G-CC-A-CACCAATG-CCAGCATCATGTCTAT--TT 1066
Db 3337 TGCAGAAAGAAGCTGAGAGCTGAGTCCGAGCACC-CTGACCAGGCTCAAGCTATCCT- 3394
QY 1067 GGTCCAGGC--GCCG--TCAGCGAGTG-----AG-CAAC--G--GCAAG 1102
Db 3395 -GTCTGGCTGCGGAGATCAGTATGTGTGGGAGAAATGAAGACAAACCTGAAGAAC- 3452
QY 1103 TCAG-----GAGG--GCAGGCTGC-----G--TCT--GG-CT-----G- 1129
Db 3453 -CGAGAGGCTCCCTGGGAGAGCCAGCAAGCTGCAGCAGTCTTCTGCGGACTTGGACGA 3511
QY 1130 CTGCC--TCTTT-----CTG-----GTCT-----TGC-----AC 1150
Db 3512 CTTCAGTCTTGGCTCTCCAGSACCCAGACTGTCTATGCTCAGAGGACATGCCCAATAC 3571
QY 1151 -----CT-----GCTTCTCA-----AATTT-----TGA----- 1168
Db 3572 CCTCACTGAGCAGAGAGCTTCTCACAGCAGCAGAGATATCAAAATGAGATCGACAA 3631
QY 1169 -TGTGAG-----TGC--CA--C-----T--TC-CCCA----- 1187
Db 3632 TTATGAGGAAGACTACCAGAAAGATCGGGACATGGCGAGATGGTCAACCCAGGGCAGAC 3691
QY 1188 -----CC-----CGGAAAGGCTGC--CGCC-----ACAC----- 1211
Db 3692 TGAATGCCAGTATATGTTCTGCGGAGCGGCTGCAGGCGTTAGA-CACCTGGTGAATG 3750
QY 1212 --CACAC-----CAACA--CAA-----CAG--CAATG-----GC 1235
Db 3751 AGTCCACAAAATGTGGGAGNACAGGCAAAACCTCTCTCCAGTCCCATGCTCATTACAGC 3810
QY 1236 A-----ACACC-GAC-AGC--AAACC-----AAT--CA-GA-TAT----- 1261
Db 3811 AGTTCCTTAGGACACCAACCAAGCTGAAGCTTTTCTTAATAACCAAGGAGTATGTTTGG 3870
QY 1262 ---ATAC--AAATG-----A-----AATTA--GAAG-----AAACA-CAG----- 1288
Db 3871 CTCATCTGAATGCCACCACCTCGGAAGGAGCTGAAGCAGCCATTAATAAAGCAGGAGG 3930
QY 1289 -CCTCATG-----GGA--CA-----GA-----AAT--TTGAGG----- 1311
Db 3931 ACTTCATGACCACCATGATGCCAAGGAGGAGAGATCATGCTGTGTGGAGACTGGCC 3990
QY 1312 -----GAG-----GGAACA-----A--AGAA--T--ACT----- 1330
Db 3991 GAAGACTGTGAGCGATGGGAACATCAACTCCGACCGCATCCAGGAGAGGTGGACTCTA 4050
QY 1331 TTG--G--G--GG--GAA-----AAG-----AGT-----T-----TTAAA-- 1352
Db 4051 TTGACGACAGACACAGGAAGATTCGAGAGCAGCAGCAGTGAATCTGTGATGAGTTAAAG 4110
QY 1353 --AA-----AGAA-----AATG--AA-----AAT- 1367
Db 4111 ACAACCGTGATCTACAGAAATTCCTGCAAGATTTGTCAAGAGCTGTCCTCTGATCAATG 4170
QY 1368 -----TGCTTT--GC--AGATAT--TTA-----G-----GTRCA 1390
Db 4171 AAAGATG--CTTACAGCTCAAGACATGCTTATGATGAAGCCAGAAATCTGCACAGTA-A 4228
QY 1391 ATGG-----AG--TTT-T-----CTT--TTCC--CAA-----AC-- 1412
Db 4229 ATGGTTAAAGCATCAGCATTTATGGCGAAGCTTGCATCCAAACAAAGAAATGCTTGCAA 4288
QY 1413 -----G--GGAA-GAA--CA-----CAGCACACCC-----G-GCT-TGG----- 1439
Db 4289 AATTGAGAGGAAGGAATGCAGCTTATTTCAGAAAGCCAGAAACAGAGCTGTGTGTA 4348
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QY 1440 -----ACCCACTG-----C-----AAG--C-TGCATC-----GTGCAA 1464
Db 4349 GGAATAACTCACTGGTTTACATAAAATGTGGGAAGTCTTGAATCCACACCCAGACCAA 4408
QY 1465 -----C-CTCTTTGGTGCCA-----G-TG-----TGGGC----- 1486
Db 4409 GGCCAGCGGCTCTTTTGAATGAATTAAGGCTGAGCTTTTTCACAAAGCTGGCAGATCT 4468
QY 1487 -----AAGGGCT-----C-----AGCC-----TC--TCTGCC-----CACAGAGTG 1515
Db 4469 TGACAAATGGCTACATGGCTGAGAGCCAGATTCATCTCTGACGACTATGGCAAAGA-- 4525
QY 1516 CCC--CCAGTG-GRACATTTCT-----G-----GA-GCTGG-CATGCCA--AA 1552
Db 4526 -CCTTACCA-GTGTCAATATTTCTTGAATAAAGCAACAGATGCTGGAGATCAGATGGAA 4583
QY 1553 -TTC-----A-ATC-----AGTCCA-----T-A-GA--G 1570
Db 4584 GTTCGGAAGAAGAGATCGAGGAACCTGCAGAGCCAGCCAGCGCTGAGTCAGAGGGG 4643
QY 1571 ACGA--ACAGATGAG-----A--CCTT-CCG-GC--CCAAG--CGTGGCGCT 1608
Db 4644 AAGAGCACAG-ATGAGGTGACAGCAACGCTTACTGTGCAGACCAAGTTTATGAGCT 4702
QY 1609 GC-GG-GCACTTTGGT-AGA-----CTGT--G--CCA-----CC----- 1635
Db 4703 TGTGGAGCCCTTGAAGTGAAGAGCATTAACCTGTTAGTCTTCAAGGAGATCCATCAGTT 4762
QY 1636 --AC-----GG-CG-----TGTGTTG-----T-GAACGT- 1656
Db 4763 CAACAGGATGTGGAGGACGAATCCTATGGGTGGCGAGAGGATGCCCTTTGCGACTTC 4822
QY 1657 ---GA-A-----ATAA-----AAA--G-AGC-----AAAAAAA 1679
Db 4823 CACAGATCATGCCATAACCTTCAAACTGTGCAGCTGTTAATAAAGAAAAA 4873
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RESULT 17

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US-08-841-349-5
; Sequence 5, Application US/08841349B
; Patent No. 5955594
; GENERAL INFORMATION:
; APPLICANT: MISHRA, LOPA
; TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT...
; FILE REFERENCE: XX/PO4470USO
; CURRENT APPLICATION NUMBER: US/08/841,349B
; CURRENT FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 8176
; TYPE: DNA
; ORGANISM: Mus musculus
US-08-841-349-5
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Query Match 41.5%; Score 697; DB 2: Length 8176;
Best Local Similarity 36.7%; Pred No. 0.00061;
Matches 1471; Conservative 0; Mismatches 168; Indels 2372; Gaps 436;
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Db 903 GATGGCATGGCTTCAATGCATCATATAAATCGGCTGACCTGATAGATTTTGTAT 962
QY 30 -----AATCT-----C-CT-----TGACAA-GC--TT-----G-AGACAA 57
Db 963 AAACCTGAAGAATCTAATGACACTCAATCTGAGAATGCAATTAACCTGCGAGAGCAG 1022
QY 58 CAC-----AATCT-----ATCA-----GGA-----A--AG 75
Db 1023 CACCTTGGCCTCACTAACTGTTAGCCCTGAAGATATCAGTGTGGACCCCTGATGAG 1082
QY 76 AA-----A-----GA-----AA-----GAA----- 85
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Db 1083 AAGTCTATCATCATAGTGGTACTTACTACCACTACTTCTCCAAGATGAAGCCCTTG 1142
Qy 86 -----AA--AAACCG-----AA-----CCTGACAA-----AAA-AGAAGAAAAA 116
Db 1143 GCTGTCGAAGAAAGCGCATTTGGAAGAGTGCTTGATATGCTATAGAAACAG-AGAAAAAT 1201
Qy 117 GA--AGAAGAA--AAAAA-----A--TC-----A-TGA--AAACCATC-- 145
Db 1202 GATTGAGNAGTACAGACACTTCTGACCTTCTGGAGTGGATTGAACAAACCATCAT 1261
Qy 146 CAGCC-AAA-AA-TGCACAAAT--CTA--TCTC-----TTGGG--CAA-----TC----- 181
Db 1362 CATCTAAACACCGCA-AAATTTGCTAATTCACCTGGTTGGGCTCCACAGCAGCTCCAAG 1320
Qy 182 -TTCA-----CG-----GG-----G-----CTG----- 193
Db 1321 CATTCACACACTACCGACAGTGGAGAAACCACTAAGTTTACTTGAGAGGGGAATTTGG 1380
Qy 194 -GCTGCTCTGTCTC--TTC--CAAG-----GAG-----TGC 221
Db 1381 AGGTGCTCTTTTCGCGATTCCAGAGCAAGATGCGAGCGAATAATCAGAAGGTCTACATGC 1440
Qy 222 CCGTGGCAGCGAGATGC-CACCT-----TC--C-----CC-----AAAG-CT----- 256
Db 1441 CC--GAGGGGAAGCTCATCTGACATCAACCAAGGCTCGGAAAGACTGGAAAAA 1496
Qy 257 -----ATG-----GACAAAC--G--TGACGG-----TC--CGGCGAGG----- 281
Db 1497 GCAGAACATGAGAGAACTGGCTCTG--CGAATGAGCTCATACGCGAGGAAAAAATCTGGA 1555
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Db 291 CCACC-----CTCAGG-----TG-----CACTATTTGA----- 312
Db 1616 CCAGCGTCTTGCTCTCAGGAACTTTTGGATTGACCTTCCCGCTGTGAGGCTGTAC 1675
Qy 313 C-----AAC-CG-GG-----TC-----AC-----CGG- 327
Db 1676 CAAAAACACAGAGCCATTGAGACAGACATCGCTGCATATGAAGAACAGTTTCAGGCCGT 1735
Qy 328 GGTGGC-CTGGC-----T-AAACCGCAG--C-ACCAT--CCTC-----TAT-----G 362
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Qy 363 CTGGAATGACAA-GTGGT--GC-CTGG--ATCGTCGCTGGTCTCTCT-----G 406
Db 1795 CGAGGAAGGCAATGTATCCGGCTCTGGGAATATCTTGC-TGSAACTGCTCAGGGCCAGG 1853
Qy 407 A-GCAAC-----ACC-----CAAAACG-----CAGTACA-GC----- 430
Db 1854 AGCAGCGCTTTGAGATGAACCTGGGATTGCAAAAGATATTCAGAGGAATGCTTTATATT 1913
Qy 431 ATCGA--GATCCA-----GAACGTG-----GATGTGT-ATGACGAGGGC--C-CTTA 471
Db 1914 ATGACTGGATGATGAAATGAAGGTGATTTGCTGTCTCAAGACTATGGCAAACTTA 1973
Qy 472 C-----ACCTG-----CTCGGT-----CCAGACA--GACAA-CC 497
Db 1974 CTTGGTGTGAAGACCTGTTACAGNAGCATGCCCT-GGTTGAAGGACATG-CNAATCC 2031
Qy 498 ACCCA-----AAGA-----CCTCT-----AG--GGT--CCAC----- 520
Db 2032 AAGCAGCGGTGAAGAGGTGAATGCTCTGCCAGAACTTTGCAACAGATGGGAAG 2091
Qy 521 -CT-----CATTTG-----CAAGTA--TC-----T-CCCA-A-----AATGT-- 549
Db 2092 GCTACAAGCCA-TGTGACCCCGAGTAATTCGAGACCGTGTGTGCCCAATGAGTCTCTGC 2150
Qy 550 -----AGAGATTTCTTCAGATATCT-CCATTATGA-----AGGGAAC-----AATA-T- 591
Db 2151 TATCAAGAGCTTT-GTCAGTGGCTGCG-----GAGCGTAGGCTCGCCTGGGAAGATC 2203

Qy 592 -----TAGCCTC--A--C--CT-----GC-----ATAGCAA--CTGGTAGACGAG- 625
Db 2204 CCCTCGCCTCTGGAAGTTCTTCTGGAGATGGCAGAAGAGGAGGTGG-ATACGAGA 2262
Qy 626 -----CCT--ACGGTTACTTGG--AGA-----CA--CAT-----CT 650
Db 2263 AGAAAAAGATCCTGTCTCTGATGATAC--GGGAAAGACTTGACCAAGTCTCATGCGCCT 2320
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Db 2321 GCTGAGCAAGCACCGGCACTTTGAGGATGATGAGTGGCGGTAGTGGCCATTTTGAACA 2380
Qy 672 -----T--GA--GTGAGAC-----GATATCTT-----GGAA--AT-- 696
Db 2381 GGCCATTAAAGAGGTGAAGACATGATGTCAGAGGAACACTTTTGGATCGGAAAGATCCG 2440
Qy 697 TCAGGGCATC-----ACCGGGAGCAG-----TG-----CAG----- 723
Db 2441 TGAGAGATCATTTTATATCCGGGAGCAGTGGGCCAACCTGGAACAGCTCTCAGCCATTAG 2500
Qy 724 G--GA-----CTAGAG-----TG-----CAG----- 738
Db 2501 GAAGAAAGCGCTA-GAGGAAGCCTCATTTACTGCACCAGTTCCAGGCTGATGCTGATGATA 2559
Qy 739 -----TGC-----CTC-----CAATGAGT--GGCC----- 757
Db 2560 TTGATTTGGATTTAGATATATCTCAAGATTGCTCCAGCAATGATGGGCCATGATG 2619
Qy 758 -G--CGCC-CG-----TGGT--ACG--G-----AGA-GTA-----AAG-G-TCACC--GT 789
Db 2620 AGTACTCCACGCAGTCTCTGTCAAGAGCATAAAGATGTAGCAGAAGAGATCACCAACT 2679
Qy 790 G-A-----ACTAT--C-CAC--CAT-----A--CA-----TTTCGAAGC-CA--AG 820
Db 2680 GCAGGCCCACTATTGACACACTGTCATGAGCAAGCCAGTGCCTTCCCAAGACCATGCAG 2739
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Db 2740 AGTCTCAGATGTGAAGGCCCGCTGGCAGGAATTTAGGAGCGCTGCAAGGATGGCAG 2799
Qy 845 -----AAGG-----GGACAC-----TG--CA 858
Db 2800 AGTTAACCGCTTAAGGAAGCAGGCTCTGCAGGACACCTTGGCCCTGTACAAGATGTTCA 2859
Qy 859 GTG-----TGA-----AGC-----CTCA-----GC 873
Db 2860 GTGAGGCTGATGCTGTGAGCTCTGATTTGACGAGAAGGAGCAGTGGCTCAACAACATGC 2919
Qy 874 AG--TCC-----CCT-----CAG----- 884
Db 2920 AGATCCAGAGAGCTGGAGCACTTGAAGTCAATCCAGACACAGATTGAGAGCCTAGAAC 2979
Qy 885 CAGAA-----TTC-----CAGTGGT--ACAAG-----GA 906
Db 2980 CAGAAATGAACAAACCGGCTTCCGGGTTGCTGTGTGAACCCAGATTGCACGCGAGCTGA 3039
Qy 907 TG-ACAAAG--AC-----TGATTGAAGGA--AGA-----AAG----- 935
Db 3040 TGCACATGGCCACCCCAAGTGA--AAAGGAATTCAGAGTCTAGCAAGACAAATCAACAC 3097
Qy 936 G-GGTGAA--AGT-----GAAAAA----- 951
Db 3098 GAGGTGAGTCACTTCAGAGAACTGGTGGACAGAAAAGGATGCTTCTTGTCTGCCCT 3157
Qy 952 -----CAG-----ACCT-----T-----TCCT-C-TC-----AAAAC 971
Db 3158 GAGCATCCAGAACTACCACTCGAGTCAATGAACCAAAATCTGCATCGGGAGAAGAC 3217
Qy 972 -----TCATC--T-T-----CTT--CA--TGTC-T-----CTGAA 994
Db 3218 CAAGGTCACTGAGTCTACCAAGACCTTGGCAATGATGCTGGCAGGTGTCTATGCCCCCTGCA 3277

QY 995 ---CA---TGACT---ATGGGAACCTACACTT---GC---GTGGCC 1024
Db 3278 GTGCAAGCTGACTGSCAT---GGAAACGAGACTTGGTAGCCATTGAGCGAAGCTGAGTGACC 3336
QY 1025 TCCA-----ACAAGCTGG-G-CC-A-CACCAATG-CCAGCATCATCTAT--TT 1066
Db 3337 TGCAGAAAGAAAGCTGAGAAGCTGGAGTCCGAGCACC-CTGACCAGGCTCAAGCTATCT- 3394
QY 1067 GGTCCAGGC--GCG--TCACGAGGTG-----AG-CAAC--G-GCAGG 1102
Db 3395 -GTCTCGGCTGGCCGAGATCAGTGATGTGTGGAGGAAATGAAGAACCCCTGGAAGAAC- 3452
QY 1103 TCGAG-----GAGG--GCAGGCTGC--G-TCT---GG-CT---G- 1129
Db 3453 -CGAGAGGCTCCCTGGGAGAGCCAGCAGCTGAGCAGGTTTCTGCGGACTTGGACGA 3511
QY 1130 CTGGC--TCCTT-----CTG-----GTCT-----TGC-----AC 1150
Db 3512 CTTCCAGTCTTGCTCTCCAGGACCCAGACTGCTATCGCTCAGAGGACATGCCCAATAC 3571
QY 1151 ---CT-----GCTTCTCA-----AATTT-----TGA-----1168
Db 3572 CTTCACTGAGGAGAGAGCTTCTCACAGCAGCAGAAATATCAAAATGAGATCGCAA 3631
QY 1169 -TGTGAG-----TGC-----CA-----C--T--TC-CCCA-----1187
Db 3632 TTATGAGGAGACTACCAAGATCGGGACATGGCGAGATGGTCAACCCAGGGCGACAC 3691
QY 1188 ---CC-----CGGAAAGGCTGC-CGCG-----ACCAC-----1211
Db 3692 TGATGCCAGTATATGTTTCTGCGCAGCGGCTGCAGGCTTAGA-CATGCTGGAATG 3750
QY 1212 -CACCAC-----CAACA-CAA-----CAG--CAATG-----GC 1235
Db 3751 AGCTCCACAAATGTTGGAGAAACAGCAAACTCTCTCCAGTCCCATGCTTACCAGC 3810
QY 1236 A-----ACACC-GAC-AGC--AACC-----AAT---CA-GA-TAT-----1261
Db 3811 AGTTCTCTTAGGACACCAACAAAGCTGAAGCTTTTCTTAATAACCAAGAGTATGTTTGG 3870
QY 1262 --ATAC--AAATG-----A-----AATTA--GAAG-----AAACA-CAG-----1288
Db 3871 CTCATCTGAATGCCACCACTGGAAGGAGCTGAAGCAGCCATTAATAAGCAGAGG 3930
QY 1289 -CCTCATG-----GGA--CA-----GA-----AAT-----TTGAGG-----1311
Db 3931 ACTTCATGACCACCATGATGCCAAGGAGAGATCAATCTGTTGTGGAGACTGGCC 3990
QY 1312 -----GAG-----GGGAACA-----A-AGAA--T--ACT---1330
Db 3991 GAAGACTGGTGAAGCGATGGGAACATCAACTCCGACCGCATCCAGGAGAAGGTGGACTCTA 4050
QY 1331 TTG-G--G--GG-GRA-----AAG-----AGT-----T-----TTAAA--1352
Db 4051 TTGACGACAGACAGGAAGAAATGAGAAGCAGCCAGTGAATCTCTGATGAGGTTAAAGG 4110
QY 1353 --AA-----AGAA-----ATTG-AA-----AAT-1367
Db 4111 ACAACCGTGATCTACAGAGTTCTTCCGAAAGATTGTCAGAGCTGTCCCTCTGGATCAATG 4170
QY 1368 -----TGCTTT--GC--AGATAT--TTA-----G-----GTACA 1390
Db 4171 AAAAGATG-CTTACAGCTCAAGACATGCTTTATGATGAAGCCAGAAATCTGCACAGTA-A 4228
QY 1391 ATGG-----AG-TTT-T-----CTT--TTCC-CAA-----AC--1412
Db 4229 ATGGTTAAGCATCAAGCATTTATGGGGAATCTTGCATCCCAACAAAGAATGCTTTGCAA 4288
QY 1413 -----G-GGAA-GAA--CA-----CAGCACACCC-----G-GCT-TGG-----1439
Db 4289 AATTGAGAAGGAGGAATGTCAGCTTATTTCAGAAAGCCAGNAACAGAGCTGTGGTAAA 4348
QY 1440 -----ACCCACTG-----C-----AAG--C-TGCATC-----GTGCAA 1464

Db 4349 GGAAAACTCACTGCTGTTTACATAAAATGTGGAAAGTCTTGAATCCACAACCCAGACAA 4408
QY 1465 -----C-CTCTTTGGTGCCA-----G-TG-----TGCGC-----1486
Db 4409 GCGCCAGCGGCTCTTTGATGCAAAATAGGCTGAGCTTTTCACACAAGCTGGCAGATCT 4468
QY 1487 -----AAGGGCT-----C-----AGCC-----TC--TCTGCC-----CACAGATG 1515
Db 4469 TGACAAATGGCTTACATGCGCTCGAGAGCCAGATTCAATCTGACGACTATGGCAAGA- 4525
QY 1516 CCC--CCACGTG-GAACATTTCT-----G-----GA-GCTGG-CCATCCCA--AA 1552
Db 4526 -CCTTACCA-GTGTCATATTTCTTCTGAAAAAGCAACAGATGCTGGAGAAATCAGATGAA 4583
QY 1553 -TTC-----A-ATC-----AGTCCA-----T-A-GA--G 1570
Db 4584 GTTCGGAAGAAAGAGATCGAGGAACTGCAGAGCCAGCCAGGCGCTGAGTCAGGAGGG 4643
QY 1571 ACGA-ACAGATGAG-----A--CCTT-CCG-GC--CCAAAG--CGTGGCGCT 1608
Db 4644 AAGAGCAG-ATGAGGTGGACAGCAAAACGCTTACTGTGCAGACCAAGTTTCATGGAGCT 4702
QY 1609 GC-GG-GCCTTTGCT-AGA-----CTGT--G--CCA-----CC-----1635
Db 4703 TCTGGAGCCTTGAGTGAGAGAAAGCATCACTGTGTAGCTTCCAAGGAGATCCATCAGTT 4762
QY 1636 --AC-----GG-CG-----TGTGTTG-----T-GAAACGT-1656
Db 4763 CAACAGGATGCGAGGAGCAAACTTATGGTTTGGCGAGAGGATGCTTTTGGCACTTC 4822
QY 1657 ---CA-A-----ATRA-----AAA-----G-AGC-----AAAAAAA 1679
Db 4823 CACAGATCGGCCATCACTTCAAACTGTGCGCTGTTAATAAGAAAAA 4873

RESULT 18
US-09-431-184A-5
; Sequence 5, Application US/09431184A
; Patent No. 6642362
; GENERAL INFORMATION:
; APPLICANT: MISHRA, LOPA
; TITLE OF INVENTION: GENES CODING FOR EARLY LIVER DEVELOPMENT...
; FILE REFERENCE: P04470051/BAS
; CURRENT APPLICATION NUMBER: US/09/431,184A
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US98/08656
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 08/841,349
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8176
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-431-184A-5

Query Match 41.5%; Score 697; DB 4; Length 8176;
Best Local Similarity 36.7%; Pred. No. 0.00061;
Matches 1471; Conservative 0; Mismatches 168; Indels 2372; Gaps 436;
QY 1 GTTG---TGCTCTCA-GCA-----AAACA-----G---TG---GATTT-----29
Db 903 GATGGCATGGCTTCAATGCACTGATACATAAAATCGGCTGACCTGATAGATTTGAT 962
QY 30 -----AAATCT-----C-CT-----TGCAAA-GC--TT-----G-AGAGCAA 57
Db 963 AAACCTGAAGAAATCTAATGACACTACAATCTGCAGATGCAATTAACCTGGCAGAGAG 1022
QY 58 CAC-----AATCT-----ATCA-----ATCA-----A--AG 75
Db 1023 CACCTTGGCTCACTAAACTGTTAGACCTTGAAGATATCACTGTGGAGCCACCTGATGAG 1082

QY 76 AA-----A-----GA-----AA-----GAA-----85
Db 1083 AAGTCTATCATCATAGTGGTCACTTACTTACCACTACTTCTCCAAAGATGAAGCCCTTG 1142
QY 86-----AA-AAACCG-----AA-----CCTGACAA-----AAA-AGAAAGAAAA 116
Db 1143 GCTGTCGAAGGAAAGCGCATTTGGAAGGTGCTTGATTAATGCTATAGAAACAG-AGAAAT 1201
QY 117 GA---AGAGAA---AAAA-----A---TC-----A-TGA---AAACCATC--- 145
Db 1202 GATTGAGAAGTACGAGACACTTGCTTCTGACCTTCTGGAGTGGATTGAACAAACCATCAT 1261
QY 146 CAGCC-AAA-AA-TGCACAATT-CTA-TCTC---TTGGG---CAA-----TC----- 181
Db 1262 CATCTTAACACCGCA-ATTTCCTAATTCACCTGTTGGGTCCAAACAGAGCTCCAAG 1320
QY 182---TTCA-----CG-----GG-----G-----CTG----- 193
Db 1321 CATTCAACAGTACCGCACAGTGAGAAACCACTTAAGTTTACTTGAAGAGGGAATTTGG 1380
QY 194 -GCTGCTCTGTCTC---TTC-----CAAG-----GAG-----TGC 221
Db 1381 AGTGCTCTCTTTTTCGCGATTTCAGACCAAGATGCGAGCGAATAATCAGAAGGTCTTACATGC 1440
QY 222 CCGTGCAGCGGAGATGC-CACCT---TC-C---CC-----AAAG-CT--- 256
Db 1441 CC---CGC-GAGGGGAAGCTCATCTTGACATCAACAGGCTGGGAAAGACTGGAAAAA 1496
QY 257---ATG---GACAAAC-G---TGACGG-----TC---CGGCAGG----- 281
Db 1497 GCAGAACATGAGAGAACTGGCTCTG-CGGAATGAGCTCATACGGCAGGAAAAACTGGA 1555
QY 282-----GAGAG-----GGAG-----GC-----G----- 290
Db 1556 ACACTGCCCGAGATTGATCGAAGGCGAGTATGAGGGAGACATGGCTGAGTGAATA 1615
QY 291 CCACC-----CTCAGG-----TG-----CACTATTGA----- 312
Db 1616 CCAGCGTCTTGCTCAGGACAACTTTGGATTGACCTTCCCGCTGTTGAGGCTGCTAC 1675
QY 313 C---AAC-CG-GG-----TC-----AC-----CCG- 327
Db 1676 CAAAAACACGAGGCCATTGAGACAGACATCGTGCATATGAAGAACGAGTTCAGGCGCT 1735
QY 328 GTGGC-CTGGC-----T-AAACCGCAG-C-ACCAT--CCTC-----TAT---G 362
Db 1736 GTGGCTGTGGCCAGGAACTTGAGCCG-AGAACTHCCATGACATCAAGCGCATCACAG 1794
QY 363 CTGGGAATGACAA-GTGGT---GC-CTGG---ATCCTCGCGTGGTCTTCT---G 406
Db 1795 CGAGGAAGGACAAATGTCTCCGGCTCTGGGAATATTGC-TGAACTGCTCAGGGCCAGG 1853
QY 407 A-GCAAC-----ACC-----CAAACG-----CAGTACA-GC----- 430
Db 1854 AGCAGCGTCTTGAGATGAACCTGGGATGCAAAAGATATTCAGGAAATGCTTTATAT 1913
QY 431 ATCGA---GATCCA-----GAACGTG-----GATGTGT-ATGACGAGGSC---C-CTTA 471
Db 1914 ATGACTGGATGATGAATGAGGTGCTATTGCTGTCTCAAGACTATGGCAAACTTA 1973
QY 472 C-----ACCTG-----CTGGT-----GCAGACA---GACAA-CC 497
Db 1974 CTTGGTGTGAAGACCTGTTACAGAGCATGCGCT-GGTTGAAGCAGACATTG-CAATCC 2031
QY 498 ACCCA-----AAGA-----CCTCT---AG---GGT---CCAC----- 520
Db 2032 AACGAGCGGTGAAGAGGTGTAATGCTCTGCCAGAGAGTTTGAACAGATGGGGAAG 2091
QY 521 -CT-----CATTTG-----CAAGTA---TC-----T-CCCA-A---AATTGT--- 549
Db 2092 GCTACAGCCA-TGTACCCCCAGTAAATTCGAGACCGTGTGCCACATGGAGTTCTGC 2150

QY 550-----AGAGATTTCTCAGATATCT-CCATTATGA-----AGGGAAC-----AATA-T- 591
Db 2151 TATCAAGAGCTTT-GTCAGCTGGCTGCC-----GAGCGTAGGCTCGCTCGCTGAAGAGTC 2203
QY 592---TAGCCTC---A---C---CT-----GC-----ATAGCAA---CTGGTAGACCAG- 625
Db 2204 CCGTGGCTCTGGAAGTTCTTCTGGGAGATGGCAGAGGAAGGCTGG-ATACGAGAGA 2262
QY 626-----CCT---ACGTTACTTGG---AGA-----CA-----CAT---CT 650
Db 2263 AGAAAAAGATCCTGTCTCTGTGATGATTAC---GGAAAGACTTGACCAGTGTCTATGCGCT 2320
QY 651 -CT-----CC-----CA-----A---A---GGGT---TGCC---TTTG--- 671
Db 2321 GCTGAGCAAGCACCGGCATTTGAGATGAGTGGCCGTAGTGGCCATTTTGAACA 2380
QY 672---T---GA---GTGAAGAC-----GAATACCT-----GGAA---AT--- 696
Db 2381 GGCCATTAAAGAGGTGAAGACATGATTGCAGAGGAACACTTTGGATCGGAAGATCCG 2440
QY 697 TCAGGGCATC-----ACCGGGAGCAG-----TCAG-----G 723
Db 2441 TGAGAGATCATTTATATCCGGAGCAGTGGGCCAACCTGGAACAGCTCTCAGCCATTAG 2500
QY 724 G-GA---CTACGAG-----TG-----CAG----- 738
Db 2501 GAAGAGCGCCTA-GAGGAAGCCTATTACTGCACCAGTTCAGGCTGATGTGATGATA 2559
QY 739---TGC-----CTC---CAATGACGT---GGCC----- 757
Db 2560 TTGATCCTTGGATTTAGATATATCAAGATTGTCTCCAGCAATGATGTTGGCCATGATG 2619
QY 758 -G---CGCC-OG-----TGCT-ACG-G-----AGA-GTA---AAG-G-TCAAC-CT 789
Db 2620 AGTACTCCAGCAGTCTCTGGTCAAGAGCATAAAGATGTAGCAGAGAGATCACCACCT 2679
QY 790 G-A-----ACTAT---C-CAC-CAT-----A---CA-----TTTCAGAAAC-CA---AG 820
Db 2680 GCAGGCCCACTATTGACACACTGCTGACAGACGCCAGTCCCTTCCAAAGCACATGCGAG 2739
QY 821 GG---TACAGTGT---CC-----CCG-----TG-GGA-----CAA----- 844
Db 2740 AGTCTCCAGATGTGAAGGCCGCTGGCAGGAATTTGAGGAGCGCTGCAAGGAGATGGCAG 2799
QY 845-----AAGG-----GGACAC-----TG-----CA 858
Db 2800 AGTTAACCGGTAAGGAAGCAGGCTCTGCAGGACACCTGGCCCTGTACAAGATGTTCAC 2859
QY 859 GTG-----TGA-----AGC-----CTCA-----GC 873
Db 2860 GTGAGGCTGATGCTGTGAGCTCTGGATTGACGAGAGGAGCAGTGGCTCAACACATCG 2919
QY 874 AG-TCC-----CCT-----CAG----- 884
Db 2920 AGATCCAGAGAAGCTGGAGGACCTGGAAGTCATCCAGCACAGATTTGAGAGCTTAGAAC 2979
QY 885 CAGAA-----TTC-----CAGTGT---ACAAG-----CA 906
Db 2980 CAGAAATGAACCAACCGGCTTCCGGGTGCTGTGTGTGAACCAAGATTCACCGCAGCTGA 3039
QY 907 TG-ACAAAAG--AC-----TGATTGAAGAA---AGA-----AAG----- 935
Db 3040 TGCACAAATGCCACCCCACTGTA--AAAGGAATCAGAGCTCAGCAGACAAACTCAACAC 3097
QY 936 G-GGTGAA---AGT-----GGAATA----- 951
Db 3098 GAGGTGGAGTCACTTTCAGAGAACTGGTGACAGGAAAGAGTGTCTTCTGTCTGCCCT 3157
QY 952-----CAG-----ACCT-----T-----TCCT-C-TC-----AAAC 971
Db 3158 GAGCATTCAGAACTACCTCCTCGATGCAATGAACCAAACTCTGATCCGGGAGAGAC 3217
QY 972-----TCATC---T-T-----CTT---CAA-----TGTC-T-----CTGAA 994

Db 3218 CAAGGTCTACGAGTCTACCCAGACCTTGGCAATGACCTGGCAGGTGTCTATGGCCCTGCA 3277
QY 995 ---CA---TGACT---ATGGGAACATACATT-----GC---GTGGCC 1024
Db 3278 GTGCAAGCTGACTGGCAT--GGAACGAGACTTGGTAGCCATTGAGCGAAGCTGAGTGACC 3336
QY 1025 TCCA-----ACAAGCTGG--G-CC-A-CACCAATG-CCAGCATCATCTAT--TT 1066
Db 3337 TCCAGAAAGAACTCAGAAAGCTGGAGTCGAGTCGAGCACC-CTGACCAAGCTCAAGCTATCCT- 3394
QY 1067 GGTCCAGGC--GCCG--TCAGCGAGGTG-----AG-CAAC--G--GCACG 1102
Db 3395 -GTCTCGGTGCCGAGATCACTGATGTGTGGAGGAAATGAAGACAACCCCTGAAGAAC- 3452
QY 1103 TCGAG-----GAGG--GCAGGCTGC--G-TCT--GG-CT--G-- 1129
Db 3453 -CGAGAGGCTCCCTGGGAGAGCCAGCAAGCTGACGAGTTTCTGCGGGACTTGGACGA 3511
QY 1130 CTGCC--TCTT-----CTG-----GTCT-----TGC-----AC 1150
Db 3512 CTTCCAGTCTTGGCTCTCCAGGACCCAGACTGCTATCGCTCAGAGGACATGCCCAATAC 3571
QY 1151 ---CT-----GCTTCTCA-----AATTT-----TGA----- 1168
Db 3572 CCTCACTGAGGAGAGAACTTCTCACACAGCAGCAGAAATCAAAATAGATCGACAA 3631
QY 1169 -TGTGAG-----TGC---CA---C---T--TC-CCCA----- 1187
Db 3632 TTATGGAAGACTACCAAGAGATCGGGACATGGCGAGATGGTCACCCAGGGGCAGAC 3691
QY 1188 ---CC-----CGGAAAGGTGC-CGCC-----ACCAC----- 1211
Db 3692 TGATCCCAAGTATATGTTTCTGCGCAGCGCTGCGAGCCTTAGA-CACTGCTGGAATG 3750
QY 1212 -CACCAC-----CAACA-CAA-----CAG--CAATG-----GC 1235
Db 3751 AGCTCCAAAATGTGGAGAACAGGCAAACTCTCTCCAGTCCCATGCTACCAGC 3810
QY 1236 A-----ACACC-GAC-AGC--AACC-----AAT--CA-CA-TAT----- 1261
Db 3811 AGTTCCTTAGGACACCAACAAAGCTGAAGCTTTTCTTAATAACCAAGAGTATGTTTG 3870
QY 1262 ---ATAC--AAATG-----A-----AATTA--GAAG-----AAACA-CAG----- 1288
Db 3871 CTCATCTGAATGCCACCCCTCGAAGAGCTGAGCAGCCATTAAGAGCAGGAG 3930
QY 1289 -CTCATG-----GGA--CA--GA-----AAT-----TTCAGG----- 1311
Db 3931 ACTTCATGACCACCATGATGCCAACGAGGAGAGATCAATGCTGTGTGGAGACTGGCC 3990
QY 1312 -----GAG--GGGAACA-----A-AGAA--T--ACT-- 1330
Db 3991 GAAGACTGTGAGCGATGGGAACATCACTCGGACCGCATCCAGGAGAGGTGCACTCTA 4050
QY 1331 TTG--G--G--GG-GAA-----AAG-----AGT-----T-----TTAAA-- 1352
Db 4051 TTGACACAGACACAGGAAGAAATCGAAGACGAGCCAGTGAATCTCTGATGAGGTTAAG 4110
QY 1353 --AA-----AGAA-----ATTG--AA-----AAT- 1367
Db 4111 ACAACCGTGATCTACAGAAAGTTCCTGCAAGATTGTCAAGAGCTGTCCCTCTGGATCAATG 4170
QY 1368 -----TGCCTT--GC--AGATAT--TTA-----G--GTACA 1390
Db 4171 AAAGATG-CTTACAGCTCAAGACATGTCTTATGATGAAGCAGCAAAATCTGCACAGTA-A 4228
QY 1391 ATGG-----AG-TTT-T-----CTT--TTCC-CAA-----AC-- 1412
Db 4229 ATGGTTAAAGCATCAAGCATTTATGGCGAACTTGCATCCCAACAAAGAAATGCTTGACAA 4288
QY 1413 -----G--GGAA-GAA--CA-----CAGCACCC-----G-GCT-TGG----- 1439

Db 4289 AATTGAGAAGGAGAGGAGTACGCTTATTTCAGAAAGCCAGAAACAGAGCTGTGTGTA 4348
QY 1440 -----ACCCACTG-----C-----AAG--C-TGCATC-----GTGCAA 1464
Db 4349 GGAATAACTCACTGCTTTACATAAAATGTGGGAAGTCTCTGAAATCCACAACCCAGACAA 4408
QY 1465 -----C--CTCTTTGTGCA-----G-TG-----TGGGC----- 1486
Db 4409 GGCCAGCGGCTCTTTGATGCAATATAGGCTGAGCTTTTTCACAAAGCTGGCAGATCT 4468
QY 1487 -----AAGGGCT-----C-----AGCC-----TC--TCTGCC-----CACAGACTG 1515
Db 4469 TGCAAAATGGCTACATGSCCTGGAGAGCCAGATTCAATCTGACGACTATGGCAAGA-- 4525
QY 1516 CCC---CCACGTG-GAACATTTCT-----G-----GA-GTGG-CCATCCCA---AA 1552
Db 4526 -CCTTACCA-CTGTCAATATTCTTCTGAAAAAGCAACAGATGCTGGAGAATCAGATGGA 4583
QY 1553 -TTC-----A-ATC-----AGTCCA-----T-A-GA---G 1570
Db 4584 GTTGGGAAGAGAGATCGAGAACTGCAGAGCCAGCCAGGCGCTGAGTCAGAGGGG 4643
QY 1571 ACGA--ACAGAAATGAG-----A--CCTT-CCG-GC---CCAG--CGTGGCGCT 1608
Db 4644 AAGAGCAG-ATGAGGTGGACAGCAACGCTTACTGTGCGAGACCAAGTTTCATGGAGCT 4702
QY 1609 GC-GG-GCACTTTGCT-AGA-----CTGT--G--CCA-----CC----- 1635
Db 4703 TCTGGAGCCTTGTAGTGAGAGGAAGACATAACCTGTAGCTTCCAGAGGAGATCCATCAGTT 4762
QY 1636 --AC-----GG-CG-----TGTGTTG-----T-GAAACGT- 1656
Db 4763 CAAAGGATGTGGAGGAGCAAAATCCTATGCTGTGGCAGAGGATGCTTTGGCACTTC 4822
QY 1657 ---GA-A-----ATAA-----AAA-----G-AGC-----AAAAAAA 1679
Db 4823 CACAGATCATGGCCATAACCTTCAAACTGTGCAGCTGTTAATAAGAAAA 4873

RESULT 19

US-09-620-312D-343
; Sequence 343, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Asundi, Vinod
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 343

LENGTH: 5273
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (328)..(4728)
US-09-620-312D-343

Query Match 41.5%; Score 696.4; DB 4; Length 5273;
Best Local Similarity 34.1%; Pred. No. 0.00026;
Matches 1471; Conservative 0; Mismatches 160; Indels 2686; Gaps 410;

QY 2 TTGTGTCCTT-----CAGCAAAACAGT-----GGAT--TT 29
DB 469 TTG--CCTTGGGCCACACCAAGCCAGTTCTTACCCTGACTTCATCTGGGAGATATT 525
QY 30 A--AATCTCCT--TGC-----ACA-----AGCT-TG--AGA-----GCAACACAA-- 62
DB 526 AGTCATGCCCTGGATGCGGTGAACACTCTCCTAGCTATGGCAGAACGGCTGCAA-ACAAA 584
QY 63 -----TCTA--TCAGGAAGAGAGAG--AATA-----AATCC----- 92
DB 585 TATAGAGCTCTAATAATCAGG--GATACAGGTAAATTCCTGCAAAACCAAGCTGGCTGA 641
QY 93 -----GAACCTGACA--AA-----AAAGAAGA-AAAAA----- 118
DB 642 ATTGTGGCTGAAGCTGATAGATGAAGTTATAGAAGACACGAGATACAGTTGCTCTCAC 701
QY 119 AGAAGAAA--AA-----A--TC-AT--GA-----AAA-----CAATCCAG-- 148
DB 702 AGAAGAAAACCAACGTCACAGTTCTCGATCTCAGATCCGAAAGCTGCGGTCCAGTGC 761
QY 149 -----CCAAA-----A-ATG-----CACA-AT-----T- 164
DB 762 TCTCTCCCAATACATGAGCGGCTGTGAGATGAGTCCGAAGCCACAGATGGAAGTC 821
QY 165 -----CT-----AT-----CT-CTTG----- 174
DB 822 CACACTGGCAGAAATTTGAGACTGGCTGTGATATAATTAATGACGTGACTGAAGGCCACA 881
QY 175 G--GCA-----ATCTTCA-----CGGG-----CTGGC----- 195
DB 882 GAACAGCATGCTGACATCATCTGTGATGATCCGGGGAGAGAGAGACTGCGCTATGC 941
QY 196 -----CCAAA-----A-ATG-----CACA-AT-----T- 199
DB 942 ACGAATTCGCGACATCAGGCTTTGTACTCCACAGTGGTGAAGATGCACTGGAAATA 1001
QY 200 CTGTG-----TC--TCT-----TCCA-AGGA----- 217
DB 1002 CTGTGGGAAACCCAAACCATCTTTCTGAAGTATCCACAGGAGAAACACGGGCCAAA 1061
QY 218 -GTGCGCG-----TGCG-----CA-----GC-----GGAGA----- 237
DB 1062 GGTGCTGTGGAGTTGGAGTGAACATCTGGCTAGGCTTAAGTCTGTGGAGAGAAAGTT 1121
QY 238 T-----GC-----C-----ACCTTCCCC-----A--AAGCT-- 256
DB 1122 TAACAGCTTCGCAAGAGAACTTTTCCCGTCTTTGCTGAAATGTATGAAATCAGCTCT 1181
QY 257 -----ATGG--AC-----A--ACGT----- 267
DB 1182 CATGTTGGAAATGGGGTACTTCTGGATTAGTAGGACGTCATAAGTTTCTGATGTCAC 1241
QY 268 -----GACGG-----TCC-----GGCAGG-----GG 284
DB 1242 AGGAATAAATACTCAAGAGGAAATTTTCTGCTTCCAAAGGCTGGGAATGGGAAGG 1301
QY 285 AGAGCG-----CC-----ACC-----CT-----CAGGT----- 302
DB 1302 AGAGTGTAGTTGATCTCTGAAAGAGCTTGTGACTGAGGACAGATCAGGTACACGGA 1361
QY 303 G--CACTATTCA-----CA-----ACC-----GGTCA-AC-----CCGG-- 328

DB 1362 GTTCACTGATGAAGTCTTATCAGAAACGAGAGCCGCTACCCCGGGGGCGACTGGAGCGGC 1421
QY 329 -GTGG-----CCT-----GGC--TAAACCGCAGCA--CCA----- 353
DB 1422 CGAGGACACCTACACGCGATGCGAAGCGGATAA--GCAGCATCACCAGGAGTTGACT 1479
QY 354 --TCCTCTATGCTGGGAAATGACAAG--TGGTGCTCGATC-----C-----TC--GGC-- 395
DB 1480 TGTCTCTCAGGTTGGGAAATGGAAGATGATGCACTGG--TCTTATGACATAAATCAGCGGT 1538
QY 396 -----TGG-----TCTTCTGA----- 407
DB 1539 GGATGAGAAAGCTGGGAATATGAATACACATTCCTCTCTGATCATAGCCCAATCCTG 1598
QY 408 -----GCA-----ACAC-----CC--AAACGC-- 422
DB 1599 GGTTCAGCAGAGAAAATGTACCACACTCATAGACGCGAAGGCTGTGCGAAACGCAA 1658
QY 423 --AG--T--ACAG-----CATCAG--AT-----CCA 441
DB 1659 GAAAGATTAAACACAGACTGCTTCAAGCACCGCAAGGGCCATGGAGGAATTGCAAGACA 1718
QY 442 -----GAA-----C--G-TGCA-----T-----GT--GT-- 455
DB 1719 AGAGGGCTGGGAATATGCTTCTCTAATTGCTGGAATTTCACTGGAAACAACGTAGTTC 1778
QY 456 --AT-----GAC-----GAG-----GGC--CCTT--ACAC----- 474
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QY 475 --CTGC--TC-----GGTG-----AGACAGACAACACCCA----- 502
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QY 524 ATTG-----TGAAGT-----ATCTCCCA----- 542
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QY 584 --AACA--ATATT-----AG-----CC----- 596
DB 2136 CCAACAAATTATTCGATGAAGTTGAAATCTATGGGAACCCCAACACAGTTCTACAGAA 2195
QY 597 T-CACC-----TG-C-AT-AGCAACTGG-----T 616
DB 2196 TCCACCCAAAGTTATCATGGAACCTTTTGACATGACCAAGTGGGCAAGATGAATTTT 2255
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QY 691 GG--AAAT-----T-----CAGGGCATCA--CCCG--GG-----AGC----- 716

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Db 2553 CCCAGTCTTGTGTGGAGTGTGGAGGAGAAAGGTGGAATCGGTGGTGTATCAAAACCT 2612
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Db 2673 GGAATTTATACATGCCCCCACTGGTGA--TCAAGGTATCGACCCACAGGCAGTTTGGCGGA 2731
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QY 838 -----GGACA-----AAAGG--GAC-----ACTG-----C--AGTG--TGAA 865
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QY 902 --AAGATGACAAA--GACTG-----AT-----TGA 924
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QY 1199 -----CTCGCGC---ACC-----ACCACC---ACCACACACACG---AA 1231
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Qy
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4027 TTTGTTTTCCGTTTGACTACCITCCAGCCGAAACACTGTGTATCTGTGGAA-AAAGA 4085

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1425 GCA---C-----ACC---CGG---CTTGA--CCCACTGCAAGCTG--CA-TG-G- 1459

Dd
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Dd
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RESULT 21
US-09-976-594-100
; Sequence 100, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCES: FA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ. ID. NO 100
; LENGTH: 6510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature

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i. OTHER INFORMATION: Incyte ID No. 6673549 234729.3
US-09-976-594-100

Query Match	41.5%	Score 696.1;	DB 4;	Length 6510;
Best Local Similarity	33.9%	Pred. No. 0.00041;		
Matches 1474;	Conservative 0;	Mismatches 156;	Indels 2723;	Gaps 412;

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Qy 691 -GG-----AAAT-----T-----CAGGGATCA--CCCG-GG-----AGC----- 716
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Qy 717 --AG--TC-AG--GGGAC--TACGA-----G-----TCGAG--TGCTCTCAATGAGT 753
Db 3692 TTGATTTCTAGCTGGGGCTTAAAGAAATATGAAATATGAAAACTTCCAGATGGCTTCTATCAT 3751

Qy 754 GGCCTGGCCC-----GTG--GTACGGA-GAGTAAAG-----TC- 784
Db 3752 --CC--CCAGTCTTGTGTGGAGTGTGGAGGAG-AAAAGGTGGAATCGGTGTGATCA 3805
Qy 785 --ACCGT--GA-----ACTATCCA-----CCATACATTCA-GAA-----G- 815
Db 3806 AAAACCTTAAAGAGACACCCAACTTTCGAATTCGTTCCTCATGAAGATGTTCTTGC 3865
Qy 816 CCAAGG-----GTACAGTGTCCCC-GTGG-GA-CAAAAAGG-----GA-CAC-TGCA 858
Db 3866 CCAAGGAGGAATTTGTACA--TGCCCCCACTGGTGATCAA--GGTCACTGACCAACAGCA 3920
Qy 859 GTGTG-----AAGCCT-----CAG-----CA-----G--TC----- 877
Db 3921 GTTTGGGCGGAAGCCTGTCTCGGCCAGTGCACCATCGAGCGCTGGACCGCTTTCGCTG 3980
Qy 878 --CCCT-----CAG-----CAG--AA-----TT----- 891
Db 3981 TGACCTTTATCGAGGAAGAGGACATCGTCCCACAGCTCAAGCTCCCTTCTGTCTGC 4040
Qy 892 ----CCAGT--GGTAC-----AA--GGATGACA--AAA-----G----- 915
Db 4041 CCCACCA--TGCCGGGACATCGTTATCGAAATGGAAGACACCAACCATTTACTGCGTCTA 4099
Qy 916 A-CTGATTG--AAGGA--AAGAAA--GG--GGTG--AAA----- 943
Db 4100 AGCTGACAGAAAGGAGGAAATCGTGGAGTCTGGAGTAAATTTTATGCTTCTCTCAG 4159
Qy 944 --G-----TGAAAAA-----CAGA--CCT--TTCC--TCTCAA----- 968
Db 4160 GGAACATGAAATGCGGACAGTATATTGAAAGGCTATTCGAAGTCAAGATATATA 4219
Qy 969 ----AACT-----CA-----T-----CTTC-----TTCA 983
Db 4220 ATTGTGAACCTAGAAATGTAGCAAAATTTGAGGCGCTGACAGACTTCTCAGATACGTTCA 4279
Qy 984 A--TGT-----C--TC--TGACATGA-----CTATG----- 1004
Db 4280 AGTTGTACCGAGGCAAGTCGGATGAAATGAAATGAAATGCTTCTGTGTTGGAGGTTTAAAG 4339
Qy 1005 ----GGAATACACT--TGC-----GTG-----G--CCTCC-A-ACA-- 1031
Db 4340 GCTCTTTTCGATCTACCTCTCGCGGATGACCCAGCGTGCCAGCCCTCCAGACAGT 4399
Qy 1032 ----AGCTG--G-G--CCACCAATGC-C--AGCAT--CAT----- 1059
Db 4400 TTCGGGAATTACCTGACAGCGTCCACAGGAATGACGGTTAGGATTTACATTTCTGCGAG 4459
Qy 1060 GCTATTTG-G-TCCAGCGGCC--GTCA-----GCGAG-GTGAGC-----AA 1095
Db 4460 GC--TTAGACTCA-GCCCGAGACAAATGCGCTGTGTGACCCCTTACATATAAAATAA 4516
Qy 1096 C---GGC-----ACGTC--G-AG--GAG----- 1110
Db 4517 CACTGGGCAAAAGATCAATTGAAGACCGAGATCACTACATTTCCCAACACTCTCAACCCAG 4576
Qy 1111 ----GGCAGGCTG--CG-TCTG-GCTGC-----TGCTC-----TT 1138
Db 4577 TCTTTGCGAGGATGTACGAATGAGCTGAGCTGCTACTTACCTCAAGAAAAAGACCTGAAAAAT 4636
Qy 1139 CTGCTCT-----TG-CACCTGCTT--CTC-----A-AAAT--TTG 1167
Db 4637 CT-GTCTATGATATGACACT--TTACCCGGGATGAAAAGTAGGAGAAACAAATTTT 4693
Qy 1168 ATGTG-----A-G-----TGCCACTT-----CCCCAC-CCGGGA-----A-AGG----- 1198
Db 4694 ATCTGAAAACCGATTCTCTTTCCGCTTTTGGGTCCCACTCGGGCATACAGAGGAGTACT 4753
Qy 1199 ----CTGCGGC--ACC-----ACCACC-----ACCAACACACAGC-----AATG 1233
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1234 --GCAA--CA-----CCGACAGCAACC-----AATCA 1256
4814 TCGCAGATCAAGGCTTC--CA-CAACCATCTTTCCGAGATGGAGTAGATCA 4870
1257 GATAT--A-TACA-----AATGAATTAGAAG-----AAA 1283
4871 GATATGAGGACGAGACTACAGCTTGGATGAA-TTTGAAGCCACAAATCTCTGCACG 4929
1284 -----GAGGCTCA-----CAGGCTCA-----TGG-- 1296
4930 CACTCGGGCCCTGAGAGCGGCTTGTCTTTCATCTCTCAGGACTCAGGGGCTGTGC 4989
1297 --GA-CA-----TTTG-----AGGGA 1313
4990 CTTGACGCTGGAACAAGGACTTTTGCACAGCAGCTTCCAGCCCAACATTTCCAGGGA 5049
1314 -----GGGG----- 1317
5050 AACTTTCAGATGTGGGTGGATGTTTCCCAAGAGTTTGGGGCCACGAGGCCCTCTTTC 5109
1318 AACA-----AAG-AATACT----- 1330
5110 AACTACACCCCGGAAGCAAGAAATACTCTGGGTGTATCATCTGGAACACCAAG 5169
1331 --TTGG-----GG--GGAAGAGT-----TTTA--AAA 1353
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1384 --AGG-----TACAATG--CA--GTTTTT-----TT- 1407
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1408 -CAA-----A-CG--G-GAAGAACACAGCA--C-----ACC--CGG--CTTG 1438
5349 ACAACTCTGTATCTGTTGCGAA-AAAAGAGCATTTCTGGAGTATTGACCAACGAATTC 5407
1439 GA-CCCACTGCAAGCTG-CA-TC-G--TG--CA--AC-----CTCT----- 1469
5408 GAATCCAC--CGAGGCTGATCATTCAGATAGGACAATGACAAGTTTCTCTGAGTAC 5466
1470 --TTGG-----TG-----CCAG-- 1479
5467 TACTTGGTTTCTAGAACCTTGCTGGTGCACAGCATCTTCTGCAAAATCACCAGAG 5526
1480 --TG-----TGGGCAAG--GG-----CT-----CA 1495
5527 AATGCAAGTTGACATGATTTCCGGACCTCAAGCCATGAACCCCTTAAAGCCAAGACA 5586
1496 GCCT--CTCT--GC-----CCA-----CAGAG-----T 1514
5587 GCCTCCCTCTTGAGCAGAGTCCATGAAGAGTGTGGCCATGCTACGAGAGAAAGAT 5646
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5647 GCGGCCCGCTAATGGCTGGGA-A--GTGAGAT--GACATTGGAATCTCTCA--CGAGA 5701
1560 --AGTCC--ATAG-----A-----GACGAAC-----AG- 1578
5702 AGAGGCCGACGAGAGCCAGCCGGGAAGGGGGGAGCAACCAACATGAACCCCAAGC 5761
1579 -----AAT-G--AGA-----CCTTCC--GG-----CCCAAGC----- 1600
5762 TGGACTTACCAATCGACAGAAACCTCTTCTGTTTCAACCAACCCATGCAAGACCA 5821
1601 -----GTGGCGCTGC-----GGG-----CA--CTT--TG-----G--TA 1623
5822 TGAAGTTTCATCGTGTGGCGCGCTTTAAGTGGGTGATCATCTGCTGCTCTCTTA 5881
1624 GACTG-TGC-CACCACGG-CGTG-----TG-----TTGTGAACGTGA 1658

5882 TCCTGCTCTTCGTGGCGGCTCTCTACTCTCTTTCGGAACACTATTGTCAA---TGA 5938
1659 A-AT-----AA-----AAA-GAGCAAAA---AAA 1679
5939 AGATTGTAAGCCAAATGTGTAACAAAGGCAA 5971
RESULT 22
US-09-534-638-2
; Sequence 2, Application US/09534638
; Patent No. 6320038
; GENERAL INFORMATION:
; APPLICANT: Panula, Pertti A.J.
; APPLICANT: Brandt, Annika
; APPLICANT: Westerlund, Johanna
; TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof
; FILE REFERENCE: 2530-104
; CURRENT APPLICATION NUMBER: US/09/534,638
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; EARLIER APPLICATION NUMBER: 09/365755
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; SEQ ID NO 2
; LENGTH: 5124
; TYPE: DNA
; ORGANISM: Mouse
US-09-534-638-2
Query Match 41.4%; Score 695.2; DB 4; Length 5124;
Best Local Similarity 39.0%; Pred No. 0.00026;
Matches 1403; Conservative 0; Mismatches 181; Indels 2012; Gaps 398;
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DB 687 GTGAGTGTGATGCTGTGATGCAAAACCACTTCCCATGTTCCCTGTGTGCCCCCAATA 746
QY 29 TAAAT-----CT-----CC-----TTGCACAAG-CT-T--GAGAGCA----- 56
DB 747 AAAATGGTCCGCTGGCTTCAGATCCCTGTGTTTGGACAAAGACTGTTCAGGAGCAGGTG 806
QY 57 --A--CA-----CAAT-----CT--A-TCAG-----G-A----- 72
DB 807 GAGGCCAGGCAATAGCTGTAGCCCCCTTCACTCCACTCAGTCTCTAGCCATCTG 866
QY 73 -----AAGAAAGA-----AAGAAAAAACCGAACCT-----G--A-----AAG 108
DB 867 TTGTTAAG--GATCCCAAGGCTACTGTGACCTTGTGCTCTCTCGGTAAACAAAAAG 923
QY 109 AAGA-----AAAGAGAGAGAA--A--A--A-----AAA--TCATGAAA 140
DB 924 ACAAGGGTTTCAAGAGGAAACAAGTCAATGTTTATTCCTTATACCTCATG--AC 981
QY 141 CCA--TCC-----AGCAAAAATGCA--CA--ATTTC----- 165
DB 982 CCAAGGCCAGAGAGAGCAGGTTTGGAGCCCAAGA--GCAGCATTTATTCAGGACTCA 1040
QY 166 -TA-----TC-TC--T-----TG-GG-C-AATC--T--TCAC--GGGGC----- 191
DB 1041 ATAGATTATCATCCATCACCACCGAATGAGGACAAATCTGTGCTGGCTGGGCGCTGTGG 1100
QY 192 ----TGCC-----TGCT-----CTGCTCT--CT--TC-CAAGG-----AGTCCCTGGG- 228
DB 1101 TTCATGGCTCTTGTCTGCTGCTTCTCTCAGTCTCAAGGACAGAG-GC--TGTT 1156
QY 229 CAGCG--GAGATGCCACCTTC-----CCCAAGCTA--TGGACACAGTGAAGGTGC 275
DB 1157 CAGAGTAGAGATGCA-CTTCTGGAGGTACCAAGCTAGGTGA-TAC---ATGGACC 1211
QY 276 GCGAGGGGAGA--GCGC-----CA--CCCTCAGGTGA-----CT 307

Db 1212 --CAGGGGAGAGGAGCAAGAGTAAAGATGCATATCCATCA-CTGCAGTGGGATGCT 1268
Qy 308 A-TTGACACACGGGTCA---CCCG-GGT---GGCCTGGCTAAACCCGACACCAT 354
Db 1269 ACTTG-CTACC-CCCCATGATCTTGAGGTACTGTAGGCGCGG-TGAGCAGCATCAC-T 1324
Qy 355 ---CCTCATGCTGG---GA---ATGACA---AGTGG-TGCTTG---A---387
Db 1325 CGGCTGCTCCCTGGTGGTGGAGAACCATACACAGTGGCTGGCTGGGTGGACAGT 1384
Qy 388 TCCTC---GC-GTGG---TC---CT---TCTG---AGCAA---411
Db 1385 TCCACTAGGCACCTGGCAGAGCCCACTCAGGCTCAGTTCTCTGGAACCAAGAAAGAGAA 1444
Qy 412 ---CAC---CZAAAGCGCA-GTACAGATCGA-GAT---CCAG 442
Db 1445 GGGAGGCACCTGGTGGGAAGGGGACCAAA-CAGTGTACA-CATC-ACCATCTCCCA- 1499
Qy 443 A---ACGTG---GAT---GT---GTATGACGAG-GGCC---467
Db 1500 ACTCCTTCATACTGCTTTGATCCAGTCCCTCCATCCCACTCT-CTAGTTGCCATA 1557
Qy 468 ---CTTACA---CTGTCTGGTGCAGA---CA---GACA-494
Db 1558 CCAATATCCAGATAGCTGACATGGAAGCCTGCTC-CT-CAGAGAGCTCACTGAGGACAC 1615
Qy 495 ---ACCA---CCCAAGACCTTAG-G-GTCCAC---CTCATTTGTGCAAG---TA 535
Db 1616 TGCAGCAGGAGAGCCAGAG-CCCTTAGAGAGCCCGGAGC-AACTGCG-AGAGGATA 1672
Qy 536 ---TCTCCA-A-AATTT---GT---AG---A-GAATTC 558
Db 1673 GGATCTTTTCTCCACAGAAATCCGCAAGGAATCCAGTGCAGCTGGCCCAAGA-TTC 1731
Qy 559 TTCAGATATC-TCCA---T---TAATGA---AG---581
Db 1732 CTCAG---TCCATCCAGCGGGAGCTACGCGCTTAATGAGATAGAGTGAAGAACGCT 1788
Qy 582 ---GGA---AC---AA---TATTA-GC-CT-CACCTG---CAT-606
Db 1789 AAGACTGTGGGACCAAGAACTGGGTATATGCTCTGACTCTCTGGCAGCCTTCTCTATC 1848
Qy 607 ---AGCAA---CT---GG---TAGACCAG---AG---CCTAC---630
Db 1849 CCAGAAAGTTGCTATAGGGCTTTTGCCTTAGCCAGCTTTTCACTAGTACCTATAC 1908
Qy 631 ---GGTT---ACTT---GGAG---A-CA---645
Db 1909 ATAGGCTGAGGGGACTTCTGGGCGCACAGGTTCAAGGGGCCCTGGGAAGAAAGCAGGCC 1968
Qy 646 CAT-CTC---TC---CCAAAG---CGGT---TG---GCTTTGTGA---674
Db 1969 CATACTCACTTCCAAACACAGACCCCAACCAATTCGTACCATGTCTCTGAGTGTGAAC 2028
Qy 675 ---GT-GA---AGACGAA---TAC-TTGGAAA---T-TCAGG---GC 703
Db 2029 CACATGTGAGCCCAACAC-AAGCCACTTACAATGGAATAATGATCGTCACTCAGGCTCTGC 2087
Qy 704 ATCA---CCCGGAGCAGTCAAGGACTACAGTGCAGTGC-CTCCAAATGA---C 751
Db 2088 CTCATTGCCATCCCGG---GCATCCAGAGG---TACAAGT---GTGCACCTGAAGGAGCATC 2140
Qy 752 ---G-TG-GC---CGC---GCCCG---TG---GT---AC-G---GAGAGT---AA 779
Db 2141 TTAGTCTGCTGTACGCTTTTGGCAGCTTTTGGAGTGCACCTGCCTGAGGTTGGGGA 2200
Qy 780 AGG---TCACC---GTGAACATATCC---ACC-ATACATTTCAAGAGC-CAAGGG 822
Db 2201 AGGAATTTTCAACTTGGGGA-T-TCTTAACAGACCAATGC-TTTC---CTCTAGG 2251
Qy 823 T-----ACAGGTGTC-CCC-GTGGGA---CA---AAAGGGA---CA---CTG---856
Db 2252 TAACTTAGACA---GTCACCAATGAGATACCACTGCAAGAGGAGGCTCAAGGCGCTGATC 2308

Qy 857 ---C---AGT---GTGAAGCC---TCA---GCAGTCCCTCAG 884
Db 2309 TTTTAACTGAGGAGTTGGTG-AGCCAGATAAGAGGGGGAAGATGGCGGAGC---AAG 2365
Qy 885 ---CAGAAATCCAG---TGTA-CAAGGA-TG---A-CAAAAGA-CT---GATT 922
Db 2366 GGAGAGACAGGAGGAGGAGCTG-AGCAGGACCTTGCAAGGCAAGAGGAGCTGGGACA 2423
Qy 923 GA---AGG-AAAGAA-A---GGGTGAAA-GTGGAAAACAGA---955
Db 2424 GAGCACAGCCAGGCAAGAACCACTTTGTTGGGTTCAGTGTGGCAAGAGAGAG 2483
Qy 956 ---CCTTT---CC-TCTCA---AAAC---TC 973
Db 2484 GTGAGTGAACCCCTTTTCCCCAGTTTACCAATCTCAATGAAGAGCTCCACCCGCAAGTC 2543
Qy 974 A---TCT---TCT---TCT---TCA-ATGT-CTCTG---AA 994
Db 2544 ATGCTGAACCTTTTGGCGTGAGCAGGCCAGACTCTTGGGTCAACATGTACTCTGGCAA 2603
Qy 995 ---CA---TG---ACTA---TG---GGA-C-TA---CA---CTT-1016
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Qy 1017 GCGTGG---CCT---CCAA---CAG---CT---1035
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Qy 1036 ---GGGCCAC---AC---CAA-TGC-CA---GCATCATG---CTATTGGTCCAG---1073
Db 2724 GGAGGACCACTTACCCACAAGTGCACACGCCCTGCTCA-GCCTACTT---CAGAG 2778
Qy 1074 ---CGGC-C-GTC---AG-CGAGG---T---GAGCA---AG---GCAC 1101
Db 2779 AAGATAGCACATGACAATGAAGACGAGGCACACCTGCGAGCACCGGCGGTTCAC 2838
Qy 1102 GTC---GAGGAG-GGCA---GGCTGCTCT---1124
Db 2839 -TCAGACTGTGAGAGAGACAGGGGCTGCACTCCATGGAGGGCTCTCTTAAGAAAAA 2897
Qy 1125 ---GGC---TGCTG---CCTC---TCTGTGCTTTG---1147
Db 2898 AGGCCCCAGGCCAGTGTCTGAGGAAAATGCAGAGGTTCTCTCTCTCTGCTCATGATCAA 2957
Qy 1148 ---CAGCT---GCT-TCT---CAAA---1162
Db 2958 GTGCCAGCCACTACCACTCCCAATTCCTCACCAGGAGCAGCTATCTGTCCAAACATC 3017
Qy 1163 ---TTT---T---GATGTGAG---TGCCACTTTCCC---1185
Db 3018 TAGCTTTTCTCCCTCCCAACACCCCAAGTAGGCTCTGCTACTTCCCGAGGAGCA 3077
Qy 1186 ---CA---CCC---GGGAAAG---GCTG-CCGC-C 1206
Db 3078 CTTAGATGTGAAATCCTTCAGCAATGTCCCTGTGATGAGGTTAAAGGAGCTGTACACAC 3137
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Db 3138 AGTCTGGAAGTACCTTTTGGGTCTCAACATGAGGCTCTTAAGATGTTTAAACAATCTA 3197
Qy 1225 ACA---GCAATGGC---AA---CA---CCGA---CAG---CAAC 1250
Db 3198 ACATTCAATGC-TTGGCTATTTTAAATCATATAATTAACCTCTAGCTCAGGCTTACCAAC 3256
Qy 1251 C---AA---TCAGATATA---TA---1264
Db 3257 CAGCTGGTCAAAATTTTCA-AT-TACACCAGCTGTCTTTTACTCTCAGGCTTCTCATC 3314
Qy 1265 ---CAA---ATGAATTAGAAG-AA-ACAC---A 1287
Db 3315 CTGACCTGCTGAGTCCAGAGGCTATGAGACTAGAACCAAGACCCCTCTCTCTCCCAA 3374

Db 704 GTGGAGAAATTTGTTCTCCCAAGTTTGAAGTACAAAGTAAAGTAAAGTAAATCACC 763
QY 326 -C-C-GG-----GTG-GCCTGG-CTAAAC-C-----GCAGCACC 352
Db 764 ATCTTGAAGAAGAGATGAATGTATCAGTGTG--TGGCCATATACATATGGAAGC-CT 820
QY 353 ATCTCTCT---ATG---CTGGGA--AT-----GACAAG-TGGTG-----CCTGGA-T- 388
Db 821 GTCC-CTGGACATGTGACTGTGAGCATTTGCAGA-AAGTATAGTAGAGCTTCC--GACTG 876
QY 389 CTTCGGGTG-G-TG---C-TTCT--GAG-----CA-----ACACCCAAAC----- 420
Db 877 CCAGC-GTGAAGATTACAGAGCTTTCTGTGAGAAATTCAGTGGACAGCTTAAACAGCCATG 935
QY 421 GCAG---TA-CAGCA-T-----CGAG---ATCCA-----GAACGTGG-ATGTGTATG-- 458
Db 936 GTGTCTTATCAGCAAGTAAACCAAGGTCTTCCAGCTGAA-GAGGAAGAGTATGAA 994
QY 459-----AC-GAGGGCCCTTACA-CC-----TG-----CT 479
Db 995 ATGAAACTTCACTGA-GGCC--AGATCCAAAGAGAGAACAGTGTGGAATTGACT 1051
QY 480-----CGTGCAG-----ACAGACACC-ACCCAAA-----GA 506
Db 1052 GGAAGGCAGTCAGTGAATCACA-AGAACCATAAACCAACTCTCATTTGTGAAGTGA 1110
QY 507 C-----CTCT-----AGGG--TCCACCTCATTTGTGCA-----AGTA----- 535
Db 1111 CTCACACTTTCAGACAGGAAATTC--CTTCTTTGGCAGGTGCGCTAGTAGTGGAAAG 1169
QY 536---TC-----TCCAAAATTTGTAGAG--AT-TTCTTTTCA-----TAT--C 568
Db 1170 GCGTCCCTATACAAA-----TAAAGTCATATTCATCAGAGGAAATGAACAACTATTAC 1225
QY 569 TCC-AT--TA-----ATGA-A-GG-----GAACA-----ATATTAGCTCACC----- 601
Db 1226 TCCAAATGTACACGGATGAGATGGCTGTGTACAGTTCTCTATCAACACCACCAACGTT 1285
QY 602 -TG-CATAGC-----AACTGGTAG-----ACCAG-----AG-CCT---ACGGTTAC 636
Db 1286 ATGGTACTCTCTTACTTGTAGGTCTAATTAACAGGATCGTAGTCCCTGTTACGGCTAC 1345
QY 637---T---TG-----GAGACACATC-----TCTCCCAA 657
Db 1346 CAGTGGGTGTGAGAAGAACACGAAGAGGCACATCACACTGTATCTGTGTCTCCCA 1405
QY 658 AGC--GGTTGGCTTTG-----TGAG-----TGAGACGA-----ATA 687
Db 1406 AGCAAG--AGCTTTGTCCACCTTGAGCCCATGTCTCATGA--ACTACCTGTGGCCATA 1460
QY 688 CT-----T--GG-----AAATTCAG-----GGCA----- 704
Db 1461 CTCAGACAGTCAGGCACATATATTTCTGAATGGAGGCACCTGTGGGGCTGAAGAAGC 1520
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Db 1521 TCTCCTTTTATPATCTGATTAATGGAAAGGAGGCAATGTCGGAAGTGGGACT-CATGGA 1579
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Db 1580 CTGCTTGTGAAGCAGGAAGACATGAAGGGCCATTTTTCATCTCAATCCCTGTGAAGTCA 1639
QY 749 GACGTGGC-----CGC-----GC-----CGTGGTAC----- 770
Db 1640 GACATGTCTCTGCTCGCTGGTTGCTCATCTATGCTGTTTACCTACCG-GGAGCTGAT 1698
QY 771---GGA-----GA-GT---AAA-----GGTCACC-----GTGAAT--A--TC 797
Db 1699 TGGGATTTCTGAAATATGATGTTTGAATTTGTCTGGCCAAAGGTGGATTTGAGCTT 1758
QY 798 CA--CCAT--ACA--T-T-----TCAGAGCCAA-----GGGT-ACAG----- 827

1759 CAGCCCATCATCAAAAGTCTCCAGCCTCACAGCCACCTCGGAGTCACAGCGGCTCCTCA 1818
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QY 865--AGC-CTCAGCAGTCC-----CCT--C-AGCAGAA-----TTCTC 893
Db 876 TGAGTCTCGGC-GTCTCTCGGTTTACAACCTGTCTACAGAAAGACCTCAGTGGCTTCC 1934
QY 894 AGTGG-----T-ACAAG--GATGACAAAAGACTG-----AT--TG----- 923
Db 1935 -CTGGCCCTTTGAAATGACAGACGATG--AAGACTGCATCATCTCAATGTCTA 1989
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Db 1990 TATTAAATGAATCAATATATCTCAGTATCAAGTACAAA--TGAAAA--GGATATGATC 2044
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Db 2045 AG--C-TTCTTAGAGGACATGGGCTTAAAGGCATTCACCAACTCAAGATTCGTAACCC 2101
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QY 1071 CAGGCGCG--TCAGC-----GAGGT--GAGCAACGG-----CA 1100
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QY 1130--CTGCTCT-TCTG-GTCTTGA--CCTGCTT-----CTCA-AAAT--TT-----T 1166
Db 2389 CACTGCTCTCTCCGAGCTTCCAGCCCTCTTGTGTGAGCTTACAATGCCTTACTCTGT 2448
QY 1167 GAT--GT--CAG-----T--GCCA-----CTTCCC-----CAC 1188
Db 2449 GATTGTGAGAGGCTTTCACACTCAAGGCCACGGTCTTAAACTACCTTCCCAATGCAT 2508
QY 1189 CCGGGAAG--GCTG-----CCGCC-ACC-----ACC-----ACCA 1216
Db 2509 CCGGTGAGTGTGAGCTGGAAGCCTCTCCGCCCTTCTGCTGTCCAGTGGGAAGGA 2568
QY 1217 CCAA-----CACAACA-----GCAA-----TGCAACA--CC--GACAGCAA--C 1250
Db 2569 ACAAGCGCTCACTGCATCTGTGCAACGGCGGCAA-ACTGTGTCTGGCAGTAAACC 2627
QY 1251 CAATCAGATATATA-CAAA--TGAATTT-A---GA-----AGAACAC--AGCCTCA-- 1293
Db 2628 CAA--AGTCAT-TAGGAAATGTAATTTCACTGTGAGCGCAGGCGCACTAGAGTCTCAAG 2684
QY 1294-----TGGACACA-----AAATTT--TGA--GGGAG----- 1314
Db 2685 AGCTGTGTGGAGCTGAGGTGCTTTCAGTTCTTGAACGGAGGAGGAGACAGTCACTCA 2744
QY 1315-----GG--GAAC--AA-----AGAA-----TACTTTT 1332
Db 2745 AGCCTCTGTGTTGTAACCTGAAGGACTAGAGAAGGAAACAACATTCACCTCCCTACTTT 2804
QY 1333 G-----GG-GG-GA-----AAGAGTTT-T--TAAAA--AAGAAAT--T-G 1362
Db 2805 GTCCATCAGGTGGTGAAGTTTCTGAAGAAATTTATCCCTGAAACTGCAACCAATGTGGTAG 2864

Qy	1363	AA-AAT-TGCC- 	-----TT-GCAGATAT-TTAGG-----T-----	1387
Db	2865	AAGAATCTGCCCGAGCTTCTGTCTCAGTTTTGGGAGCATATTAGGCTCTGCCATGCAAA	2924	
Qy	1388	---ACAA- 	-----TGGAG-----TTT-----TCCTTT-1404	
Db	2925	ACACACAAATCTCTCCAGATGCCCTATGGCTGTGGGAGCAGAAATATGGTCTCTCTTTG	2984	
Qy	1405	-TCCCAA- 	-----ACGGG-----AA-G-AAACACAGCA-----C-1430	
Db	2985	CTCCTAACATCTATGTACTGGAATTATCTAATATGAACACAGCAGCTTACTCCAGAGTCA	3044	
Qy	1431	---CG--GGC-TTGG--ACC- 	---CACTG---CA-----AGCTGCATGTGCAAA---1464	
Db	3045	AGTCCAGGCCAATTTGGCTATCTCAACACTGTGTTACCAAGAGACAGTTG-AAC-TACAAACA	3102	
Qy	1465	-----CCY- 	-----CTTTGG-----TGCCAGTG-----TGGGCNA---G 1489	
Db	3103	CTATGATGGCTCTACAGCACCTTTGGGGAGCGATATGGCAG-GAACCGAGGGCAACACCT	3161	
Qy	1490	GGCT--CAGCC- 	-----TCT---C---TGCCCCAG--AGTGCC--C--C--CA-CG-T 1524	
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Qy	1525	GGA---ACATP-CTGGAGC- 	-----TGGCCATCCCA-----AA-----1552	
Db	3221	GAAGCACACATTACCCAGCCCTCATATGGCTCTCCAGAGCGCAAGGACAAATGGCTGT	3280	
Qy	1553	TTCA-A- 	-----TCAGT-----CCAT--AGAGACCAACAGA--ATGA--G 1584	
Db	3281	TTCAGGAGCTCTGGGTCACTGCTCAACAATGCCATAAAGGAGGAGTAGAAGATGAAGTG	3340	
Qy	1585	A-CCT-TCGG- 	-----GCC-----CA-AG-----CGT 1602	
Db	3341	ACCTCTCCGCTATATCACCATCGCCCTCTTGAGATTCCTCTCAGATCACTCACCT	3400	
Qy	1603	G-----GC--GC- 	-----TGC--GG-G-CA-CTTTGGTAGAC-----1626	
Db	3401	GTTGTCGCAATGCCCTGTTTGTGCTGGAGTCAGCCT--GGAAGACAGCACAAAGGGG	3458	
Qy	1627	---TG--TGCC- 	-----ACCA-----C-GCGGTGTG---TTG---TG-----A 1651	
Db	3459	ACCATGCAGCCATGTATATACCAAAAGCACTGTGGCCTATGCTTTTGCCCTGGCAGGTA	3518	
Qy	1652	A-----AC- 	-----CTGAATA--AA-----AA-CAGCA--AA-AAA---1677	
Db	3519	ACCAGGACAGAGGAAG-GAAGTACTCAAGTCACTTAATGAGGAAGCTGTGAAGAAAGAC	3577	
Qy	1678	AA 1679 		
Db	3578	AA 3579 		

RESULT 24

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US-09-241-606-1
? Sequence 1, Application US/09241606
? Patent No. 8472140
? GENERAL INFORMATION:
? APPLICANT: Tanzil, Rudolph E.
? APPLICANT: Kovacs, Dora
? APPLICANT: Saunders, Aleister J.
? TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
? TITLE OF INVENTION: Alzheimer's Disease
? FILE REFERENCE: 0609.4460003
? CURRENT APPLICATION NUMBER: US/09/241.606
? CURRENT FILING DATE: 1999-02-02
? NUMBER OF SEQ ID NOS: 27
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 1
? LENGTH: 4577
? TYPE: DNA
? ORGANISM: Homo sapiens

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995 ATGAACCTTCACTGA-GGCC--AGATCCAAAGAAAGGAACAGTGGTGAATTGACT 1051
480 -----CGGTGCAG-----ACAGACACC--ACCCAA-----GA 506
1052 GGAAGGCACTCCAGTGAATCACA-AGAACCATAACCAAACTCTCAATTTGTGAAGTGA 1110
507 C-----CTCT--AGGG--TCCACCTCATTTGTGA-----AGTA-----535
1111 CTCACACTTTTCAGACAGGAATCC-CTTCTTTGGCAGGTGGCCCTAGTAGTGAAGAA 1169
536 ---TC---TCCAAATTTGTAGAG--AT--TTCTTCAGA-----TAT--C 568
1170 GGGTCCCTATACCAAA--TAAAGTCATATTATCATCAGAGGAATGAAGCAAACTATTAC 1225
569 TCC-AT--TA-----ATGA--A-GG-----GAACA-----ATATTAGCCTCACC-----601
1226 TCCATGCTACACGGATGAGATGGCCCTGTACAGTTCTCTATCAACACCACCAAGCTT 1285
602 -TGATPAGC-----AACTGGTAG-----ACCAG-----AG--CCT--ACGGTTAC 636
1286 ATGGGTACCTCTCTTACTGTAGGTCAANTTACAAGGATCGTAGTCCCTGTTACGGCTAC 1345
637 ---T---TG-----GAGACACATC-----TCTCCCAA 657
1346 CAGTGGGTGTCAAGAAACACGAAGAGGACATCACACTGCTTATCTTGTGTTCTCCCA 1405
658 AGC--GGTTGGCTTTG-----TGAG-----TGAAGACGA-----ATA 687
1406 AGCAAG--AGCTTTGTCCACCTTGAGCCCATGTCTCATGA--ACTACCTGTGGCCATA 1460
688 CT-----T---GG-----AAATTCAG-----GGCA-----704
1461 CTCAGACAGTCCAGGCACATTAATTTCTGAATGGAGGCCCTGTGCTGGGCTGMAAGAC 1520
705 TCACC-----C---GGGA-GCA--GTCAG-----GGGACTAC--GA 732
1521 TCTCCTTTTATATCTGAATTAATGGCAAGGGAGGCATTTGCCAACTGGGACT-CATGGA 1579
733 -----GT--GCAG-----TG-----CC-TC-CAAT-----748
1580 CTGCTGTGAAGCAGACATGAAGGCCATTTTCCATCTCAATCCTGTGAAGTCA 1639
749 GACGTGGC-----CGC-----GC-----CCGTGGTAC-----770
1640 GACATGTCTCTGCTGCTGCTGCTCACTATGCTGTTTACCTACCG-GGACGTGAT 1698
771 ---GGA-----GA-GT---AAA-----GGTCACC--GTGAAT--A--TC 797
1699 TGGGATTTCTCAAAATATGATGTGAATAATGTCTGGCCCAAGAGGTGGATTTGAGCTT 1758
798 CA--CCAT-ACA--T-T-----TCAGAAGCCAA-----GGGT-ACAG-----827
1759 CAGCCCATCAAAAGTCTCCAGCTCCACAGCCACCTGCGAGTCAAGCGGCTCCTCA 1818
828 GT--GT-----CC-CCGTG--GGACAAAG-GGGAACATGC-----ATGTGA---864
1819 GTCCGTCTGCGCCCTCGTCTGTGAGCAAAAGCGTG--CTGCTCATGAAGCCTGATC 1875
865 --AGC-CTCAGCAGTCC-----CCT-C-AGCAGAA-----TTCC 893
1876 TGAGCTCTCGGC-GTCCCTCGTTTACAACCTGCTACCAAAAGGACCTCACTGGCTTCC 1934
894 AGTGG-----T-ACAAG--GATGACAAAGACTG-----AT--TG-----923
1935 -CTGGCCCTTTTGAATGACCGAGGACGATG--AAGACTGCATCAATCGTCAATATGTCTA 1989
924 ----AA-GGA-----AAG-----AAGGGGTGAAGTGAAGAA--AC 952
1990 TATTAATGAATACATATACCTCCAGTATCAAGTACAAA--TGAATAA--GGATATGTAC 2044
953 AGACCTTTCTCT-----CTCAAA--ACTCA-----TC-----TTCTT---C 982
2045 AG--C-TTCTTAGAGGACATGGCTTTAAGGATATCCCAACTCAAGATTCGTAAACCC 2101

983 AA-----TGTC-----TC-----TGAA-----CATG-----AC-----1000
2102 AAAATGTGTCCACAGCTTCAACAGATGAAATGCAAGCTTGAAGGTCTACGTGTAGGT 2161
1001 -----T-ATGGAA--C-TACA--CT--TGCGTG-----GCCT 1025
2162 TTTTATGAGTCAGATGTAATGGAGAGGCCATGACGCTGTGTCATGTTGAAGAGCT 2221
1026 CCAACAAGGTG--GGCCACACCAA-----TGCC--AGCATCATG--CT--ATTGGTTC 1070
2222 C--ACA--CGAGAGCCGTACGAAAGTACTTCCCTCAG-A-CATGATCTGGGATTTGGT- 2274
1071 CAGGCGCCG-----TCAGC-----GAGGT--GAGCAACGG-----CA 1100
2275 --GGTG--GTAACTCAGCAGGGGTGGCTGAGTAGGAGTAACAGTCCCTGACCATCA 2330
1101 COTCGA--GGAGGGCAGG-----CTGC--GTCTG-----GCTG-----1129
2331 C--CGAGTGAAGGAGGGCCCTTCTGCTGTCTGAAGATGCTGGACTTGGTATCTCTTC 2388
1130 --CTGCTCT-TCTG-GTCTTGCA--CCTGCTT-----CTCA-AAT--TT-----T 1166
2389 CACTGCTCTCTCCGAGCCTTCCAGCCCTTCTTTGTGGAGCTTACAATGCTTACTCTGT 2448
1167 GAT--GT--GAG-----T--GCCA-----CTTCCC-----CAC 1188
2449 GATTCGTGAGAGGCTTCACTCAAGCCACGGTCTCTAAACTACCTTCCCAATGCTAT 2508
1189 CCGGAAAG-----GCTG-----CGCC-ACC-----ACC-----ACCA 1216
2509 CCGGTCTAGTGTGAGCTGGAAGCCTCTCCGCCCTTCTTGTGCTGCCAGTGGAGAAGA 2568
1217 CCAA-----CACACA-----GCAA-----TGGCAACA-----CC-GACAGCAA--C 1250
2569 ACAAGCGCTCACTCATCTGTGCAACGGGCGGCAA--ACTGTGTCTGGGCGAGTAACCC 2627
1251 CAATCAGATATATA-CAAA--TGAATT-A-----AGAAACAC--AGCCTCA-- 1293
2628 CAA--AGTCAT-TAGGAATGTGAATTTCACTGTGAGCGCAGAGGACTAGAGTCTCAG 2684
1294 -----TGGGACAGA-----AATT--TGA-----GGGAG-----1314
2685 AGCTGTGTGGGACTCAGGTGCTTCACTTCTTGAACCGAAGGAAGACAGATCATCA 2744
1315 -----GG-CAAC--AA-----AGAA-----TACTTT 1332
2745 AGCCTCTGTGTTGAACCTGAAGGACTAGAGAAGGAACACATTCACCTCCCTACTTT 2804
1333 G-----GG-GG-GA-----AAAGAGTT-T-----TAAAA--AAGAAAT--T-G 1362
2805 GTCCATCAGTGTGAGGTCTTGAAGATTTATCCCTGAACTGCACCAATGTGGTAG 2864
1363 AA-AAT-TGCC-----TT-GCAGATAT-TTAGG-----T-----1387
2865 AAGATCTGCCGAGCTTCTGTCTCAGTTTGGGAGACATATTAGGCTCTGCCATGCAA 2924
1388 -----ACAA-----TGGAG-----TTT-----TCITT- 1404
2925 ACACACAAATCTTCTCAGATGCCCTATGCTGTGGAGGACGAATATGTCTCTTTG 2984
1405 -TCCCAA-----ACGGG-----AA-G-AACACAGA-----CA-----C- 1430
2985 CTCCTAACATCTATGCTAGTATCTTAATGAACACAGAGCTTACTCCAGAGATCA 3044
1431 ---CC--GGC--TTGG--ACC-----CACTG-----CA-----AGCTGATCGTGA-- 1464
3045 AGTCCAGGCCATTTGGCTATCTCAACACTGTTACAGAGACAGTTG-AAC-TACAAACA 3102
1465 -----CCT-----CTTTGG-----TGCCAGTG-----TGGCAA---G 1489
3103 CTATGATGGCTCTACAGCACTTTTGGGAGCGATATGGCAG-GAACAGGCGCAACCT 3161

Qy	1490	GGCT--CAGCC-----TCT-----C-----TGCCACAG--AGTGCC--C--C--CA--CG-T	1524
Db	3162	GGCTCACAGCCTTTGTTCTGAAGACTTTTGCCCA-AGCTCGAGCCTACATCTTTCATCGAT	3220
Qy	1525	GGA---ACATT-CTGGAGC-----TGCCCATCCCA-----AA-----	1552
Db	3221	GAAGCACACATTACCAGAGCCTCATATGGCTCTCCAGAGGCAGAAGGACATGGCTGT	3280
Qy	1553	TTCA--A-----TCAGT-----CCAT--AGAGACGAACAGA--ATGA--G	1584
Db	3281	TTCAGGAGCTCTGGGTCACTGCTCAACAATGCCATAAAGGAGGAGTAGAAGATGAAGTG	3340
Qy	1585	A-CCT-TCCG-----GCC-----CA-AG-----CGT	1602
Db	3341	ACCCTCTCCGCGCTATATCAATCGCCCTCTTGAGATTCCTCTCAGTCACTCACCCCT	3400
Qy	1603	G-----GC--GC-----TGC--GG-G-CA--CTTTGGTAGAC-----	1626
Db	3401	GTGTGCGCAATGCCCTGTTTGGCTGGAGTCAGCCT--GGAAGACAGCACAGAAGGGG	3458
Qy	1627	TG--TGCC-----ACCA-----C-GGCGTG--TTG--TG-----A	1651
Db	3459	ACCATGCGAGCCATGTATATACCAAGCACTGTGTGGCTATGCTTTTGCCCTGCGAGTA	3518
Qy	1652	A-----AC-----GTGAAATA--AA-----AA-GAGCAA-----AA-AAA--	1677
Db	3519	ACCAGGACAGAGGAAG-GAAGTACTCAGTCACTTAATGAGGAACTGTGAAGAAGAC	3577
Qy	1678	AA	1679
Db	3578	AA	3579

RESULT 25

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US-09-125-635-1
; Sequence 1, Application US/09125635
; Patent NO. 6562589
; GENERAL INFORMATION:
; APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steroid receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6835
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(4463)
US-09-125-635-1

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1118	Db	TCATAATGATGGCAGTCATGGTCCCGAAGACGTCACTATCAAGAAGCTTATCTTAATGG	1177
133	Qy	---CATG-A-AAACC---ATC---ATC---CA	147
1178	Db	CCATGCGAAGAACCCAGTATATCGATTCTCGTTGGCTGATGGAACATATAGTACTGCACA	1237
148	Qy	GCACAAATGCA---C-AATCT---ATC---TCT--	172
1238	Db	GACAAAAA-GCAAACCTTCCGAAATCTCTGTAAACAATGATCGACATGGCTTTGTCTCAA	1296
173	Qy	-----TG-----G-----C-AATC---TT---CAGC	187
1297	Db	CCCACTTCCTTCAGAGAGAACAGAAATGGATATAGACCAAAACCAATCTGTTGGACAAG	1356
188	Qy	-----GGCTGGCTGC-----TC-----TG-----TGCTCTC--T	209
1357	Db	GGATTAGACACCTATGGCTGGATGCAACAGTTCGGTAGCGGCGCATGATATGTCGCAA	1416
210	Qy	TCCAAGG-----AG-TGCCCGTCGCGAGCGAG--ATGCC-----ACCTT--CCCCA	251
1417	Db	ACCAAGGCTTACAGATGCC--GAGCAGCAGGCGCTATGGCTTTGGCAGACCTAGCACCA	1473
252	Qy	AAGCTATGGACAAG-TGA-CGGTCC--GGCA-GGGGG--AG-----AGCGCCA---	293
1474	Db	CAG-----GG-CA--GATGAGTGAGCTAGGATGCGGGGTTCCAGTAACATAGCTTCATTG	1526
294	Qy	--CCCT--CAGG--TG-----CACTAT-----T-----G-ACAAC-C--GGG-TCA--	323
1527	Db	ACCCCTGGCGCAGCATGCAATCACCATCTTCCTACCAGAACAACTATGGCTCAAC	1586
324	Qy	-----CCC-----GGGTGGCTGG-CT-----AAACC-GCAG-----CACCA--	353
1587	Db	ATGAGTAGCCCCCACCATGGGAGTCTCGTCTTTCGCCCAACACGACAGATATCATGATT	1646
354	Qy	--TCCTC-T-ATGCTGGGA-----AT-G-----ACA-AGT-----GGT	380
1647	Db	TCCTCTGTAATCGTGGAGTCCAAGATAGCCTCACTCAGTTTCTCCTGTGTCAGGT	1706
381	Qy	GCCTGGATCCTCGGTGGTC--CTTCTGACAAAC--C-----CCAAACGCAG--TACA	428
1707	Db	G--TGCACCTCCCATGG-CATCTCTG-GCAATACTGGGAACCA---CAGCTTTTCCA	1758
429	Qy	GCA-----TCGAG-----ATCCA-----GAAGCT-----GGA-----	450
1759	Db	GCAGCTCTCTC-ATGTCCTCGAAGCCATCAGTGAAGGTGTGGGACTTCCCTTTTATCT	1817
451	Qy	--TGTGT-ATGACGAGGCC--TT--ACACCTGTCTGGTGCA---GACAGA-----C	493
1818	Db	ACTGTGTCATCACAGGCCCCAAATTGGATPACT-CTC---CCAATATGA-ATATTACCC	1872
494	Qy	AACCA-----C-----CCAA-AGACTCTAGG-----GTCCA--	519
1873	Db	AACCAAGTAAAGTAAGCAATCAGATTCCAGAGTCTCTGGGCTTTTATTGCGACCAA	1932
520	Qy	--CC-----TCATTGTG---CAAGT-----ATCTCC-----CAAA-ATT	547
1933	Db	ATCAGTGGAGAGTTCAATGTGTCAGTCAATAGACAGATCACTCAGTGACAAAGAA	1992
548	Qy	GTA--GAGA--TTTCTT-----CAGA-TATC-----TCCATT--AATG--AAG--	582
1993	Db	GTAGGAGAGCAGTGTGTAGGGGGCGAGAATCAAAGGGGTCTCTTTGGAAGCAAGGTC	2052
583	Qy	-GAACATATTA--GC-----CTCAGCTG-----CAT-----	606
2053	Db	ATAA-AAAAATCTGCAGTTACTTACTGTCTCTTGATGACCGGGGTCACTCTCTTG	2111
607	Qy	AGCAACT-----GGTAGA--CCAG-----AG--CCTACGGTTA-----CT-T	638

Db 2112 ACCAACTCCCTAGATTCAAGTTGTAAAGAACTCTCTGTAGTGTACCAGGCCCTCT 2171
QY GGAGAC-----ACATCT-----CTC-----CCAA-A-CC-----GT-----TG 665
Db 2172 GGAGTCTCCTCTTACATCTGGAGAGTATCCTCTATCAATCAATATCATGGGTCACTG 2231
QY 666 GCTTTGTGAGTGAAG-AC--GAAT-----AC-----TTG-----GA-----AATTC----- 698
Db 2232 ---TTACAAGAGAAGCAGCCGGATTTTGCACAGTTTGTCTGAGATGGGAATTCACCACT 2288
QY 699 -AGG--GC--ATCAC-----CC--GGG-----AGCAGTCA----- 721
Db 2289 GAGGTAGCCAAGATTACTGCAAGACCCTGGGAAAGACACCAAGCAGT-ATAACTTCTTG 2347
QY 722 -GGGGA-----CTA--C-----GAG-----TGC 736
Db 2348 TGGGACGGAAATGTTGTCAAGCAGGAGCAGTAACTCTTAAGAAGAGGAGATAATATGC 2407
QY 737 ---AG-TGCCT-C---CA---ATCA--C-GTG--GC---CGC----- 759
Db 2408 ACTTCTTAGATACCTGTCTGGACAGGATGATCCTAGTGTATGCACTCTCTAAAGAACTACA 2467
QY 760 GCCC---GTGTACGGAG---AGTAA--G-GTCACGTGGACTA--TCCACCAT--- 803
Db 2468 GCCCAAGTGG--AAGGAGTGGATATAAATAGTCA--GTGCACCACTCCACCATTC 2524
QY 804 -----AC-----ATTTCAGA--AGCCAAG----- 820
Db 2525 TAGCTCAAGTCAGAGAAGACCTTAAATTAAGACAGACACAGTGAAGAGGATCTGG 2584
QY 821 ---GG-----TACA-----GGTG----- 830
Db 2585 AGACTTGGATAATCTAGATGCTATTCTTGGTGTCTGACTAGTCTCTGACTTTTACAATAA 2644
QY 831 -TCC-----CC-----GT-----GGGA-----CAAAAGG-----GGA----- 851
Db 2645 TTCCATATCTCAAAATGTAGTATCTGTGGGACTAAGCAACAGGTGTTTCAAGGAATAA 2704
QY 852 -CACTG-----CAG--TGTGAAG-----CCTC-----AGC 873
Db 2705 TTCTCTGGGTTTGAAGAGTTTCACTCTGTGCAGTCTATTCTGTCTCTCCATATAACCGAGC 2764
QY 874 AGT-----CCC-----CTC-AG-----CAG-----AATTCAGTG- 897
Db 2765 AGTGTCTCTGATAGCCCTGTTTCTGTGTCTCAAGTCTCCAGTAAATAATATCAGTGC 2824
QY 898 -----G-TAC--AAGGA-----TGACAA--AAGACTGATTGA-----A 925
Db 2825 TTTCCCAATGTTTACCAAGGAACCCATGTTGGTGGGAATCCAGAATGATGATAGTCA 2884
QY 926 GGAAGA-----AAG--GGGTG-----AAA--G--TG-GA-----AAACAGAC-C 957
Db 2885 GGAATATTATGGCTCAAGTATGGTGGCCCAACCGAAATGTGACTGTGACTCAGACTC 2943
QY 958 TTTCTCTC-----T-CAAACTCA--TCTTCTTC--AATGTCTCTGAAC-- 995
Db 2944 CTTCCTCAGGAGACTGGGCTTACCAACTCAAGGC--CGGCAAGATG-----GAACT 2996
QY 996 ATG-----ACT--ATGGGA-----C-TAC-----ACT 1016
Db 2997 ATGAATTCAACTCCATGGGAAGACAGAGGAGATATAATATCTTTTATCCAGACCT 3056
QY 1017 GC-----GTGGC-C--TCCAAACA-----AGC-T-----GG-GCCACA 1043
Db 3057 GCACTGGGTGGTCTTATCCCATTTGCTCTTCGTCTAATAGCATACCAGTGGGAGA 3116
QY 1044 CCA--A-TGC-----CAGATC--ATGCT-----ATTGTCCAGCG-----CCGTCA-G 1083
Db 3117 CCAGTATTGCAACAGCAGCAGCAGATGCTTCAATGAGG--CTGTGTGAATCCC--CATG 3173
QY 1084 CCA--GGTGAGC-AA--C--GGCACGTGAGGAGGCGAG-----GCTGGCT-- 1122
Db 3174 GGAATGG--GGGCTAATCTCTATATGGC-----CAAGCA--GCAGCATCTAAACCACTGGGTT 3226

QY 1123 CTGGC---TGCTGCTCTT---C-TGG-----TCT-TG-----CA-----CCT 1152
Db 3227 CTGGCCCGATG--GCATGTTGTCCATGGACAAAGTTTCTCATGCATCAAAATAGGCT 3284
QY 1153 GCTTCTCA--AATT---TTGATG---TG-AGTGCCA-CTTCCCAACCCGGGAAAGGC-- 1199
Db 3285 -CTTCTTAGGAATTCCTCGATGATCTGTGGGCCACCTT--CCAACCTGG-AAGGCCA 3340
QY 1200 ---TGCCG-----CCA-C-CACAC-----CACCAACACA-----A 1225
Db 3341 GAGTGACGAAGAGACATTTATGGACCAGTGCA-CACTCTTCTCAGCAACACAGATGCCA 3399
QY 1226 CAG--C-----AAT-----GGC-----AAC-----ACC--GACA-G 1246
Db 3400 CAGCCTTGGAGAAATTCACAGAGCTTTGGGCATCTCTGACCTTGTCAATCAGGACAGG 3459
QY 1247 CA---A--CAATCA-GAT-----ATATA---CA--AATGA----- 1271
Db 3460 CATTAGAGCCCAACAGAGATGCTTTTCCAAAGGCCAAGA-AGCAGCAGTAATGATGATCAG 3518
QY 1272 ---A-ATTA---GA-AGA-----AACACAG-----CC-----T 1291
Db 3519 AAGCAGATTATATGGACAGACATACCAGCACAGGGGCTCCCAATGCAAGAGGCTTT 3578
QY 1292 CAT-----GGGACA-----GAG-----GGA-----G----- 1302
Db 3579 CATCTTCAGGACAAATCACCATCTTTAACTCTATGATGAATCAGATGAACCAAGGC 3638
QY 1303 AATTG-----AGG-----GAG-----GGGA-----ACAA----- 1322
Db 3639 AATTTCTCTTCCAAAGAAATGCACCCAGCAGCAACATCATGAGACCCCGGCAACACC 3698
QY 1323 -----AGAAT--A-CTT-----TGGGGGAAAAGAGTTT--AA----- 1351
Db 3699 CCCAAGCACTTAGAATGACGCTTCAGCAGAGGCTGCAAGGCCAGCAGTTTGAATCAG 3758
QY 1352 A---AAAG--A---AATTGAAAATTG---CCT--TGCAAT-----ATT 1382
Db 3759 AGCCGACAGGCACCTTGAATTTGAAATGGAATGGAACCCCTACTGCTGTGTGCTGGTGA-T 3817
QY 1383 TAGG--TACAATG-----GAGTTTCTT----- 1403
Db 3818 GAGCCTATGATGAGCCGCCAGCAGGCTTTTCTTAATGCTCAAATGCTCGCCCAACGACG 3877
QY 1404 -----TTCCCA-AAC-----GGG----- 1415
Db 3878 CAGAGAGCTGCTAAGTCACTCTCCGACACAGAGGTGCTATGATGATGACGACGA 3937
QY 1416 ----- 1415
Db 3938 GCAGCAGCAACACAGCAGCAGCAGCAGCAGCAACAGCAACAGCAACAGCA 3997
QY 1416 --A--AG-AACA-CAGCACACC----- 1432
Db 3998 ACAGCAGCAACAGCAGCAACCCAGGCTTCAGCCACCTCCTAATGTGACTGTCTCC 4057
QY 1433 -----GGCTT-----GGACCCAC--TG--CAAGCT-----GCATC-GT----- 1460
Db 4058 CAGATGATGGCTTTTGGCAGGACCCCAATGCCACAGCTCTCTCGCAACAGTTTCC 4117
QY 1461 ---GCAACC---TCTTTGG--TG-----CCAG--TGTTGGCAAGGGCTC- 1494
Db 4118 ATATCAACCAAT-TATGGAATGGCAACAAACACAGATCCAGCCTTTGGTCAAGTG-TCT 4175
QY 1495 AG-CCTCTC--TGC-----C-CACAGA-----GTGCC-CCCACGTGGAA---CATTC 1533
Db 4176 AGTCTCCCAATGAATGATGTCGTCA-AGAATGGTCCCTCCCA-----GAATCCCATGA 4230
QY 1534 TGGG-----GCTGGC--CATCCCAATTTCAATCAGTCCATAGACAGCA----- 1575
Db 4231 TGCAACCCCGAGGCTCATCC---A-TCTATCAGTCTCAGAAATGAAGGGCTGGCCA 4286

QY 1576 -CAG-AAT--G-AG--A--CCTT--CC-----G--GCCA--AGCGTG- 1604
Db 4287 TCAGAAATTTGGCCAGAACAGCTCTTTTCCAGCAGCAGTTTGGCCACCAG-G-GGA 4344
QY 1605 ---CGCTGC-----GG-GCAGTT-----TGCT--A--GAC--TG 1628
Db 4345 ATC-CTGAGGTATAGTATGGTGCACATGAATGGCAGCAGTGGTCACTGGGACAGATG 4403
QY 1629 ---TG---CCA---C-GGC-G---TGCT--TG-T--GAA--AC-G-TGA 1658
Db 4404 AACATGAACCCATGCCATCTCTGGCATGCTTGGTCTGATCAAAATCTGCTGA 4463
QY 1659 AAT-----AAAAAGAGC---AA--AAA-----A-AAA 1679
Db 4464 CATCTCTGCACAGGACCTCTTAAGGAAACCACTGTACAAA 4504

RESULT 26

US-09-566-921-42
; Sequence 42, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ. ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 42
; LENGTH: 6856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 401746.2
US-09-566-921-42

Query Match 41.4%; Score 694.5; DB 4; Length 6856;
Best Local Similarity 41.5%; Pred. No. 0.00049;
Matches 1381; Conservative 0; Mismatches 198; Indels 1747; Gaps 393;
QY 1 GTGTGTCTCT-----TCAG-----CHAAAACAGTGGATTT 29
Db 2301 GTGTGTCTCTGGAAACCATCCGAATCAGTGGCGCGGTTTCCCTC-ACGGTGGACTT 2357
QY 30 A-----AAT-----C---TCCT--T---GCACNA-----GCT---TG--A 51
Db 2358 ACCAGAAATTTTTCAGCGGTACCGTGTCTCTAATGAAGCAGAGATGTGCTGAGTGACA 2417
QY 52 G-AGC-AACA-C---AATCTATCAG-GAAA-GAAA---GA-AA-GAAAAAACCC--- 92
Db 2418 GAAAGCAACATGCAAGAAATGTGTAGAGAACTGATCTGGACAGGACAAATACCAGT 2477
QY 93 ---G-AACCTGACAAA-A-----AAG-----A--AGAAAA--GA 118
Db 2478 TTGGTAA---GACAAAGATCTTTTTCGTGCGGTCAAGTGGCGCTATCTAGAAAAATTGA 2534
QY 119 -AGAAGA-AAA-AAA-----ATC---AT---GAAACCATCC-A-----GC--C 150
Db 2535 GAGCTGACAACTAGAGAGTGCCTGCTCCGATCCAGAGACCATCCGAGGGTGGCTGC 2594
QY 151 -----AAAAATGCAAAATCTATCTCTTG-----GGCA-----ATC-----TTCA----- 185
Db 2595 TGAGAAAGAGTAC-----CTA-CGCATGCGGAAGCAGCCATCACCATGCAGATACGT 2649
QY 186 -CGGGGCT---GSC-----TGCTCTG-T--GTCTCT-----TCCAAGG----- 216
Db 2650 GCGGGGTACAGGCCCGATGCTATGCTAAAGTTTCTGCGGAAACCAAGCAGCAACCAT 2709
QY 217 -----AGT-----AGCC-----GTG-----CGCAG-----C-----G--GAGATGC 240

Db 2710 CATTCAAAGTACTGGCGCATGTATGTGGTCCGACGAGGTACAAGATTAGACGAGCTGC 2769
QY 241 CAC-----CTTC-----C-----CCA-----AAGCT 256
Db 2770 CACTATTGTCTTTCAGTCTTACTTGGAGGCTTCTTGGCCAGAAATAGTATCGCAAGAT 2829
QY 257 A-----TGG-ACAA-C-GT-----GA-CG-GTCCGCGCAGG--GG--GAGAGCG 290
Db 2830 ACTCCGTGGCACAAGCAGTCACTCATTCAAGACGAGTCCGG--GGCTGGCTG-GCCG 2886
QY 291 C-CACCT-C---AGG---TGCA--CTATTGACA--ACC-----GGG-----TCACCG 327
Db 2887 CACACACTACAAGAGGAGCATGATGCCAT---CATCTACCTTCAGTGTCTTCAAGCG 2943
QY 328 G--G-TGGCC-----TG-GCTAAACGCGACACA-----TC-CT-----C 358
Db 2944 GATGATGGCCCAAGCGTGAGCTAAA--GAAGCTCAAAATCGAGCTCGCTCAGTGGAGCG 3001
QY 359 TAT-----GCTG-----GGAATG-----ACAAG-TGGTGC--CTGGATCCTCGC-- 395
Db 3002 TATAAGAGCTGGCATCGCATGGAGACAAGATCATGCAGCTGCA-----CGCNAAG 3056
QY 396 -TGGT-----CCTTCT-GAGCAAC-ACCCAAAC--GCAG-- 424
Db 3057 TTGATGAGCAGAAACAAAGACTACAATGCCTTGTGGAGAACTAACCAATCTGGAAGAA 3116
QY 425 ---TACAGCATC-----GAGA--TCC-----AGAACGT----- 447
Db 3117 TATACAACT-TCGTGAGACTGAGAAACTACGAAGTGAATTAGAACGTCTTCAACTAAGTGAA 3175
QY 448 --GGATGTGTA--TG--AC--GAGGGCCCTTA----- 471
Db 3176 GAGGAAGCGAAAGTTGCCACTGGCGGGTCTTAGTCTGCGAGGAGAAATTTGCCAAGCTC 3235
QY 472 C-----ACCTG-----CTC-----GG-----TGCG----- 487
Db 3236 CGGAAGAGCTGGAGCAAACTCGTTCAGAGAAAAAATGCAATTCAGGAACATGCGAGATCGA 3295
QY 488 -ACAGAC---AAC---CACC-----CAAA-----GA-----C-----CT--- 509
Db 3296 TACAAACAGAAACACAGCAGCTGGTATCAATCTGAAGAGAAATACTTTGCTGAAG 3355
QY 510 CTAG-----G--G--TC---CACCTCATTTGCA--AG--T-----ATCTCCAAAAT 546
Db 3356 CAAGAAAAAGAGCCCTCAATCACCGCATCGTGCAGCAGCTAAGGAGATGACAGAACT 3415
QY 547 -TGAG-AGA-TTCTTTCAGA-----T--ATCTC--CATTAATG-----AA 580
Db 3416 ATGGAGAGAAAGTAGT--AGAAGAAACGAAACAACTGGAACCTCGACCTTAATGATGAA 3473
QY 581 GG-----GAAC-----AAT-A-TT-AGCCTCACCTGCATAGCAACTGGTA--- 617
Db 3474 GGTGAGATATCAGAACCTTCTGAATGAGTTCAG--TCGCTTGA-AGAA--GATATGA 3528
QY 618 -GACC-----AGAG-----CC-TACGCT-----TA-CTTGGAGAC-----AC 646
Db 3529 TGACCTCAAGAGAGATGACCCCTTATGCTGATGTCCTAAGCTTGGACACAGAGAAC 3588
QY 647 A---TCTCTCCCAAG-----CG-GT-TG-----GCTTTG-----TG-AG--- 675
Db 3589 AGACTC-CACCCACAGCAGCAAGCTGGAATATATCTTTAGCTCTGAAATTCGAGAA 3647
QY 676 T-GAAGAC-----GAA-----GAA--TA-CT-TGGAAT--T 697
Db 3648 TGAAGACATTCATCAAGCAGAGAACCAAGTGAAGAGAGGTACTCTTGGATGT 3707
QY 698 CA-----GGGCATCAC-----CCGGAGCAG-----TCAGG----- 723
Db 3708 CATTGTCTTAACTCCAGAGCGGG--TCACAGAGCTGGAGCAGGAGAGCAGGTGAT 3765
QY 724 ---GGA---CT--AC-----GA-GTGCA-GTGCTC-----CAATGACGTGGCC--GC 759

3766 GCAGGATGAGTGGACCGCAAGGAGGAGCAGGTG-CTCCGACAGAA-----GGCCAAAG- 3817
QY 760 G-----CC-C-----GTG-GTAC-CCA-----GAGT-A---AAG-GTAC 786
Db 3818 GAAGAAGAAGACCACAAATAGAGTGCAGAACTGGATATGATGACTCAAGCGTCA- 3876
QY 787 COTGAAC--ATC-----CACCATACATTTTCAG--AGC-----CAAGG-- 821
Db 3877 --AGACTAGATCAGAAACAAACAACTGAGAAATGAGCTAAATGAGTTGGCAAGGCC 3934
QY 822 ----GT-----ACAGGTGTCCCGTGG-GA-----CAAAAGGGACA-CTGC-A--GTGT 862
Db 3935 CTCAGTGAAAGAGTCCCGCAGAGGTGACCGCCCC-----AGGTG-CACCTGCCTACTGTGT 3990
QY 863 -----GA--AG-----CCTC-----AGC--A-GTCC-----CCT 881
Db 3991 CCTCATGGAGCAGTCACTCTGTGAGCGAGGAGCTTGTGTCGCAAGGAGGAAGTCTCT 4050
QY 882 CAGC---AG-----AATT-----CCAG-----TGG--T---A--CAAGGATGACAA--- 912
Db 4051 CATCTTAAGGTCTCAACTGCTGAGCCAGAAAGAGGCCATCCAAACCAGATGACAGAA 4110
QY 913 ---AA-GACTGATT-----GAAG-----GAAAG--AAAGGGGT 939
Db 4111 TACAATGACAGATTCCACAATACTTTTGAAGATGTACAAATAATGAAAGATAAA--GGT 4168
QY 940 GAAAGTGGG-AAACAGACCTT--TCCTCTCA--AAAC-----TCATCT--TC---T 980
Db 4169 GAAATAGCACAGCATACATTTGT--T-TGAAGAAACAAATAGATCATCTGCTCTGGAT 4225
QY 981 T-CAATGTCTTGAACATGACTATGG-GAATACACTTGC--GT-----GSCCTCCAA 1029
Db 4226 TACCATGAGT-TGA--ATGAGGATGAGAGCT--GTGGCTGTTTATGAAGGTTTAAA 4279
QY 1030 CRAAGC---TGGGCCACACC--AATGCCA--GCA-TCA-----TGCTATT---T 1066
Db 4280 CRAAGCAATAGG--CTCTGGAATCCAGCTGCAGTGCAGTCAAGAAGAGGAGCCATGAGAAT 4336
QY 1067 G-GTCC-AGGCGCGTCAGCGAGGTGAG--CAAAG-GC--ACGTGAGAGGAG----- 1110
Db 4337 GAGGCGAGGC-CC-TC--CGTGGGAGATCCA--GAGCCTGAG--GAGGAGAACAAAC 4388
QY 1111 G---CGAG-GGTGGGTCTGG-----CT--GCTGCTCTTC--TGGTC-----TTG- 1147
Db 4389 GACAGCAGCAGCTG--CTGGCCAGAACCTGACGCTGCCCC--CAGAGSCCGCATGA 4443
QY 1148 ---CA-CTGC-----TTCTC-----AAATTTGATGTAGTG---C 1177
Db 4444 GGCCAGCCTGCAGCAGAGATCACCGGCTGACCAACGAAAACTTGGATTTGA-TGAAAC 4502
QY 1178 CACT-----TCC-----C-----CACCGGGAAG--GCTGC 1202
Db 4503 AACTTGAAAAACAGGATAAGCGTCCGTAAACTGAAAAACAAAC--TGAAAGTATTTC 4560
QY 1203 C-----GGCACCACA-----CCA-----CAACA-----CA-ACAG--C 1229
Db 4561 CAAAAAAATTTGGCGA--ACTAGAGTGGGCCAGGAGGAGACATATCCCCAGGACAGATC 4618
QY 1230 A---ATGGCAA--CA-CCGA-CAG-CAA-----CCA-----AT---CA--GA 1258
Db 4619 ATGTATG--AACCATCCAGCAGTCAATTTCCAGGAAAGAAAGGATTTCCAGGGA 4676
QY 1259 T-----ATATACAA-----ATG-----AAA-----TT-AGAA--GA-----AAC- 1284
Db 4677 TGTGGA-ATACAAGAGGAGGTGAGCAAAACTTTGTAAGAACTGATTTCTGNACTG 4735
QY 1285 ACAGCTCATGG-G-A-CAG-AAATTTGA-----GGGA-----GG----- 1315
Db 4736 A-AGCCAGTGTGTAGCAGTCAATTTGATTCAGGATTAACCGCATATATCTGTTCAT 4794
QY 1316 -----G-GA--AC--AA-----AGAA--TA-----CTTTG----- 1333
Db 4795 GTGTGTCACATGCTGACTACTGTAATGATGATCAGAAAGTAAAGTCTGTGCTAACATC 4854

QY 1334 -----GGGGHAAAGAGT-TTTAA-AAAAGA--A-A--TTGAAA----- 1365
Db 4855 AACAAATTAACAGCATCAAAAAAGTATTGAAGAAAAGAGGTGATGATTTTGAACCGTCTC 4914
QY 1366 ATT--GC--CT-----TGCAATATTTT--A-----G-----GTACAATGGAG-- 1396
Db 4915 CTTCTGGCTCTTAACACATGCCGATTTTGTGACTGCTTGAACACAGTACGTGGAGAAGA 4974
QY 1397 ----TTT-T-----CTTTTC-CCAAACGGGAA-GAACACAG--CAC----- 1428
Db 4975 GGGCTTTATGAAGCACACACATCTCGCCA-----GAATGAACACTGCTCCACCAATTT 5029
QY 1429 ACCCGGCT-----TG---GAC-----CCA-----CTGCAAGCTGCAT 1457
Db 5030 GACCTGGCTGAGTATCGGAGGTGCTGAGTGAATCTGGCCATTCAGATCTACCAAGCAGC-T 5088
QY 1458 COTGC-----AACCTCTTTGGTGCCAGTG--TG-----GGCAAG--GG----- 1491
Db 5089 CGTGGGGTGTAGAGACATCTTT-CAGCCATGATTTGCTCAGGCATGCTGGAACATG 5147
QY 1492 ---C---TCA--GCCTCTCT-----GCCCACAGAGT-----GC-----CC----- 1518
Db 5148 AAACGATTTCAGGGCGTGTCTGGGGTGAAGCCCAACAGGTTGAGAAAAGCGAACCTCCAGTA 5207
QY 1519 ---CC-ACGTGG--A---ACATTTCTGGAGCTGCCATCC-----CA-----AA-----TTCA 1556
Db 5208 TCGCCGAGAGGGACCTACACTGGA-CT--CAATCTCCGGCAGCTCAACTCTCTCC 5264
QY 1557 A-----TCA--GTC--CATAG-A-GAC--GAACAGA-----A 1580
Db 5265 ACTCGGTATGTTGTCAGCATGCGATGCGCCCTGAACTGATCAAGCAGGTGGTCAAGCAGA 5324
QY 1581 TG-----AG-----ACCTTC-----CGGCCAAG--CGTG- 1603
Db 5325 TGTTCATCATATAGGGGCCATCACCTGAAACAACTTCTCTCTGCGG--AAGGACATGT 5381
QY 1604 GC-GCTGGG-----GGCA--C---TTTGGTAGACTGT--GCCACC-----ACGGC-G 1641
Db 5382 GTCCTTG-GAGTAAAGGATGCGATCAGATCAATGTCAGTCAACTGGAAGATGGCTG 5440
QY 1642 TGTG-----T-TG-TGAACGCTG-----AAATAAA-----AA----- 1666
Db 5441 CTTGACAAAGATCTGATGATGATGAGTGGGGTAAAGAAACCTGGAACCTCTCATTCAGGCT 5500
QY 1667 G----A-----GCAA-----AAAA-AA 1679
Db 5501 GCTCAACTTTTGAAGTGAAGAAAGAA 5526

RESULT 27

US-09-620-312D-345

; Sequence 345, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yuning

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: John Tillinghast

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and


```
QY 740 ---GCC---TC-CA-ATGAGT---G-G-CCG-----CG----- 760
Db 3106 GAGGGCTCAGACACTTCTCAGAT-ACGTTCAAGTTGTACCGAGGCAAGTCGATGAATA 3164
QY 761 -----CC-C-GTGGTACGAGAG-TAAAGGTACCGT---GAACTA----- 795
Db 3165 TGAAGATCCTCTCTGTGGT-TGGAGAGTTTAAAGGCTCCTTTCGGATCTACCTCTGCGG 3223
QY 796 -----T-CCA-----CCATACA-TTTC-----A-AG-AG-----CCA- 818
Db 3224 ATGACCCGAGGTGCCAGCCCTCCAGACAGTTTCGGGAATTAACGTGACAGCGTCCAC 3283
QY 819 AGG---GTAC---AGG-----TGT-----CCCCGTGGGACAA 844
Db 3284 AGGAATGCACGTTAGATTATACATTTGTCGAGGCTTAGAGCTCCAGCCCC--AGGACAA 3341
QY 845 -AAGGG-----G-----ACACT--GC-----AGT-GTGAAG-CC- 868
Db 3342 CAATGGCCTGTGTGACCTTACATAAAAATAACACTGGGCAAAAAGTCATTGAAGACG 3401
QY 869 ---TCA--GCAGTCCC-----CTCA-----GCAGAT-TCC-----AG-TG 897
Db 3402 AGATCACTACATTTCCCAACACTCTCAACCCAGTCTTTGGCAGATGTACGAACCTGAGCTG 3461
QY 898 GTA-----CAAG--GATGAC-----AAAA---GAC--TGAT--TGA-----A--- 925
Db 3462 CTACTTACCTCAAGAAAAGACCTGAATAATTTCTGTCTATGATATGACACCTTTACCCG 3521
QY 926 GGA--AAGAAAG-GGGTGAAA-----G-----TGAAAACAGA-CCTTTTC----- 962
Db 3522 GGATGAA-AAAGTAGGAGAAACAATTTATGTCTGGAACACCGATTCCTTTCCCGCTTTG 3580
QY 963 ---TCTCAAACT---CAT-----C-----TTCT---TCAATGCT--C-TG 992
Db 3581 GGTCCC---ACTGGCGCATACAGAGGAGTACTGTGTCTTGAGTCAATACCTGGCGAG 3637
QY 993 AACATGACTPANGGAACCTACAC--TTGC-----GTGGCC---TCCAACAAAGCTGGGC 1039
Db 3638 ATCA--AC--TGACGACCAACACAGCTGCTTCAAAATGTGCCAGATTCAA-AGGCT-TCC 3691
QY 1040 CAC-ACCAATGCC-----ACATCATGCTATTTGGTCCAGG-CG---C 1077
Db 3692 CACAACCCAT-CCTTTCCGAAGATGGAGTAGAATCA--TATATGG--AGGACGAGAC 3744
QY 1078 CGT-CAGC---CAGG---TG-AG-CAAC-----G-----GCAGCTCAGG----- 1108
Db 3745 --TACAGCTTGATGAAATTTGAAGCCAAACAATCTCTGCACCAACCTCGGGGCCCTG 3802
QY 1109 -AGGCGAGGC-TGCGTCT-----GG-CT-----GCTG--CCTCTTCTG-----G 1142
Db 3803 AAGAGC-GGCTTGC-TCTTCATATCCTCAGGACTCAGGGCTGGTCC---CTGAGCAGC 3856
QY 1143 T-----CCTT---GCACCT---GC-----TTC-----TCAA 1162
Db 3857 TGAACAACAGGACTTTGCACAGACCTTCACGCCCAACATTTCCAGGGAATACTCAGA 3916
QY 1163 T-T--TTGATGT-----GAGT-----GCCAC-----TTC-----CCAC 1188
Db 3917 TGTGGGTGATGTTTCCCAAGAGTTTGGGGCCACAGGCCCTCTTTCACATCAACAC 3976
QY 1189 CCGGAAAG-----G---CTGCC-GC---CACACC---ACCACCA-CA-C-A--- 1224
Db 3977 CCGGAAAGCCAAAGATATCTACCTCGTGTGATCATCTGGAACACCAAGGACGTTATCT 4036
QY 1225 ---AC-AGCAATGGCAACCG-ACAGCAACCAATCA--GATATATA---GAAA---T-G 1270
Db 4037 TGGACGAG-AAAGCATCAGAGAGGA--AATGAGTGCATCTACGTCGAAGGCTGG 4092
QY 1271 A-----AATTAGAG-----AAAC-----ACAGCCTCATG---G-GACAGAAATTTG 1308
Db 4093 ATTCTGGCAAT--GAAGAAACAACAGAAACAG-----ATGTCGTTACAGTCTTTG 4146
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QY 1309 -----AGGGA-----GGCGA-----ACAA-----A---GAA 1326
Db 4147 GATGTGAGGGAATTTTAACTGGCGATTTGTTTCCGTTTGACTACTCTCCAGCCGAA 4206
QY 1327 -TACTTTG-----GGGGAAAAGAG-TTT-----TA---A---AAAAGAAATTT--GA 1363
Db 4207 CAATCTGTATGTTTGGCGAAAAAGAGCATTTCTGGAGTATTGACCAACGGAATTTTCG- 4265
QY 1364 AAAT-----TG--CCTTGAGATATTAGTACAATG--GAGTTTCT----- 1402
Db 4266 -AATCCCAACCCAGGCTGATCAAT--CAGATAT---GGGCAATGACAAGTTTTTCTCTGAT 4320
QY 1403 -----TTTCCCA-AAC-----GGG---AAGAACA---CAGCA---CACCC 1432
Db 4321 GACTACTTTGGGTTTCTAGAACTTGACTTGCCTCACAGATCAATCTTGCAAAATCACA 4380
QY 1433 G-----GC---TTGGAC-----CC--A-CTGCAAGCTGCAAT-----CGT---G-CA 1463
Db 4381 GAGAAATGCAGATTGGACATGATTCGGGACCTCAAAGC--CATGAACCCCTTAAAGCCA 4438
QY 1464 A-----CCTCTTTG-----GTGCCAGTGTG---GGCAAG--GGCTCAGCTCTC 1502
Db 4439 AGACAGCTTCCCTCTTTGAGCAGAAAT-CCA---TGAAGG-ATGGTGGC-CA----- 4485
QY 1503 TGC-CCACAGAG-----T-GCCCCCAGCT-----GGAACATTTCTGGAGCTGGCCATC 1547
Db 4486 TGCTAGCGCAGAAAGATGCGCCCGCTGAATGGCTGGGAA-A--GTGAGAT-GACATTT 4541
QY 1548 CCAAT--TCAATC-----AGTCC--ATAG-----A-----GACGAAC 1576
Db 4542 GGAATCTCTCAA-CGAGAAGGAGGCGCGACGAGCCAGCCGGAAGGGGGGAGCGAAC 4600
QY 1577 -----AG-----AAT-G--AGA-----CCTTTC--GG--- 1593
Db 4601 CCAACATGAACCCCAAGCTGGACTTACCAATTCGACAGAAACCTCTCTCTGGTCA 4660
QY 1594 -----CCCAAGC-----GTGGCGTGC-----GGG---CA--- 1615
Db 4661 CCAACCCATGAAGACCATGAGTTTCATCGTGTGGCGCGCTTTAAGTGGGTATCATCG 4720
QY 1616 -CTT--TG-----G--TAGACTG-TGC-CACACGG-GGT-----TG----- 1645
Db 4721 GCTTCTCTTCTGTTTATCTCTGCTCTTCTGTCGCGTCTCTCTACTCTTTTGGCGA 4780
QY 1646 -----TTGTGAAACGTGAA-AT---AA---AAA-GAGCAAAAAA---AAA 1679
Db 4781 ACTATTGTCAA--TGAAGATTGTAAGCCCAATGTGTACAAAGGCAAA 4828
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RESULT 28

US-09-220-132-24

; Sequence 24, Application US/09220132

; Patent No. 6506607

; GENERAL INFORMATION:

; APPLICANT: Shyjan, Andrew W.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT

; FILE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANC

; TITLE REFERENCE: 07334-074001

; CURRENT FILING DATE: 1998-12-23

; PRIOR FILING DATE: 1998-03-25

; PRIOR FILING DATE: 1997-12-24

; NUMBER OF SEQ ID NOS: 191

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 24

; LENGTH: 7672

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-220-132-24

Query Match

41.3%; Score 694.2; DB 4; Length 7672;

QY 926 ---GGAA---AGA---AAGGGTGAAAGT---GGAAA---ACAGACCT--- 958
Db 4039 CTGGGGAACAGTCAGATCAGGCGAAG---CAAAGTTGGGTGATCCCCAC-GACCTGCA 4094
QY 959 ---TTCCTCT---CAA---AACTCATCTTCT---TCAA--- 984
Db 4095 GCGCTTCTCT-TAGCGATTTCCGGGACCTCAT-GTCTTGGATCAATGAATAACGGGGTTG 4152
QY 985 TGT-CTC---TGAAC---AT---GA-CT---AT---G--- 1004
Db 4153 GTGTCTCAGATGAGCTAGCAAGGATGTCAACCGAGCTGAGGCATTTCTGAGCGACAC 4212
QY 1005 ---GGAACCTAC---AC---T---TGC---G-TGGC-C---TCCA--- 1028
Db 4213 CAGGAAC-ACCGGACAGAAATCGATCCAGGCTGCGACTTTCCAGGCATTTGAGCAGTT 4271
QY 1029 ---ACA---AGCTG---GGC-CAC---AC-CAATGCCAGC---ATCA---TGC 1061
Db 4272 TGGACAGCAGCTGTTGGCTCAGGACACTATGCCAGCCTGAGATCAAGCAGAACTTGA 4331
QY 1062 TAT---TTG---GTCAGGC---GCC---G-TCAGCG-AGG-TGA--- 1091
Db 4332 TATTTCTTACCAGGAGCTGTCAGACTGAGAAAGCCTGGGTTCAGCGCAGGATGATGCT 4391
QY 1092 ---GC---AACGGCA---CGTCGAGGA---GGGCGAGCTGCG-TCTGGC 1127
Db 4392 GGATCAGTGCTTGAATGACGCTGCTTCCATCG-GGACTGTGAGCAGCTGAGAACTGGA 4450
QY 1128 T-GCTGCTCTTCTG---TCTTG---TCTTG---CAC---CTGC 1154
Db 4451 TGGCTGCC---CGGGAGGCTTCTTGAATACCGAAGACAAAGGAGACTCACTGGACACG 4506
QY 1155 -T---TC---TCAA---AT---TTTG---ATGTGAGTGCCACTTCCCCACCC 1190
Db 4507 GTAGAGCTCTGATCAAAAACATGAGACTTTGACAAAGCGATT--AACGT--CCA--- 4559
QY 1191 GG-CA-AAG---GCT---GCC-ACCA-C-CA---CC--- 1216
Db 4560 GGAAGAGAAGATTGCTGCTCTGAGGCTTTTGGCGACCACTCATCGTGGCGGCAATTA 4619
QY 1217 ---CCAAACA-ACA---GCAATGGCA---ACA---C---CGACAG 1246
Db 4620 TGCCAAAGGAGACATTTCTAGCGGCGCAATG--AGGTCTTGGACAGGTGGCGAGCTGTG 4677
QY 1247 CAA-CCAATCAGAT-AT-ATACAA--TGAAA-TTAGAAGA--- 1285
Db 4678 AAGGCC---CAGATGATTGAGA-AAGGTCAAAGCTAGGAGAACTCAAACCTCCAACA 4733
QY 1286 ---CAGCC---TCA---TG---GGA-CAG---AAATTTG---AGGGAG 1314
Db 4734 GTTCAGCGGGATGTGGATGAGATTGAGGCTTGGATCAGTGAAATAATTTGCAACAGCGAG 4793
QY 1315 GG-GA---ACRAAGA---AT-A-CTTT---G-G---GGGAA--- 1340
Db 4794 TGATGAGTCGTACAGGATCCCAACATCAGCTTTCCAAAGCTGCTGAGCAAGCAACA 4853
QY 1341 -AAG---AG---TTTTAAA---AAAG---AA--- 1360
Db 4854 GAAGCACCAGGCTTTTGAAGCAGAGCTGCATGCCAACGCTGACCGGATCCGTGGGGTTAT 4913
QY 1361 TGA-----AA-----ATT-----GCCT-TGC-----A-GAT-----A 1380
Db 4914 CGACATGGGCACTCCCTCAITTGAACGTGGAGCCTGTGCGGCGAGTGAGGATGCTGTCAA 4973
QY 1381 -----T---TTAGGT-A-CAATGG-AGTTTCTTT-T-----TC----- 1406
Db 4974 GCGCCGCTGCTGCTTGTAGTGACGAGTGGCGAG--TTCTTTGGTCAAAAGTCAGCGGAA 5031
QY 1407 -----CC---AAACGG---GAAG---AAACA---CAGC-----ACAC----- 1430
Db 5032 AAGGCCAGAACTGAAGAGGCCCAACAGCAGCAGAACTTCAACACAGGGATCAGGAC 5091

QY 1431 -----COGGCT-----TGA---CCCACTGC-----AAG 1451
Db 5092 TTTGACTTCTGCTGTCTGAGTGGAGGCC---CTGCTGGCATCCGAGATTATGGCAAG 5149
QY 1452 ---CT-GCATC-GTG---CAACCT-CT-----T-TGG-----TG 1475
Db 5150 ACCTGGCTTCTGTGAACAACCTGTGAAAGAGCATCAACTGCTGGAAGCAGATATATCTG 5209
QY 1476 CCAGTGTG---GC---AAGG-GCT---CAGCC-TG---TCTGCC---CACAG-AGT 1514
Db 5210 CCCATGAGGATCGGCTGGAAGACCTGAACAGCCAGGACAGACGCTGTATGAC-CAGCAGT 5268
QY 1515 GCC-----CCACGT---GGA-----ACA-----TTC----- 1533
Db 5269 GCCTTGCACACCTCCCAAGTAAAGGACNAGAGGACACCATCAACGGCGGCTTCAGAG 5328
QY 1534 -----TGG-----AGCTG---G---CCAT---CC---CA---AA 1552
Db 5329 ATCAAGAGCATGGCGGCTCCCGCGAGCCAAAGCTGAATGAATCCCATCGCTGCACAG 5388
QY 1553 TT-----CA---AT-C---AGTCC---AT-A-GAGACGAA----- 1575
Db 5389 TTCTTCGGGACATGGATGACGAGGAGTCTCTGGATCAAGGAGAGAAAGCTGCTGTGGGC 5448
QY 1576 -CAGA-A-T-----GAGACCT-----T---CC-----G---GCCAAGCG- 1601
Db 5449 TCAGAGGACTACGGCGGACCTTAACCTGGCTGCAGAACCTGAGGAAGAGCAAGCGG 5508
QY 1602 -TGG-----C-GTGGG-----GGCATT-----TGG---T---AG 1624
Db 5509 CTGGAAGCAGAACTGGCTGGCTGCGCATGAGCGGCTATTGAGGCTGCTGGACACTGGCAAG 5568
QY 1625 A-CTGTGC-----CACCA-----CGGC-----GTGT 1644
Db 5569 AAGCTGTCCGATGACACACCATCGGAAAGAGAGATCCAGCAGCGCTGCGCAGTTT 5628
QY 1645 GT-----TG-----TGAA-----A-CG----- 1655
Db 5629 GTGGAGCACTGGAAGAGCTGAACGAGCTGGCAGCTGCCGGGCTCAGCGGCTGGAAGAG 5688
QY 1656 ---TGAAATA-----AA-----AAGACGCAAAA----- 1675
Db 5689 TCCTTGAATATCAGCAGTTTGTAGCCAATTTGAGCAATTTGGAAGAGGAGAAAGCCTGGATCAATGAG 5748
QY 1676 AAAA 1679
Db 5749 AAAA 5752

RESULT 29

PCT-US96-01735-5
; Sequence 5, Application PC/TUS9601735
; GENERAL INFORMATION:
; APPLICANT: Marks, Andrew R.
; TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01735
; FILING DATE:
; CLASSIFICATION:

```

, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: 08/386,039
, , FILING DATE: 09-FEB-1995
, , ATTORNEY/AGENT INFORMATION:
, , NAME: Kole, Lisa B
, , REGISTRATION NUMBER: 35,225
, , REFERENCE/DOCKET NUMBER: A30042 - 165/30555
, , TELECOMMUNICATION INFORMATION:
, , TELEPHONE: 212-408-2628
, , TELEFAX: 212-765-2519
, , TELEX:
, , INFORMATION FOR SEQ ID NO: 5:
, , SEQUENCE CHARACTERISTICS:
, , LENGTH: 8791 base pairs
, , TYPE: nucleic acid
, , STRANDEDNESS: single
, , TOPOLOGY: linear
, , MOLECULE TYPE: cDNA
, , HYPOTHETICAL: NO
, , ANTI-SENSE: NO
, , FRAGMENT TYPE:
, , ORIGINAL SOURCE:
, , FEATURE:
PCT-US96-01735-5

```

Query Match	41.3%;	Score 694.1;	DB 5;	Length 8791;
Best Local Similarity	39.9%;	Pred. No. 0.00081;		
Matches 1384;	Conservative 0;	Mismatches 194;	Indels 1895;	Gaps 384;
QY	2	TTGTGTC----	CTTCAGCAAAA--CAGTGG-	-----26
DB	3477	TGTTGTCAGGGGCCCTGCAGCTCCTCTTCGGCACTTCAGCAGGCA--GGAGTGCT	3534	
QY	27	-----TTTAAA-----T-----CTCCTTG--CA--CAAGCT--TGAGAGCAAC-----A	59	
DB	3535	CCAGGCCTTCAAAACAGGTTCACCTGCTGGTTACCGAGCCAAGATGTG-GA-CAACTACAAA	3592	
QY	60	CA-ATCTATCA-----GGA--AA-----G-AAAGAAGA-----	84	
DB	3593	CAGATCAAAACAAGCTTGGATCACTCAGGTCCATCGTGGAAGAAGTCAGAGCTTTGGGTG	3652	
QY	85	-AAAAA-----A-----CCGA-----AC-----CT-GACAAA--AA-AGAAG	111	
DB	3653	TACAAAGGGCAGGGCCCGATGAGACTATGAGTGTGTCATCTGAGAAAAATGAACATAAG	3712	
QY	112	AAAAA--AGAA--AAGAA-AA-----AAAAATCATGAA--ACCATCCAGC--CRA--	152	
DB	3713	AAACGGAGGAGGAATATACAGCCACAAGCATGAAGACCA--GCAGCTACAACTA	3771	
QY	153	-A-AATG--CACA--ATTCT-ATCTCTTGG-----GCAA--TC-----TTCAAG--GGGC	191	
DB	3772	CAGAGTGGTCAAAAGAGATTTTGAT-TC--GGCTTAGCAAACTCTGTGTTCAAGAGAGTGC	3828	
QY	192	-----TG-----GCTGC--TCGTGTCTCTCC--AA-----GGAGTGC--C	222	
DB	3829	CTCAGTGAGAAAGCAGGAGCAGCAAGCGTCTCTCCGGAACATGGGCGCAGCG	3888	
QY	223	CGTGGCAGC--GGAGATGC--CACCTTCC-----CCAAAGCT-----ATG--	259	
DB	3889	CGTG-G-TGCTGAGCTGTCTGCAGATTCCTTATGAGAAGCCGAAGATACCAAGATGCAA	3946	
QY	260	--GACAACTGACGGTCCGG--CAGG-----GGGAGA-----GGCC--CACCC--	296	
DB	3947	GAGATAA--TGA--GGT--TGCTCATGAATTTTGCAGAAATTTCTGGCGCAGGCAACGACA	4002	
QY	297	---TCAGG---TGC-ACATATTGAC-----AACCGG---GTC-ACCC--GGG-TGGCCT--	335	
DB	4003	GAATCAAGCTTTGCTAC-ATAAACACATAAACCTGTTTCTCAACCCAGGAT--CCTGGA	4059	
QY	336	GGCTA--AACC--GCAGCAC-----CA--TCC--TCTATGC--TGGG--AATG	371	
DB	4060	GGC-AGTAACCATGACGACATCTCATGAACAAATTTCCAGCTTTGCAGTGAATCAACG	4118	

QY	372	ACA-AGTGGT--GC-----CTG-----GATCTCGC-GT--G-----GTCC-----	401
DB	4119	AGAGAGTTGTTTCAGCACTTCGTTCACTGCAATAGAGACTCAGGTCGGAATGTCAGTATA	4178
QY	402	-----TTCT-----GA-----GCA-----	413
DB	4179	TAAAGTTCCTTACAGCAAAATGTCAAGCGAGNAGGAAATTTATTAATAATGCCAGACA	4238
QY	414	-----CC-----CA-----	424
DB	4239	TGGTTATGGCCGAGCTGGTCAATTCGGGAGAGGATGTCCTCGTGTCTCTACAACGACAGAG	4298
QY	425	-----TACAG--C--ATCGAGAT--C--CAGAACCTGGAT--G--TGTATGACGAG	463
DB	4299	CCTCTTCCAGACTCTGATCAGATGATCGGTGAGAACG--GGATCGATGGATGAGAAC	4357
QY	464	GGCCCT-----TA-CAC-----CT-----GCTC-----G-GTGCA--GACAG--AC	493
DB	4358	AGCCCTCTCATGTACCACATCCACTTGGTCGAGCTCCTGGCTGTGTGTCACGGAGGGTAAG	4417
QY	494	AA--CCACCAAGACCTCTAG-----GTTCC-----AC-----CTCA	524
DB	4418	AATGCTACACAGAGA--TCAAGTGCAACTCCCTGCTCCGCTGGATGACATCGTTTCGGC	4475
QY	525	TTGTG---CA--AGTA--T-C--TCCC-----AAAATTGTAGAGAT--TT--CT--TC	561
DB	4476	TTGTGCCACGAGGACTGCATCCCTGAGGTTAAATGTGATACATTACTTCTGATC	4535
QY	562	A--GATATCTCCAT-----T--AATGAAGG-GA-----A-CAAT-----	589
DB	4536	ACTGCTATGTGATACAGAGTGGTGAATGAAGGAGATTTATACAGCAATCACATGTGGA	4595
QY	590	-ATT-----AG-----CCT-----CACCTGCA-----TAGCA--ACTGGT--AG--	618
DB	4596	AATTGGTTGGAATTCCTTGTAGACATCTGCGAGGCGCTGTAAACACACTAGTGCAGGA	4655
QY	619	-AC---CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCG-----G--TTG--	665
DB	4656	AACATGCAGA--CT--CGATT--TTGAGAGAAGTATGACCGAAATCGTATGAGTATTGT	4710
QY	666	-----GCT-----TTGT-----GAGT--GA-----AGAC-----	682
DB	4711	TACTACTTCTTCAGCTCTCCCTCTCAGACAGAGTACGACTTTCGAGACTCGCCAGCC	4770
QY	683	-----GAATACT--TGGA--AFTCAGGG-----CA-T-CACCGG-----G--	713
DB	4771	TGCTTTGTGCA-ACTGCTCAAGGCGTGTTCAGGGTTTACCACTGCACTGTTTAATGC	4829
QY	714	--AGC-----AG--TCAGGGA--C--TA--CGAGTGCAGTCCCT-----CCAATGA	750
DB	4830	CAAGCCAAAAGCCTCCGTGGAGAGCTGTATTCGGGTGC--TGTCTGATGATGCCAA--GA	4886
QY	751	--CGTGCC--GC--GCCCGTGGTAC--GGAGAGTAAAGGTCAACCGTGAA--CTATC	797
DB	4887	GCCG-GGCCCATTGCCATTCCCGTGG-ACCTGGACAGCCAA-GTCAAC--AACCTCTTC	4940
QY	798	-CA---CCATA-CATT-T-CAGA---AGCCAAG--GGTACAGGTGTC--CCCG-----	836
DB	4941	TCAAGTCCCAACAGCATGTGCAGAAAACAGCCATGAATGG--CGGCTCTCAGCCCGCAA	4998
QY	837	TG--GGACAAAAGGGGACACTG-----CAG-----TG--	861
DB	4999	TGCCGACGCA--GGGACTCTGTTCTGGCAGCTTCAGAGACTACCGGAATATCATTTGAG	5056
QY	862	-----TGAAG-----C-CTC-----AG-----CAGTCCCT-----CA-CGAGAA	889
DB	5057	AGATTGAGGACATCGTCTCCGCGCTGGAGGACCGCTCAGGCCCTCGTGCAGGCGAG	5116
QY	890	TT--CCAGTG--GTACNAGATG-----ACAAA-----AGACTGATT-----	922
DB	5117	TTATCTGTGCTCGT---GGATGTTCTCCACAGACCCGAG-CTGCTTTTTCCAGAGAAC	5171
QY	923	-----GAAGGAAA--GAAAGGG-----TG-----AAAG--TGGA	949

Db 5172 CAGAGCCAGAGGAATGTAAGAGTGGCGGTTTCATTTGCAAGTTAAATAAGCATACAA 5231
QY 950 AACAGACCTTTCT-CTCA--AAACTCA--TCTTCTCAATGT-CT-----989
Db 5232 AACAG-----CTGCT-AGAAGAAATGAAGAGAGCTCTGCAATTAAGTCTCTACAGAC 5283
QY 990 -CTGA--ACATGA-----CTATGG-GAACTACACTTGGCT--GSC-CT 1025
Db 5284 CTTGAGGGAATGATGACCAAGATAGAGCTATGGAGAA--A-A--GGGTGAGCGCT 5337
QY 1026 CCAA--CAAG--CTGGGCCAC--AC-----CAATGCCAG--CATC-----1057
Db 5338 C--AGCAAGTCTTGCTCAACCTTACTATGAAACGTCAGACCTTCGGGCAAGAGAG 5395
QY 1058 ATGC--TA-----TTTGGTCCA--GGCCGC--GTGAGC--GAGGTGACCAAGCGACGT 1103
Db 5396 A-GCCTTACCAGCTTTGG--CAATGGC-CCACTGTGACGAGGAG--GACC--CGGCAAGC 5447
QY 1104 C-----GAGGAGGG-----CAG-----GC-----TGCGTCTGG 1126
Db 5448 CCGGGGAGAGGGGAGGTTCCGGATCCAGCTCTATGAGCAGGGGTGAGATGAGTCTGG 5507
QY 1127 CTGCTGCTCTTCTGTCTTTG-CACT-----GCTTCTCAA--ATTT-----1165
Db 5508 CCGAGG-----TTTCAG-----TGTCACTTGACAAGAGGGGGCTTC-CAATCTAGTTATCG 5558
QY 1166 -----TG-----AT-----CT-----GAGTG--CCA-----C--T-TCC--CCA-----1187
Db 5559 ACCTCATGTAAGCGTATCCAGTGACCGAGTGTTCATGAAGAGCAATCTCTCGGCCATTG 5618
QY 1188 CCC-----GGGAAGGCTGC--CGCCACCA-CCACCAC-----C-----1218
Db 5619 CCTTCTGG--AAGGAGGCAACACCACTCATCAGACTCTTTTCTGTGCTTGACAGA 5676
QY 1219 -----AA--CA-----C-----AA-----CAGCA 1230
Db 5677 AGATAAGAGTCAGAGAAATTTCTTAAGGTGTTTATGACCGGATGAAGGTGGCCACGA 5736
QY 1231 ATG-----GCAACACCGACAG--CAACC-----AATCA-----1256
Db 5737 A-GAAATCAAGCAACAGTGACAGTGAAC-ACAGTGACTTGGGAATAAAGAAAGAC 5794
QY 1257 GAT-A--TATACA--A-----AT-----GAAATTAG--AAGA-----AAACAG--1288
Db 5795 GATGAGTAGACAGGATGCCCATCAGCAAGAAAGCTAAAGAGCCCAACACACAGATA 5854
QY 1289 -----CC--TCA-----TGG-----GACA-----GAAA-----1304
Db 5855 ACAGAGAGGTCGGGATCAGCTCTGAGGCGCTCGCTGCCACCGAGGAAGCTTCACC 5914
QY 1305 --TTT--GAGGGAG--G-----GGA-----1318
Db 5915 ACTTTCAGAGGAGGCTGATCCCGACGACCACTACCGCTTGGAGAGGCGACCCAGGCC 5974
QY 1319 -----ACAA-----AGA-----1325
Db 5975 ACTGCCGACAGGCCAAGGACGACCTGGAGATGAGCGGCTCATCACCATCATGAGGCC 6034
QY 1326 ATACT-----TT-----G-----GGGGHAAA-----GAG-----TT-----1347
Db 6035 ATCTCTCGCTTCTTTCAGCTCTGTGTGAAACCAACCAACCGAGACCTGCAGAACTTCCTC 6094
QY 1348 --TT--AAAA--AAGA--AATTGMAATT-----G-CCTTGCA-----GA 1378
Db 6095 CGTTGCCAAATAACAGACCAACT-ACATTTGATGTGAGACCTGCGATTTCTCGA 6153
QY 1379 ---TATTT---AGGTACAA-TGGAG--TT-----TTCT-----TTCCCAACGG 1414
Db 6154 CTGTATTTGTGAAGCACAACTGGAGGCTTGTCTTCTGGGCTGTATAT--AAATGA 6210
QY 1415 GAAGAACACAGC-----AC-----ACCC-----GG--C 1435

Db 6211 AAAGAAGCTAGCGCTTATCAACCAACCCCTGAAAGTCTGACCCGATACTGTCAAGGACC 6270
QY 1436 TTG-----GAGCC--ACTGCA-AGC-----TGATC-----GTGCA--ACCTCTT--1470
Db 6271 TTGCCATGAGAACCAAGAACTGATAGCCACCACCATGAATCCAAATG-GCATTGACATCATCA 6329
QY 1471 -----TGGTGC-CAGTG-----TGGGCAAG-----GG-----1491
Db 6330 CAGCCCTGATCTCAATGATATCAATCCCTTTGGGAAAGAGAGGATGGACCTTGTGTGTTAG 6389
QY 1492 --CT-----CA--GCCT-----CT-CTGCCCA-----CAG-----AGTG 1515
Db 6390 AACTGAAGAACAACTGCTCGAAGTTGCTCCTGGCCATCATGGAAGACGACGACAGTG 6449
QY 1516 -----C-----C-----CCC-----AC--GTGA-----1527
Db 6450 AAAACGACAGAGGATACTTTTATACATGAGGCCCAAGAACTGGTGGAAATGATCAAGA 6509
QY 1528 -----ACATTC-----TGGAG--C-----TGG-----1542
Db 6510 AAGCCTCATGCAAGGTGAAGTGGAAATTTGAGGATGGAGAAACCGTGAGGATGGCGG 6569
QY 1543 -----CCA-----T-----CCCAA-----ATT-----CAATCAG--TC--CATA 1567
Db 6570 CGTCCCCCAGGAACGTGGGGCACACATCTACATATTAGCCCATCAGTTGGCTCGGCATA 6629
QY 1568 GAGAC--GAA--CAGA--A--TGAGACCT--TCCGGCCCAAG--CG--TG--G 1604
Db 6630 ---ACAAAGAACTTCAGAGCATGCTGAAACCTGGT--GG--CCAGTGGACGAGATGAAG 6683
QY 1605 CGCTG-----CGG--GCA-----C--TT-----1618
Db 6684 CCTGGAGTTTATGCCAAGCACACGCGCGAGATAGAGATTGTGAGATTAGACCAACAA 6743
QY 1619 TGG-----TAGACT-----GTGCCACACCGCGT--GTG--TT-----GTGA 1651
Db 6744 TGGACAGATAGTCTTTCCCGTGC--CCA--GCATATGTGAATTCCTAACCAAGAGTCA 6799
QY 1652 AACGT--GAA-----ATA-----AA--AAG--AGCAAAA--AA 1676
Db 6800 AACTACGAATTTACTATATCTACAGAGAGACGCAACCAAGGACGCAAAATCAA 6852

RESULT 30
US-09-566-921-45
; Sequence 45, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 9610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 996794.11
US-09-566-921-45

Query Match 41.3%; Score 694.1; DB 4; Length 9610;
Best Local Similarity 39.9%; Pred. No. 0.00096;
Matches 1384; Conservative 0; Mismatches 194; Indels 1895; Gaps 384;
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QY 27 -----TTTAAA-----T-----CTCCTTG-----CA--CAAGCT-TGAGAGCAAC-----A 59
Db 3480 CCAGGCGCTTCAACAGGTTCAACTGCTGCTGTTACAGCCAGATGTG-GA-CAACTACAAA 3537
QY 60 CA-ATCTATCA-----GGA-AA-----G-AAAGAAAGA-----84
Db 3538 CAGATCAACAAAGACTTGGATCAACTGAGTCCATCGTGGAAAGTCAAGGCTTTGGGTG 3597
QY 85 -AAAAA--A-----CCGA--AC-----CT-GACAAA-----AA-AGAAG 111
Db 3598 TACAAAGGCGAGGCGCCGATGAGACATATGATGGTGCATCTGGAGAAATGAAATGAATGAAG 3657
QY 112 AAAA--AGAAG--AAGAA-AA-----AAATCATGAAA--ACCATCCAGC--CAA---152
Db 3658 AAAACGAGGAGGGAATAAACAAGCCACAAAGCATGAAGCACCA--GCAGCTACACTA 3716
QY 153 -A-AATG--CACA--ATTCT-ATCTCTTGG--GMA--TC-----TTACAG--GGGC 191
Db 3717 CAGAGTGGTCAAGAGATTTTGTAT-TC--GGCTTAGCAAACTCTGTGTTCAAGAGAGTGC 3773
QY 192 -----TG-----GCTGTC-TCTGTGCTCTTCC--AA-----GGAGTGC--C 222
Db 3774 CTCAGTGAAAGAGCAGGAGCAGACACAGCTCTGCTCCGGAACATGGCGCGCAGC 3833
QY 223 CGTGGCAGC--GGAGATGC--CACTTTCC-----CCAAAGCT-----ATG---259
Db 3834 CGTG-G-TGCTGAGCTGCTGCAGATTCCTATGAGAAGCGCGAAGATACCAAGATCAA 3891
QY 260 --GACACAGTGACGCTCGG--CAGG-----GGGAGA-----GGCG--CACCC---296
Db 3892 GAGATAA--TGA-GGT-TGGCTCATGAATTTTTCAGAAATTTTCGCGAGCAACACGCA 3947
QY 297 ---TCAGG---TGC-ACTATGAC--AAACCG--GTC-ACCC--GGG-TGSCCT---335
Db 3948 GAATCAAGCTTTGTAC-ATAAACACATAAACCTGTTTCTCAACCCAGGAT--CCTGGA 4004
QY 336 GGCTA--AACC--GCAGAC-----CA--TCC-TCTATGC--TGGG--AATG 371
Db 4005 GGC-AGTAACCATCAGCAGACATCTTCATGAACAATTTCCAGCTTTGCAGTGAGATCAACG 4063
QY 372 ACA-AGTGGT--GC-----CTG-----GATCCTCGC-GT--G--GTCC-----401
Db 4064 AGAGAGTTGTCAGCACTCGTTCACTGCACTAGAGACTCAAGTTCGGAATGTCAGATTA 4123
QY 402 -----TTCT--GA-----GCA-----ACA 413
Db 4124 TAAAGTTCTTACAGACAATTTGCAAGGCGAGAGGGAATTTATTAATAAATGCCAAGACA 4183
QY 414 -----CC-----CA-----AACG-CAG--424
Db 4184 TGGTTATGCGCGAGCTGGTCAATTCGGGAGAGGATGTCCTCGTGTCTTACAAGCAGACAG 4243
QY 425 -----TACAG--C-ATCGAGAT--C--CAGAACGTGGAT--G-TGTATGACGAG 463
Db 4244 CCTCTTTCCAGACTCTGATCCAGATGATGGGTGAGAACG--GGATCGATGGATGAGAAC 4302
QY 464 GGCCT-----TA-CAC-----CT-----GCTC-----G-GTGCA--GACAG--AC 493
Db 4303 AGCCCTCTCATGTACCACATCCCACTTGGTGGAGCTCTGCTGTGTGTCAGGAGGTTAG 4362
QY 494 AA--CCACCAAGACCTCTAG-----GGTCC-----ACCTCATT-----526
Db 4363 AATGTCTACAGAGA--TCAAGTGCAACTCCCTGCTCCCGCTGGATGACATCGTTGCGG 4420
QY 527 --GTG--CA--AGTA-T-C-TCCC-----AAATTTGAGAGAT--TT-CT--TC 561
Db 4421 TGGTGACCCACAGGAGCTGATCCCTGAGGTTAAATTTGATACATTAATCTCTGATC 4480
QY 562 A--GATATCTCCAT-----T-----AATGAAGG-GA-----A-CAAT-----589
Db 4481 ACTGCTATGTGATACAGAGGTGGAATGAAGAGATTTTATACCAGCAATCACATGTGA 4540

QY 590 -ATT-----AG-----CCT-----CACCTGCA-----TAGCA--ACTGGT--AG--618
Db 4541 AATTGTTTGAAGATTTCTTGTAGACATCTGCAAGGCGCTGTAAACAACACTAGTGACAGGA 4600
QY 619 -AC---CAGAGCCTTACGTTTACTTTGGAGACACATCTCTCCCAAGCG-----G--TTG--665
Db 4601 AACATGCAGA--CT-CGATT--TTGGAGAGATGTGTCACCGAATCGTCACTAGATATTGT 4655
QY 666 -----GCT-----TTGT-----GAGT--GA-----AGAC-----682
Db 4656 TACTACTTTTCTCAGCTCTCCCTTCTCAGACCAGATACGACTTTGACAGACTGCCAGCC 4715
QY 683 -----GAATACT--TGGAA--ATTACAGG-----CA-T-CACCGG-----G--713
Db 4716 TGTCTTTGTGCA-ACTGCTCAAGGCGTGTTCAGGTTTACCACCTGCACTGGTTAATGC 4774
QY 714 --AGC-----AG--TCAGGGGA--C--TA--CGAGTGCAGTGCCT-----CCATGA 750
Db 4775 CAAGCCAAAAGGCTCGTGGAGAGCTGTATTCGGGTGC--TGTCTGATGTAGCCAA-GA 4831
QY 751 --CGTGGCC--GC---GCCGTGGTAC--GGAGGTAAAGTCAACGTGAA--CTATC 797
Db 4832 GCCG-GGCCAATGCCAATTCCTCGGTGG-ACCTGGAGACGCCAA-GTCAAC--AACCTCTTC 4885
QY 798 -CA-----CCATA-CATT-T-CAGA--AGCCAAAG--GGTACAGTGTG--CCCG--836
Db 4886 TCAAGTCCCACAGCATTTGCGAAGAACAGCCATGAACCTGG--CGGCTCTCAGCCCGCAA 4943
QY 837 TG--GGAACAAAAGGGGACACTG-----CAG-----TG--861
Db 4944 TGCCGACGCA--GGGACTCTGTTCTGGCAGCTTCCAGAGACTACCGGAATATCATTTGAG 5001
QY 862 -----TGAAG-----C-CTC-----AG-----CAGTCCCT--CA-GCAGAA 889
Db 5002 AGATTGAGGACATCTGCTCCGCGCTGGAGACCGCTCTCAGGCGCTTGGTGCAGGCAGAG 5061
QY 890 TT--CCAGTG--GTACAAAGATG-----ACAAA--AGACTGATT-----922
Db 5062 TTATCTGTGCTGT-----GGAATGTTCTCACAGACCCGAG-CTGCTTTTCCAGAGAA 5116
QY 923 -----GAGGAAA--GAAAGGG-----TG-----AAAG--TGGAA 949
Db 5117 CAGACGCCAGAGAAATGTGAAGTGGCGGTTTCAATTTGCAAGTTAATAAGCATACAA 5176
QY 950 AACAGACCTTTCTCT-CTCA--AAACTCA-----TCTTCTCAATGT-CT-----989
Db 5177 AACAG-----CTGCT-AGAGAAATGAAGAGAGCTCTGCATTAAAGTCTCTACAGAC 5228
QY 990 -CTGA--ACATGA-----CTATGG-GAACTACACTTTCGT--GGC-CT 1025
Db 5229 CCTGAGGAAATGATGACCAAGATAGAGGCTATGGAGAA--A-A--GGTGAGGCGCT 5282
QY 1026 CCAA--CAAG--CTGGGCCAC--AC-----CAATGCCAG--CATC-----1057
Db 5283 C--AGCAAGTTCTGTGTCAACCGTTACTATGAAACGTCAGACCTTCGGGACGAGAGAG 5340
QY 1058 ATGC--TA-----TTTGGTCCA--GGCGCC--GTCAGC--GAGGTGACCAAGCGCACCT 1103
Db 5341 A-GCCTTACAGCTTTGG--CAATGCC-CACTGTGACGAGAG--GACC--CGGACAG 5392
QY 1104 C-----GAGGAGG-----CAG-----GC-----TGCGTCTGG 1126
Db 5393 CCGGGGAGGAGGAGGAGGTTCCGGATCCAGCTCTATGACGAGGGGTGAGATGAGTCTGG 5452
QY 1127 CTGCTGCCCTTCTGCTCTTG-CACCT-----GCTTCTCAA--ATTT-----1165
Db 5453 CCGAGG-----TTGAG-----TGTCACCTTGACAAGGAGGCGGCTTC-CAATCTAGTTATG 5503
QY 1166 -----TG-----AT-----GT-----GAGTG--CCA-----C-T-TCC--CCA---1187
Db 5504 ACCTCATCATGAACGATCCAGTCCAGTCCAGGCTGTTCCATGAAGAGCATTTCTCTGGCAATG 5563
QY 1188 CCC---GGGAAAGGCTGC--CGCCACCA-CCACCAC-----C----1218

Db	5564	CCCTTCGG--AAGGAGCAACACCCATCCAGCACTCCTTTTCGTGCTTGACAGA	5621
Qy	1219	-----AA--CA-----C-----AA-----CAGCA	1230
Db	5622	AGATAAGAAGTCAGAGAAATCTTTAAGGTGTTTTATGACCGGATGAAGGTGGCCAGCA	5681
Qy	1231	ATG-----GGAACCCAGCAG-----CAACC-----AATCA-----	1256
Db	5682	A-GAAATCAAGACCAAGTCAGCAGTGAC--ACCAAGTCAGCTGGGAAATAAAGAAAGAC	5739
Qy	1257	GAT-A--TATACA--A-----AT-----GAATTAG--AAGA-----AACACAG--	1288
Db	5740	GATGAGGTAGACAGGATGCCCATCAGGAAAAAGCTAAGAGGCCCAACAACAGATA	5799
Qy	1289	-----CC--TCA-----TGG-----GACA-----GAAA-----	1304
Db	5800	ACAGAAGAGTCCGGGATCAGCTCTGTGAGGCCTCCGCTGCCACAGGAAGCGCTTCACC	5859
Qy	1305	---TTT---GAGGAGG-----GGA-----	1318
Db	5860	ACTTTCAGGAGGAGGCTGATCCCGACGACCACTACCAGGCTGGAGGGCCACCAGGCC	5919
Qy	1319	-----ACAA-----AGA-----	1325
Db	5920	ACTGCCGACAGGCCAAGGACGACCTGGAGATGAGCGGTCATCACCATCATGCAGCCC	5979
Qy	1326	ATACT-----TT-----G-----GGGGAAAA-----GAG-----TT-----	1347
Db	5980	ATCTCCGCTTCCTTCAGCTCCTGTGTGAAAAACCAACCGAGACCTGCAGAACTTCCTC	6039
Qy	1348	--TT-----AAAA--AAGA--AATTGAAAAAT-----G-CTTTGCA-----GA	1378
Db	6040	CGTTGCCAAAAAACAAGACCAACT-ACAATTTGGTATGTAGACCCCTGCAGTTCTTCTGGA	6098
Qy	1379	---TAATTT---AGGTACAA--TGGAG---TT-----TTCT-----TT-----TCCCAACGG	1414
Db	6099	CTGTATTGTGGAGACCAACTGGAGCCCTTGSTCTTCTGGGCTGTATAT---AAATGA	6155
Qy	1415	GAAGAACACAGC-----AC---AGCC-----GG--C	1435
Db	6156	AAAGAACTAGCGCTTATCAACCAACCTTGGAAAGTCTGACCGAATCTGTCAAGGACC	6215
Qy	1436	TTG-----GACCC---ACTGCA--AGC-----TGCATC---GTGCA---ACCTCTT--	1470
Db	6216	TTGCCATGAAACCAAGAACTGCTATAGCACCCATGAATCCAATG-GCATTAATCATCA	6274
Qy	1471	-----TGGTGC-CAGTG-----TGGSCAAG-----GG-----	1491
Db	6275	CAGCCCTGATCCTCAATGATATCAATCCTTTGGAAAGAGAGATGACCTTGTGTAG	6334
Qy	1492	--CT-----CA--GCCT-----CT-CTGCCCA-----CAG-----AGTG	1515
Db	6335	AACTGAAGAACAAATGCCTCGAAGTTGCTCTCTGGCCATCATGGAAGCAGCAACAGTG	6394
Qy	1516	-----C-----C-----CCC-----AC--GTGGA-----	1527
Db	6395	AAAACGACGAGAGATCTTTATTAACATGAGGCCCAAGAACTGGTGGAAAGTGAATCAAGA	6454
Qy	1528	-----ACATTC-----TGAG-----C-----TGG-----	1542
Db	6455	AAGCCTACATGCAAGGTGAAGTGAATTTTGAGGATGGAGAAACGGTGAGGATGGGGCGG	6514
Qy	1543	-----CCA-----T-----CCCA-----ATT--CAATCAG-----TC--CATTA	1567
Db	6515	CGTCCCCCAGGAACGTGGGGCACAACATCTACATATTAGGCCATCAGTTGGCTGGGCATA	6574
Qy	1568	GAGAC---GAA---CAGA--A---TGAGACCT---TCCGGGCCAAG---CG-----TG--G	1604
Db	6575	---ACAAGAACTTCAGAGCATGCTGAACCTGTT--GG--CCAAGTCGAGGATGAAG	6628
Qy	1605	CGCTG-----CGG-GCA-----C-----TT-----	1618

Search completed: May 28, 2004, 21:12:45
Job time : 342.763 secs

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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 15:19:20 ; Search time 4830.37 Seconds
(without alignments)
10379.861 Million cell updates/sec

Title: US-10-017-084A-522

Perfect score: 1679

Sequence: 1 gttgttccttcagcaaac.....ataaaagagcaaaaaaa 1679

Scoring table: IDENTITY NUC

Gapop 1.0 , Gapext 0.1

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:**

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1319	78.6	1808	11	AK045973 Mus muscu
2	1319	78.6	1808	11	AK046377 Mus muscu
3	923.4	55.0	1083	12	BM090927 AGENCOURT
4	894.9	53.3	1033	12	BM07426 AGENCOURT

5	892.4	53.2	3166	11	AK042854	Mus muscu
6	866.4	51.6	874	29	AY406347	Homo sapi
7	844.2	50.3	1085	9	AL533026	AL533026
8	834.8	49.7	1039	10	BE798585	BE798585
9	769	45.8	865	12	BI666583	BI666583
10	761.3	45.3	856	13	BU15617	BU15617
11	757.6	45.1	773	29	AY406348	Pan trogl
12	739.5	44.0	2798	11	AK028345	Mus muscu
13	724	43.1	874	29	AY406349	Mus muscu
14	708.8	42.2	2768	11	AK030681	Mus muscu
15	707.7	42.2	14278	11	AY318958	Rattus no
16	707.7	42.2	14278	11	AY321317	Rattus no
17	707.2	42.1	770	10	AW117456	xd92a06.x
18	702.2	41.8	4667	11	BC049868	Mus muscu
19	701.1	41.8	5570	11	BC044081	Xenopus l
20	701	41.8	11415	29	AY418622	Mus muscu
21	699.9	41.7	4754	29	AY408639	Homo sapi
22	698.9	41.6	4035	11	AK044634	Mus muscu
23	698.5	41.6	5118	11	AK036018	Mus muscu
24	698.5	41.6	4728	11	AK087828	Mus muscu
25	698.2	41.6	10481	11	AK090138	Mus muscu
26	697	41.5	3971	11	AK054393	Mus muscu
27	696.7	41.5	4540	11	AK087352	Mus muscu
28	696.4	41.5	9022	29	AY402248	Mus muscu
29	696.2	41.5	4379	11	AK086942	Mus muscu
30	695.5	41.4	4529	11	AK014607	Mus muscu
31	695.3	41.4	4059	11	AK083598	Mus muscu
32	694.9	41.4	4000	11	AK031491	Mus muscu
33	694.7	41.4	3955	11	AK054356	Mus muscu
34	694.4	41.4	3808	11	AK087443	Mus muscu
35	694.3	41.4	3970	11	AK049454	Mus muscu
36	694	41.3	7626	29	AY406123	Pan trogl
37	693.9	41.3	7886	11	BC034956	Homo sapi
38	693.8	41.3	8315	11	AK090135	Mus muscu
39	693.4	41.3	784	12	BI549918	BI549918
40	693.2	41.3	4626	11	AK052174	Mus muscu
41	692.9	41.3	4463	11	AK083374	Mus muscu
42	692.8	41.3	5002	11	AK029828	Mus muscu
43	692.5	41.2	8329	11	AK090130	Mus muscu
44	692.4	41.2	4827	11	AK042675	Mus muscu
45	692.3	41.2	4168	11	BC060216	Mus muscu
46	692.3	41.2	5855	29	AY418964	Mus muscu
47	692.2	41.2	5072	11	AK082062	Mus muscu
48	692	41.2	4213	11	AK085022	Mus muscu
49	692	41.2	4384	11	BC036366	Homo sapi
50	692	41.2	4729	11	BC035209	Mus muscu
51	691.9	41.2	3885	29	AY403281	Homo sapi
52	691.9	41.2	3912	11	BC049876	Mus muscu
53	691.9	41.2	4257	11	AK029726	Mus muscu
54	691.9	41.2	4441	11	AK081990	Mus muscu
55	691.8	41.2	4126	11	AK015017	Mus muscu
56	691.8	41.2	4346	11	AK046357	Mus muscu
57	691.7	41.2	7211	29	AY419435	Mus muscu
58	691.5	41.2	8528	11	AK090134	Mus muscu
59	691.2	41.2	3744	11	AK030109	Mus muscu
60	691	41.2	3595	11	AK032617	Mus muscu
61	690.8	41.1	4187	11	AK029952	Mus muscu
62	690.5	41.1	4253	11	AK034140	Mus muscu
63	690.5	41.1	4484	11	AK082497	Mus muscu
64	690.3	41.1	4831	11	BC018614	Mus muscu
65	690.3	41.1	4857	11	AK049216	Mus muscu
66	690.2	41.1	4751	11	AK038568	Mus muscu
67	690.2	41.1	7060	11	BC043838	BC043838
68	690.1	41.1	4294	11	AK083129	Xenopus l
69	690.1	41.1	4329	11	AK054507	Mus muscu
70	690	41.1	3379	11	AK088860	Mus muscu
71	690	41.1	5400	29	AY407796	Homo sapi
72	689.8	41.1	7529	29	AY406124	AY406124
73	689.7	41.1	3441	11	BC023933	Mus muscu
74	689.6	41.1	5550	11	BC054077	BC054077
75	689.5	41.1	4694	11	BC027787	Mus muscu
76	689.2	41.0	3685	11	AK034114	Mus muscu
77	689.1	41.0	3839	11	AK054229	Mus muscu

78	689.1	41.0	5758	11	AK038638	Mus muscu	
79	689	41.0	7596	11	AY383707	Rattus no	
80	688.9	41.0	6882	11	AK029252	Mus muscu	
81	688.7	41.0	3829	11	AK014481	Mus muscu	
82	688.6	41.0	4187	11	AK087617	Mus muscu	
c	83	688.5	41.0	4195	11	BC021044	Homo sapi
84	688.5	41.0	4561	11	AK054014	Mus muscu	
85	688.5	41.0	7008	29	AY414399	Homo sapi	
86	688.3	41.0	5400	29	AY407798	Mus muscu	
c	87	688.2	41.0	4051	11	AK086467	Mus muscu
88	688.1	41.0	3429	11	AK052117	Mus muscu	
89	688.1	41.0	3939	11	AY325194	Rattus no	
90	688.1	41.0	5487	29	AY404243	Mus muscu	
91	688	41.0	4489	11	AK028459	Mus muscu	
92	688	41.0	4805	11	AK040543	Mus muscu	
c	93	688	41.0	8259	11	BC038478	Mus muscu
94	687.9	41.0	3602	11	AK080960	Mus muscu	
c	95	687.9	41.0	4510	11	AK039975	Mus muscu
96	687.9	41.0	5433	29	AY406469	Mus muscu	
97	687.7	41.0	4193	11	AK033851	Mus muscu	
98	687.7	41.0	4193	11	BC034785	Mus muscu	
99	687.6	41.0	3590	11	AK036419	Mus muscu	
100	687.5	40.9	6333	29	AY414807	Homo sapi	

ALIGNMENTS

RESULT 1	AK045973	1808 bp	mRNA	linear	HTC 20-SEP-2003
LOCUS	Mus musculus adult male corpora quadrigenina cDNA, RIKEN				
DEFINITION	full-length enriched library, clone:B230328N06 product:NEUROTRIMIN				
ACCESSION	AK045973				
VERSION	AK045973.1	GI:26337738			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				

REFERENCE

AUTHORS

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PUBMED

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Db 1073 TGGGAACATACATCTGGTGGCTCCAAAGCTGGGCCACACCAATGCCAGCATCATGCT 1132
QY 1063 ATTGGTCCAGCGCGCTCAGCAGGTGAGCAACGCGACGCTCAGGAGGCGAGGCTCGGT 1122
Db 1133 ATTGGTCCAGCGCGCTCAGTGGGTCAACATGGGACATCAAGAGGCGAGGCTGCAT 1192
QY 1123 CTGGCTGTGCTCTCTCTGCTCTGCTGCTCTCAATTTTGAATGATGATGCTCACTT 1182
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QY 1183 CCCACCCGGGAAAGGCTGCCGCCACACCAACCAACCAACCAACCAACCAACCAACCG 1242
Db 1253 CCTGCTGGGAGA-GCTGCTGCCACC-GCATC-TCATACAAAGCACT-GCAA-AATG 1307
QY 1243 ACAGCAACCATCATGATATATACAAATGAATTAAGAGAAACACAGCCTCATGGACAGA 1302
Db 1308 A-AGCAACAAGTCAAG--AT-CAAAATGAATTCGGAGAATCACAGCC-AATGAGACAGA 1361
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QY 1356 GAAA-TTGAATTCCTTTGAGATATTTAGGTACAATG--GAGT---TTCTTTTCCC 1408
Db 1422 GAAATTTGGAATTCCTTTGAGATATTTGCGTAC--CGTGAGTTTCTTTTCTTCCC 1479
QY 1409 AAACGGGAGAACAGACACACCCCGCTTGGACCA-CTGCAAGCTGATGTCGCAACT 1467
Db 1480 AAGTGGGAGAA--GGCACACCTAGCTTGGACCCACCAACCAAGCTGCTGTGACCT 1536
QY 1468 CTTTGTGCCAGTGTGGGCAAGGCTCAGCTCTCTGCTGCCAC-AGAGTGCCC--CCAGT 1524
Db 1537 CTCTGTGCCAGGTTGGGCAAGGCTCAGCACTCTGCCCACTAAAGTGCCCCACCA--T 1594
QY 1525 GGAACATCTGAGCTGGCCATCCCAATTCATCAGTCCATAGAC--GAAACAGA--A 1580
Db 1595 GAAACATCTGAGTTGGCCATCCCAATTCATCAGTCCATAGAC--GAAACAGA--A 1654
QY 1581 TGAGACCTTCC---GGCCCAAG-CGTGGCGCTGGGGGCACTTTGTGTAGACTGTGCCCA 1636
Db 1655 AGAAA-----CAAGGGCCTTAGATGTGCCACAGGGGCCCTTTGTGTGGGCTGTGTGA-CA 1708
QY 1637 CG--GCGTGTGT-----TGTGAACCTG-----AAATAA-AAGAGCAAAAAA 1677
Db 1709 -GTGCGTGTGTGATGAAGTGTGAATCTGGAGGAGAAAAAACAAGAGCAAAAGAA 1767
QY 1678 AA 1679
Db 1768 AA 1769

RESULT 3
LOCUS BM809227 1083 bp mRNA linear EST 05-MAR-2002
DEFINITION AGENCOURT 6582414 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5468221
5', mRNA sequence.
ACCESSION BM809227
VERSION BM809227.1 GI:19126050
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1083)
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AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: L10M1971 row: h column: 14
High quality sequence stop: 656.

FEATURES
source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5468221"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 55.0%; Score 923.4; DB 12; Length 1083;
Best Local Similarity 90.6%; Pred. No. 2.6e-11;
Matches 977; Conservative 0; Mismatches 33; Indels 68; Gaps 30;

QY 663 TTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGGCATCACCGGGAGCAGTCAG 722
Db 1 TTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGGCATCACCGGGAGCAGTCAG 60

QY 723 GGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCGGCCCGTGTGATCGAGAGTAAAGG 782
Db 61 GGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCGGCCCGTGTGATCGAGAGTAAAGG 120

QY 783 TCACCGTGAATATCCACCATACATTTTCAGAACCAAGGGTACAGGTGTCCCGTGGGAC 842
Db 121 TCACCGTGAATATCCACCATACATTTTCAGAACCAAGGGTACAGGTGTCCCGTGGGAC 180

QY 843 AAAAGGGGACACTCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACA 902
Db 181 AAAAGGGGACACTCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACA 240

QY 903 AGGATGACAAAGACTGATTTGAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCC 962
Db 241 AGGATGACAAAGACTGATTTGAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCC 300

QY 963 TCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACATTTGGGTGG 1022
Db 301 TCTCAAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACATTTGGGTGG 360

QY 1023 CCTCCAAAGCTGGGGCACCAACCAATGCCAGCATCATGCTATTT----- 1066
Db 361 CCTCCAAAGCTGGGGCACCAACCAATGCCAGCATCATGCTATTTGAAGTGAAGAACTACAG 420

QY 1067 -----GGTCCAGGGCCCGTCAAGGAGGTGAGCAACCGGACCGTCGAGGA 1109
Db 421 CCCTGACCCCTTGGAAAGGTTCCAGGGCCCGTCAAGGAGGTGAGCAACCGGACCGTCGAGGA 480

QY 1110 GGGCAGGCTCGGTCTGGCTGCTGCTCTTCTGGTCTTGGTCTGGACCTGCTTCTCAAAATTTGAT 1169
Db 481 GGGCAGGCTCGGTCTGGCTGCTGCTCTTCTGGTCTTGGTCTTGGACCTGCTTCTCAAAATTTGAT 540

Db 475 COTGAGTAACACCCAGACCCAGTACAGCATTTGAGATCCAGATGCGATGCTACGATGA 534
Qy 463 GGGCCCTTACACCTGCTGGTGCAGACAGACACCCAGACCTCTAGGTCACACT 522
Db 535 GGGCCCTTATACCTGCTGGTGCAGACAGACACCCAGACCTCTAGGTCACACT 594
Qy 523 CATTGTGCAAG-----TATCT-----CC-----CAA 543
Db 595 CATTGTCAAGGTGGGTGGGCTTGGCTGGGAGGCTGAGTGGGTGGCTGGGAATATCAA 654
Qy 544 AATTGTAGAGATTTCTT---CAGATATCTCCATTAAT---GAAGGGAACATA---TTAGC--- 595
Db 655 CAT---TACTGATTTTTTTCACA-A---TCC---TAATCAA---C---TAGGTGGCTG 701
Qy 596 ---CTCACCTGCATAGCAA---CTGGTAG---ACC---AG---AGCCTACGG----- 632
Db 702 TTCTCCCC---AGCAATGCTCTCTGCTGGTGTATCTTTGAAGCTAGAC---ACGGNACGTT 755
Qy 633 ---TTAC---TTGGAG---ACACA---TCTC---TCC----- 654
Db 756 TCATCAATTTACTTTTGTAGTTGAAC-CAGTTTTTCTCTATTCAGTATTATGTTTGT 814
Qy 655 -CAAA-----G---CGTTGGCTTT-----G----- 671
Db 815 ACATAATTTATGCTAATTTATTTGTTCCCTTGGCTTTTCCCTCTTAGCATTTTTAAAA 874
Qy 672 TG-----AG---TG-----AAGAC---GAA---TA-----CTT---GG--- 692
Db 875 TGTTCATACAACTACAAAGTTGTTTATTTAAGACAAGAATTTATGTTCTTCGGTT 934
Qy 693 ---AAAT-T---CAGGCAAT-CACCG-----G-----AG---CAGT 719
Db 935 GCTGTACATATATACCATGCCATAGACCCGCTTCCATGATGACAAAGCCAAAGAACAGT 994
Qy 720 ---CAGG-----GGA-----CT-----AC-----GAGTGCAGTG 740
Db 995 ACCCAGGATCTTATCGCAACCATCCCTCCACACACCCATTATAGTATAGGGTGCT-TG 1053
Qy 741 C-----C-TCAATGAC-G---TGG---CGCG---GCCGTGGT-----AC-GG--- 772
Db 1054 CTCCTCTCCATCCAAT--CCAGTTTGGCTTCCCATGCTCTGCTATAAGACTGGAT 1111
Qy 773 --AGAGT-----AAAGGTAC--CGTGAATATCCACCATACATTTTCAGAGCC- 817
Db 1112 TCAGAGTCTCTTCTCTATGTTCTCTCTTCTG---TTT---ATAC-TTT---GTAGGCT 1160
Qy 818 -AAGG---GTACAGGTGC---CCC-----GTGGG-----A-----CAAAAG 847
Db 1161 TAATGTTTGT--TTGGGTCTCCCGTGTGTTTGTGGCTTTGGCATTTCTCCA--- 1215
Qy 848 GG-----G-----ACA---CTGAGTGTGAAGC-----TC 870
Db 1216 GGTTCATCTCTCTGCTCTCATATCACAGGTCTG--GTGTCAGCCCTTTTCAAAATC 1273
Qy 871 AGCA-GTCCCT---CAGCAGA---ATP---CCAG---TG-----GT----- 899
Db 1274 AGAATGCT--CTGAGCGCAGCAGACACATTTACAGTAGATGAATTTCTAGTTACTGA 1331
Qy 900 ACAA-----GG---A-----TGAC---A-AAAG-----ACT 918
Db 1332 ACAACAGCTTTGGGTCTACATTTGTTCTGTTTCTGACGGAGAGAGGCCCTCAAAATTAAT 1391
Qy 919 G-A-----TTG---AA---GG-AAA-----GAAAGGGTGAA----- 942
Db 1392 GCACCCCTGGGGCTTTTCTTGGAAATAGGGTAAATGTGAGAGTGGGTGAAGATTAC 1451
Qy 943 -----A-GT-GGAAAC---AGACCTT-----TCCTCTC-----A-A-A---A 970
Db 1452 ATTATATGTAGTAACTAAAGCCCTTAGGAGAGGCCCTCACCTGTGGAGGACTATTA 1511
Qy 971 C-----TCATC-T---TCTTCAATGTC-----TC-----TG----- 992
Db 1512 CCTGTTGTCTATGCTATTGAATGTCCTTGAATTTCTTTTCAAAATACAGTGAATAT 1571

Qy 993 -----AACAT---GAC-----TATGGAACT-----ACACTTGC-GTGGCTC---CAAC- 1030
Db 1572 TTTTAAACATTTAGTCATGTTTATAGTAATTAATACTATGCTTTGTTCTCTGAGACT 1631
Qy 1031 -AAGCTGGCCACACCAATGCCAGA---TCATGCT---ATTT-----GG---TCCAG 1073
Db 1632 AAA-----CATACC-ATG-AAGTAAATTTCTTTGGATTTTTTGGGGTTCTCC--- 1680
Qy 1074 GCG-C-CGTC-----AG-CGA-----GG-----T-GACA--AC 1096
Db 1681 TCGTCTCGTCTCTCTCTTTCTTAGTCTAATCCCTGGCTTTCTCTCATCCAGCATGAT 1740
Qy 1097 GGCACGTCG-AGG-AGGGC-----AGCTCGCTCGCTGCTGCTCT---CTT-CTG---G 1142
Db 1741 GGCAGGT-GTCAGGCAGAGCCATGAAG--TTGCTTTGCAACAGCCTTCTCTGGAAG 1797
Qy 1143 T---CTTG-----CACCTG-----CT----- 1155
Db 1798 TACACTTGAGAGTAGGATGAACCTCGAGTGACTGGAGAGACAAAAGATAGGGA 1857
Qy 1156 TCT-----CAAAAT---TTGATGTAGTGCCACT-TCCCCACCCG---GGAAG 1197
Db 1858 T-TGAGAAGACAAATTTGGAAGAGTGA-GCAGAGCCCACTGT---GAGCAGAGAAGGAAA- 1911
Qy 1198 GC-----TGCCGCCACCAACCACCAACA---CAAC-----AGCAAT--GGCAACACC 1241
Db 1912 GCAGAAATGCCATCATGA--ACCA--AACAGAGCTACGAGGAGTAG-AATGGGCA----- 1961
Qy 1242 GACAGCAACCA---ATCAGA-TAT-----AT-----ACAAATGA-A-A-TTGA- 1278
Db 1962 ---AGCAGCATGAGATGAGACTATGTTAGAAATGAGGGGACACTTGAGCATATGTTAGAG 2018
Qy 1279 -A---CAA---ACACAGC-----C-----TCA-----TGG-GA-----C 1299
Db 2019 GAGGTGAAGTA-GCAGCTGACTGGCAATGATCGCTGTGTAGATATGTCACCTC 2077
Qy 1300 AG-----AAATTTG-----AGG-----GAGG--- 1315
Db 2078 AGGTTTTTATCATTCTTGTCTGCTGTTTCTCTCCCCCAAGAGAAATATGATGTTT 2137
Qy 1316 ---GGA---ACAAA-GAATACTTT-----GG---GGGAAA-AGAG 1345
Db 2138 CTTTTATTGATTTCTATAAATGACTACTTTTTTTTTTGCAACAGGTTAGTGCAATAGAG 2197
Qy 1346 TTTTAAAGAAATGAA-----A---ATTGCTT-----GCAGATATTTAGG 1386
Db 2198 TTTTAAATAG-AATTCATAGCCAGTACTTGTAGTGTTTATAAATAGCAGA---TTAGG 2253
Qy 1387 TA---CAATG-GA-----GTTT-----T-C-TTTTC--C---CAAAACG----- 1413
Db 2254 TACTGCTATGTAATTTTTTGTGTTGTTATACATTTTCAACGTACAAAAGCTTTTCT 2313
Qy 1414 -----GGAAGA--ACACA-----G-CACA---CCCG-----GTTTG- 1438
Db 2314 TGTAGATAGAAGATAGACAAAATAAAGTTAAGGTCACAGTTCTGTGGGGTAGCTGG 2373
Qy 1439 -GACCCACTGC-----AAGCTGCATCGTGCAACCTCT--TT--G-GTCCC-----AG- 1479
Db 2374 TGA---A-TGCTCGGGGAAGC--CATC-TGCCATCTCTATTAGGCGATACCTCACAGT 2426
Qy 1480 ---TG--TGGG-----CAAG---GGCT-----CAGCC 1498
Db 2427 CCTTGTGGGCAAGATGCTCCTCAATGACCAAGATGGCTAGGAGATTGGAGCACAGCT 2486
Qy 1499 TCTCTGC-----CCAC-A-GA--GTG-----C-----C 1517
Db 2487 TTGCTCGAGGAGCAGCACCATGAGACCTTGAACCTTGAACAGCAAAAATAGAAAAGAGC 2546
Qy 1518 CCCACGT-G-----GAACA--TTCTGGAG-C-TG-----G---CCATC--C--- 1548
Db 2547 ACCTTTAGAAAATAAAGAACAGTTTTT---AGTCATTTGTTTTTGTATATCATCTTCTGG 2604

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QY 1549 -CAAAATTC--A-AT--CAGTCC--ATAG-AGAC----- 1572
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QY 2605 ACACATTCGTATATACCTGTCTGCTAAATAGTAGTACTGACTTTTACACATTTGGGAATTAAT 2664
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QY 1573 -----GAA-CA-----GAAT-----G-----AGACTTCC-----GGCCC--- 1596
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QY 2725 GAGAAAGAGTATAGTACTGGAGTTGGGGGGGCGAGCAGAGGAGGGAGGACACAGC 2784
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QY 1617 -----TTTG-----GT--AG--ACTG-----TG-----CCA---CCACGG-- 1639
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QY 2844 TTACGTCTGTGACTTGTGGCTAGTGCCCTTTCCCATGACACACCACCTTTGAGTATTGGA 2903
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QY 1674 -----AAAAAA 1679
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RESULT 6
AY406347
LOCUS
DEFINITION
Homo sapiens HCM2527 gene, 874 bp DNA linear GSS 12-DEC-2003
genomic survey sequence.
ACCESSION
AY406347
VERSION
AY406347.1 GI:39762321
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferred nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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/locus_tag="HCM2527"
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Best Local Similarity 99.3%; Pred. No. 3.6e-10;
Matches 868; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
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QY 1 GTGCACATTTGACAAACGGGTACCGGGTGGCTTAAACCGCAGACCATCTCTTA 60
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QY 361 TGTGGAATGACAAAGTGTGCTGGATCCTCGCGTGTCTTCTGAGCAACACCCAAAC 420
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QY 61 TGTGGAATGACAAAGTGTGCTGGATCCTCGCGTGTCTTCTGAGCAACACCCAAAC 120
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QY 421 GCAGTACAGATCGAGATCCAGAACGTGTGTGTATGACGAGGGCCCTTACACCTGTCTC 480
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QY 481 GGTGACAGACAGAACCCACCAAGACCTCTAGGGTCCACCTCATTTGTCAGTATCTCC 540
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QY 181 GGTGACAGACAGAACCCACCAAGACCTCTAGGGTCCACCTCATTTGTCAGTATCTCC 240
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QY 541 CAAAATTGTAGAGATTTTCTTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCAC 600
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QY 241 CAAAATTGTAGAGATTTTCTTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCAC 300
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QY 601 CTGCATAGCAACTGTGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCCAA--- 657
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QY 658 ---AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCGGGA 714
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QY 715 GCAGTCAGGGGACTACGAGTGCAGTGCCTTCCAAATGACGTGGCGGCGCGTGTACGGAG 774
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QY 421 GCAGTCAGGGGACTACGAGTGCAGTGCCTTCCAAATGACGTGGCGGCGCGTGTACGGAG 480
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QY 775 AGTAAAGTTCACCGTGAAGTATCCACCATACATTTTCAGAGCCAAAGGTGTACAGGTGTCCC 834
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QY 661 ACCTTTCTCTCAAACTCATCTTCTCAATGTCTCTCAACATGACTATGGGAATACAC 720
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QY 721 TTGCGTGGCCCTCCAAACAGCTGGGGCCACACCAATGCCAGCATCATGCTATTGGTCCAGG 780
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QY 1075 CGCGTACAGGAGTGAGCAACGGCAGCCTCAGAGGAGGCGAGGTGCTGCTGCTGCTGCC 1134
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QY 781 CGCGTACAGGAGTGAGCAACGGCAGCCTCAGAGGAGGCGAGGTGCTGCTGCTGCTGCC 840
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QY 1135 TCTTCTGTCTTGTGACCTGTCTTCAATTTTGA 1168
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QY 841 TCTTCTGTCTTGTGACCTGTCTTCAATTTTGA 874
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RESULT 7
AL533026
LOCUS
DEFINITION
Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CSODN005YD20 5-PRIME, mRNA sequence.
ACCESSION
AL533026
VERSION
AL533026.2 GI:31070858
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```


NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW779 row: d column: 04
High quality sequence stop: 849.
Location/Qualifiers
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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match.	49.7%;	Score 834.8;	DB 10;	Length 1039;
Best local Similarity	69.6%;	Pred. No. 4.3e-09;		
Matches 964;	Conservative 0;	Mismatches 37;	Indels 385;	Gaps 71;
QY	176	GCAATCTC-----ACGG--GGCTGGCT-GCTCTGTGTCT-CTTCCAAGGAGTGCCCGTG	226	
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QY	227	CGCAGCGGAGATGCCACTTCTCCCAAGCTATGGACACGTCGCGTCCGCGAGGGGAG	286	
Db	53	-----C-AGAT-----CTT-----CAGG-----64		
QY	287	AGCGCCACCTCTCAGGTGCATTTTGACAAACCGGCTACCCGGGTGGCTGTGCTAAACGC	346	
Db	65	-----CAGGTGCATTTTGACAAACCGGCTCGCCGGGTGGCTGTGCTAAACGC	113	
QY	347	AGCACCATCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGGCTGTCTCTCTG	406	
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QY	407	AGCAACACCCAAAGCGAGTACAGATCGAGATCCAGAAACGTGGATGTGTATGACGAGGCG	466	
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QY	467	CTTTACACCTGCTCGGTGCAGACAGACAAACCAACCAAGACCTCTAGGGTCCACCTCAT	526	
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QY	527	GTGCAAGTATCTCCCAAAATGTGAGATTTCTTCAGATATCTCCATTAAATGAAGGGAAC	586	
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QY	587	AATATTAGCCTCACCTGCATAGCACTGGTAGCCAGAGCCTACGGTTACTTTGGNACAC	646	
Db	354	AATATTAGCCTCACCTGCATAGCACTGGTAGCCAGAGCCTACGGTTACTTTGGNACAC	413	
QY	647	ATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAATACTTTGGAATTCAGGGCATC	706	
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QY	707	ACCGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAAATGACGTGGCCGCGCCCGTG	766	
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Qy	996	AT-GACTAT--GGGAACCTACACTTTCGTGGCCTCCAAAGCTCGGCCACACCAATGCCAG	1053
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Qy	1054	CATCATGCTATTGGTCCAGGCCCGTCA GCGAGGT- GAGCAACGGCACGTCCAGGAGGG	1112
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Db	882	AGAGCCAC-----AA---TGCCG-----G--AT	899
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Db	900	AG-----GACAG--TCCAGTC-----T-----ACAGCC-C	921
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Db	922	-----CAG--TGTGAGCGAG--CCAAAGAAGA--GCAGGGGCG--CGAG--	958
Qy	1349	TAAAAAGAAATTGAAATTTGCCTTGCGAGATATTTAGGTACAATGGAGTTTCTTTTCCC	1408
Db	959	-----TGA-----GCA-----AGCTA-----GA-----	971
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Qy	1521	ACGTGG	1526
Db	1031	ACGTGG	1036

RESULT 9
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LOCUS
DEFINITION Bi666583.1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5' , mRNA linear EST 12-SEP-2001
mRNA sequence.

ACCESSION
VERSION Bi666583
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health. Mammalian Gene Collection (MGC)
DATE 1 (bases 1 to 865)

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11787 row: j column: 18
High quality sequence stop: 742.

FEATURES

source

1. 865
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/note="Organ: Brain; Vector: pBluescriptR (modified
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insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 45.8%; Score 769; DB 12; Length 865;
Best Local Similarity 96.94; Pred. No. 1.1e-07;
Matches 791; Conservative 0; Mismatches 11; Indels 14; Gaps 14;

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QY 61 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120
DB 110 AATCTATCAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 169
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DB 230 CTTTCAGGGGCTGGCTGCTGTGTCTCTTCAAGGAGTGCCTGCGCAGCGGAGATGC 289
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DB 410 TGCTGGGAATGACAAGTGTGTCCTGGAATCTCGCGTGGTCTCTTCGAGCAACCCAAAC 469
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QY 481 GGTGCACACAGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 540
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RESULT 10
BUI55617

LOCUS

DEFINITION

BUI55617

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BUI55617 856 bp mRNA linear EST 03-SEP-2002
AGENCOURT 7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
5', mRNA sequence.
BUI55617
BUI55617.1 GI:22669149
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13527 row: m column: 16
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FEATURES

source

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Technologies."

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Query Match 45.3%; Score 761.3; DB 13; Length 856;
Best Local Similarity 89.9%; Pred. No. 1.7e-07;
Matches 805; Conservative 0; Mismatches 22; Indels 68; Gaps 25;
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RESULT 11
AY406348
LOCUS
DEFINITION
Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY406348
VERSION
AY406348.1 GI:39762322
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 773)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
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TITLE
Gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 773)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Location/Qualifiers
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Query Match 45.1%; Score 757.6; DB 29; Length 773;
Best Local Similarity 98.4%; Pred. No. 1.5e-07;
Matches 761; Conservative 0; Mismatches 6; Indels 6; Gaps 1;

QY 301 GTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGGAGCACATCTCTA 360
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TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 695-690 (2001)
5

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2768)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imorani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, O., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, I., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

TITLE
JOURNAL

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
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misc_feature
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Matches 1255; Conservative 256; Indels 1276; Gaps 265;

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DB 324 AACTC---GCCGAGGCCACCATGGTCGGAGAGTTTCAGCCCGATCGAAACAGATTGCCGCT 381
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DB 495 AGGTG---TGTGGTAGAAGACAA---GAACTCA--AGAGTGGCTGGTTGAACCGCTCT 545
QY 347 AGCACCATCTCTATGTCTGGGAATGACAAGTGGTCTGGATCTCGGCTGGTCTCTCTG 406
DB 546 GGCATCACTTC---GCTGGACATGACAAGTGGTCTCTGGACCCCTCG---GGT-----TG 594
QY 407 AGC-----AA--CACCACAAAGC-----AGTACAGCAT--CGAGATCCAGAGACGTGGATGTG 454
DB 595 AGCTGGAGAGAGCGCC---ATGCTCTGGAATACAGCCTCCGA--ATCCAGAGTGGATGTC 650
QY 455 TATGACAGAGG---CCCTTACACCTGTCTGGTGGAGAGAGACAAACCA-----CCAAAGACC 508
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VERSION
AY318958.1
KEYWORDS
HTC.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM

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Rattus norvegicus Aal064 mRNA, complete cds.
AY318958
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HTC.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.
 1 (bases 1 to 14278)
 Xu, C.S., Li, W.Q., Li, Y.C., Wang, G.P., Chai, L.O., Yuan, J.Y.,
 Yang, K.J., Yan, H.M., Chang, C.F., Zhao, L.F., Ma, H., Wang, L.,
 Wang, S.F., Han, H.P., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
 Liver regeneration after PH
 Unpublished
 2 (bases 1 to 14278)
 Xu, C.S., Li, W.Q., Li, Y.C., Wang, G.P., Chai, L.O., Yuan, J.Y.,
 Yang, K.J., Yan, H.M., Chang, C.F., Zhao, L.F., Ma, H., Wang, L.,
 Wang, S.F., Han, H.P., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
 Direct Submission
 Submitted (09-JUN-2003) Henan Bioengineering Key Lab, Henan Normal
 University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
 China

FEATURES
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ORIGIN

Query Match 42.2%; Score 707.7; DB 11; Length 14278;
 Best Local Similarity 38.5%; Pred. No. 0.079;
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AV321317
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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JOURNAL
FEATURES
SOURCE

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AY321317.1 GI:32527694
HTC.
Rattus norvegicus
Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 14278)
Xu, C.S., Li, W.Q., Li, Y.C., Zhao, L.F., Ma, H., Wang, L., Wang, S.F.,
Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J., Yan, H.M.,
Chang, C.F., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
Liver regeneration after PH
Unpublished
2 (bases 1 to 14278)
Xu, C.S., Li, W.Q., Li, Y.C., Zhao, L.F., Ma, H., Wang, L., Wang, S.F.,
Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J., Yan, H.M.,
Chang, C.F., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
Direct Submission
Submitted (11-JUN-2003) Henan Bioengineering Key Lab, Henan Normal
University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
China
Location/Qualifiers
1. 14278
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41. 14272
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QY 603 GCA-----TAG-----CAAC-----612
Db 2054 TCACCTTGATCTCTTTGAGATTGGTTAGAAAGAAAGGGCTTTGAGCAACACTGGAAGCT 2113
QY 613 -----TGGA-----GA-----CCAGA-----GCCTAC-----GG-----T-TACTTGG-----640
Db 2114 CTTTGTGGTAAGCAAGGATCTCTCCAGACAGAGTGTCACAAAGGCTTTGTA-TTGGGTCAA 2172
QY 641 -----AG-ACACATC-----TCTCCCAAGCGG-----TTGG-----CTTTG-----671
Db 2173 TGGTCAAGTTCCAGATCGTGTCTCC-AA-GGTCTTGGTAGACCACCTTTGGCTACACTA 2228
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QY 692 -----GAAAT-----CAGGGC-----ATCACC-----C-----GG-----712
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QY 713 -----GAGC-----AGTCAGG-----GGA-CTAGAGTGC-----AGTCCCTCC-----AATG 749
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QY 896 TG--GTACAAGATGA-CAAA-----AGACT-GA-T-----921
Db 2695 CGGTGTTCA--GATGAATACAAACTTCTTCCAGAGTCAGGCCCTGGAGGCTCGAGTGGCC 2752
QY 922 -TGAAG-----GAA-----A-----GAA-AGG--GGTCAA-----942
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Db 2813 AGTGGCAGCAACGCTGCACCTGGT--CTTACCAACCAAAACGGAAGTGTATCCACCTT 2870
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QY 1044 CCAATGCCAG-----CATCATCTAT-----TTG--GTCCA-----GGCGCC 1078
Db 2984 CCCTGACAGAGACA-CAAGGTATGAGCTGGAGTTGAAGCCCAACAGGAGAGGTGGAGCA 3042
QY 1079 G---TCAGCGAG-G-----TGAGC-----AA-CGG-CACGTC-----1104
Db 3043 GTATTCGCCAGTGCACCTATGAGTCTCTTAAGAGAGCAAGTCTTTTGGTTGACACACT 3102

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Db 3103 GAAGTTCTCTAGTGCAGCAGAGAGGAGTCCAGCAGTCTGAAGCTTACTTGCATGTTCAATA 3162
QY 1140 ---T-----GG-----TCT-TG-----C-ACC-----TG-----CTT 1156
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QY 1157 -----CTCAAAATTT--TGATG-----TGAGTGC-----CACTT-C-----CCCA- 1187
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QY 1209 -----CA-----CC-ACCAC-----CAA-CACAA--1225
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QY 3226 CAGCAAT--GG--CAACACCGACAG-----CAACCAATCAGATATATACAAATGAA--A 1273
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Db 3520 GAAATCGAATTTGATTTGGAACACGGGACCAATGTGATACCAAAAGGTGGGCTCCAA 3579
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Db 3580 T--TTCCCTGTG-----GATCTTTCCTGTTATCTTAGATGTCATGATGATGCCA 3630
QY 1360 T-----TG-----A-AAATTTGCT-TG-CAGATA-----TTTAGGTACA-ATGG-----1394
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QY	1251	CAATCAGATATATCAAAATGAAATTAAGAAGAAACACAGCCTCATGCGACAGAAATTTGAG	1310
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QY	1551	AATTCATCAGTCCATAGACAGAAACAGATGAGACCTTCGCGCCCAAGCGTGGCGTGC	1610
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Db	4	AAAA 1	
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BC049868			
LOCUS			
DEFINITION	BC049868	4667 bp mRNA linear	HTC 17-DEC-2003
ACCESSION	BC049868		
VERSION	BC049868.1	GI:29437204	
KEYWORDS	HTC		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 4667)		
	Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,		
	Altshul, S.F., Zeeberg, B., Buetow, K.H., Schenken, C.M., Schuler, G.D.,		
	Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,		
	Diatchenko, L., Marudina, K., Farmer, A.A., Rubin, G.M., Hong, L.,		
	Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,		
	Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,		
	Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,		
	Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,		
	McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,		
	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,		
	Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,		
	Pahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,		
	Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,		
	Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,		
	Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., R.M.,		
	Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,		

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 4667)

Strausberg, R.
Direct Submission
Submitted (31-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mgc@nih.gov

Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Shantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, J.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 99 Row: h Column: 5

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 6678965

This clone has the following problem: frame shifted.

Location/Qualifiers

1. 4667
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5097177"
/tissue type="Liver, normal. 5 month old male mouse."
/clone_lib="NCI CGAP_Li9"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"

ORIGIN

Query Match 41.8%; Score 702.2; DB 11; Length 4667;
Best Local Similarity 37.0%; Pred. No. 0.0022;
Matches 1441; Conservative 0; Mismatches 169; Indels 2284; Gaps 409;

QY 1 GT-----TTGT-----T-CC-----TT-CAG--CA-----AAAC 20
DB 838 GTGACTGTCATGTGGAAATATACCTATGGAAGCCTGTTCCAGGACATGTGAAGATAAAC 897

QY 21 -----AG--TGGAT-----TTAAATCTC-----CTTG-C-ACAA--GC 47
DB 898 GTCTGCGGTGAGCTGAGCTGGATGCGAGAGTCAATTCCTCAGCTAGACAACAATGGC 957

QY 48 TTGAGAGCA--ACACAA--T-----CTATCA--G-G-----AAAGAAA--CAA----- 81
DB 958 T-----GCAGTACACAGAGAGTGAAC-ATCACTGAGTCCCATCAAGAAAGGAATAT 1011

QY 82 -AG-----A-----A--AA-----ACCGAA----- 95
DB 1012 GAGGTTCAGCTTTTCCATGTGAATGCAACTGTTACAGAGAGGGACAGGATGGAGTTC 1071

QY 96 ---C---CTG--ACAA--AAAA--G-NAGAA-----AAAGAA-----GAAG--- 123

DB 1072 AGTCGATCTGGACCAACATAAATTTGAAGAATATCAAAACAGCTCATATTTCTGAAGCA 1131
QY 124 -----A-----AAAA--AAT--CA-----TGAAA-----ACC-----ATCCAG 148
DB 1132 GATTCACACTTTCAGACATGGAATTCATTTCTTTGAAAGTCCGCTAGTGATATCAAG 1191
QY 149 -----CCAAA-----AATGCACAA-----TT--CTAT----- 168
DB 1192 GGAGACCTATCCCAATATGAGAAAGTCTTATCAAGACCAAGAACTTTAGCTATACCAGT 1251
QY 169 ---CT---CT-----TG-----GGCA-A--TCT-----T--CAC--G-----G 188
DB 1252 GCTACTACCACTGATCAGATGGCTGCGAGAGTCTCCATAGATACACATGATCTCG 1311
QY 189 GGCT-----GG-----C-TGCT--CTGTGTCTCT 209
DB 1312 GGCTCTTTCCCTCCATATCAAAAGTCAACCAAGAGGAAGATTTCATGTTCTTATTTCTAT 1371
QY 210 TCCAAGGAG-----TGCCCGTGC--GCA--GGG--AGATGC--CACCTTCCC--- 249
DB 1372 TGCATGGAGGAAAGACATGCAAGTCAAGATGTGGCTATGCTGTTTAC--TCCCTCA 1429
QY 250 -CAA-AGCTA-----TGGACA-----AC-----G---TG----- 268
DB 1430 GCAAGAGCTACATCTTACCTTGACACAGAGACCAGCAGCATCTTGCCTTGCAACCAAGATTC 1489
QY 269 --AC--GGTCCGGCA-----GGGG-----AGAGCGC----- 291
DB 1490 ACACAGTTTCAGGCAATTTTATTCTGAAGGGGAGCTTGGGAGTCTGAAAGAGCTCATTT 1549
QY 292 -C-AC--CC--TCA--GGTGCA-----CTAT--T---GAC-----AAC-----CGGCTAC 324
DB 1550 TCTACTACTTGGTCTATGCGCGAGGAAGC-ATCATCCAGATGGAACCATAC--TCA-- 1604
QY 325 CCGGGTG--GCCTG--GCT-----AAA--CC-----G---C----- 346
DB 1605 CCAGGTGGAGCCAGGAGAGCTCCAGTAAAGGAAATTTGCCCTTGGAGATCCCTGTGGA 1664
QY 347 ----AGCA-----CCA-----TCTCTTA-----TG-CTGGGAAT--GACA 374
DB 1665 GTTTAGCATGGTCCCAATGGCTAAATGCTCATCTACAGCATCTTGCTG--ATGGAGA 1721
QY 375 AGTG--GTGC-----CTG-----GA-----TCCTGCG-----GTGG----- 398
DB 1722 AGTATTCAGATCTCTTAACCTTGAATTTGAAGTGTCTTCGCAACAAAGTGGACCT 1781
QY 399 ----TC-----CTTCTGAGCAA-----CACC-----CAAAAC-----GCA--GT--ACAGC 430
DB 1782 GCGCTTCAGCATTCT--CAAAAGTCTTCCGCTCTCAAAACCCGCTGCGAGGTTCACAGC 1838
QY 431 ATC-----GAGATCC-----AGAAC--GTGA-----TGTC--TA-----TGA--- 459
DB 1839 TTTCTCTCAG--TCCCTTGTGGCTGAGAGCTGTGGACCAAGAGTGTGCTACTCTCTGAAC 1897
QY 460 -CGAG--G-G-----CCCTT-----AC-ACCTGTCTGG--TGCACACAGACAA-- 495
DB 1898 CCGAGTCTGAGCTCTCCCTTCTCGGATATAGATCTGCCAGGTATGCAACAAACAAAT 1957
QY 496 ----CCA-----CCC-----AAAGACC-----TCTAGGGTCCACCTCATTTGT 528
DB 1958 TCGTTCAAGTCTCCGCTCTGTGAAAGACCAAGAGACTGTATACTGTACAGTTCATGGT 2017
QY 529 -----GCA-----AGTATCTCC--CA-----AA-----AT 546
DB 2018 TGGCTGAGAGCACAAACTTAGTA--CCACATGGAACGTGAGAAGGATGTCTATAGAT 2074
QY 547 -TGTAGAG--A-----TTT-----C--TTCA-----GAT--ATC-----TCCATTAA-- 576
DB 2075 ATGTGGAGGACATGGGGTTTAAACAGCATTCACAACTTGATGATCAAACTTCTTATATTT 2134
QY 577 ----TGA--AGGAA-----CAATATTAG--CCTC-----A--CCTGCAT--- 606
DB 2135 GTTTTGACTATGGCATGGTTCCAATATCAGCACCTCTGTGTGGAATTTGATCTTGCATTTA 2194

QY 607 -----AG-----CAAC--TG-GT-----AGACC--AGAGCC----- 627
Db 2195 CCCCCTGAAATTCCTGGAGTTTACGCCAACATTTAGTAAAGAGACCTTGAGAGCCACCAC 2254
QY 628 -TA-----CG--GTT--ACTT--GGAGACACATCTC-----TCC-CA 656
Db 2255 GTAAAGATCCATCATCAATGAATGATCCATTTACAGAGAC-CAT-TGAAATATTTTCTCGA 2312
QY 657 AAGC--GGT-T-GGCT--TTGT--CAGTGAA-----GAC-----GAATACTTGGAAAT 696
Db 2313 AACCTGGGTCTGGATATAGTACAGTAAACTCCACAGGACTGGCTGAA--GTGGAAAT 2369
QY 697 ---TC---AGGCATACCCCG---GGAGCAGTCAGGGGACT-ACGAGTGCAGTGCCT 743
Db 2370 GACTGTCCCTGACACCATCA-CAGAAATGA-AAGCAGGAG-CTCTC--TGC-TTG--T 2419
QY 744 CCAATGAC-----CTG-----GCC-----GC----- 759
Db 2420 CCAATGACATGGCCTTGGCCTCTCTTCTGTGTGTACCTCTCAAGCCTTCAAGCCTTCT 2479
QY 760 -----GCC-----GTGCTAC--GGAGA-----G-TAAAGTCA 785
Db 2480 TTGTGGAGTCTCATTTGCCCTATCTGTGTGTCTGGAGAGCCTTCATGCTCAAGGCCA 2539
QY 786 CCG---TGAATAT---CCAC--CATACA-----T-TTCA---GAAGCC----- 817
Db 2540 CTGTGATGAATCTATCTCCACAGCATGCAATGAGTGTGAGTGTGAGGCTCTCTCTG 2599
QY 818 AAGGGT---ACAGGTGTCCTGGGA-----CAA-----AAG 847
Db 2600 A-----TTTCAAGTGTCCAGTGGGAGACGACCAAGATTTCTTACTGCTCAGTGCCAAT 2655
QY 848 GGA-----CA-----CTG-----CA----- 858
Db 2656 GGGAGGCACACCTCATCTGGCTGGTAACTCCCAAGTCTTTAGGGAATGTGAATTTCTCT 2715
QY 859 GTCT---GAAG-----CCTCAGAGTCCC-----CTCAG-----CAGAATTC 892
Db 2716 GTGTCTGGGAGACACACAGTCTCTCAG-AG-CCCTGTGGTCTGAGGTGGCCACAGTTC 2773
QY 893 C-----AGTGTACAGGATGACA-----AAAG-ACTGAT-----TGAAGGA--A 929
Db 2774 CTGAATCTGGAGAA--AGGACAGTAGTCAAGTCTCTGAGTGTGAGCCTGAAGGAATCA 2831
QY 930 AGAAGGG-----GTGAA--AG-----TG-----GAAACA 953
Db 2832 AGCAAGAGCATACCTTCAGTCACTCTGTCTGTGTCATCAGATCTGAGATATCTGAATAA 2891
QY 954 -GACCTT--TCCCTCA-----AAA-----CTC----- 973
Db 2892 TGTCCCTGGTCTCCACCAAGTAGTGAAGATTCAGAAAGGCCATTTCTCTGTGA 2951
QY 974 -----ATCTT--CTTCA--AT--G-----TCTC-----TGAAC-ATG 998
Db 2952 TGGGTGATATCTTGAGTTCAGCCATAAGAAACACACAAAACCTTCTCCATATGCCCTATG 3011
QY 999 ACTAT--GGA--ACTACATTTGGTGGCCT-----CCAACA--A-G--CTG----- 1036
Db 3012 GCTGTGGGAGCAGAAC--TG-GT--CCTTTTGTCTCCCAACATCTACGTACTGAATA 3066
QY 1037 ---G---GCCACCAATGCCAGC-----ATCATG-CTA-----TTTGT--C 1070
Db 3067 TCTGAATGAAC--CCAA--CAGCTGACTCAGAAAGATCAAGACTAAAGCCTTGGGTTC 3122
QY 1071 -CAG-GC-GCCG---TCAGCGAG-G-TGAGC-----AAC-----GGC---AC-GT-- 1103
Db 3123 TCAGAGCTG--GTATCAGAGAGCTGAATACAAACACAAAGAGTGGCTCTCAGTGC 3180
QY 1104 -----CG--AG-GAGGG---CA---GGCT-----GGCTCTG-GCT--- 1128
Db 3181 CTTCCGGGATCAAAATGGGAAAGAGAGAAACACTTGGCTCAGAGCCTTTGTCTCA 3240

QY 1129 -----GCT---GCC-----TCTT----- 1138
Db 3241 GTCTTTTCCCAAGCTCGAGCCTTCACTTTCATGATGAATCACATCACCATGCCCTT 3300
QY 1139 ---CTGG-TCTT---GC-----AC-----CTGCTT---T 1158
Db 3301 CACCTGGCTCTCCCAAAAGCAGAGGACCAATGCTGCTCCGGAGCTCCGGATCATGTT 3360
QY 1159 CAA--AT---T-----T-----TGATG--TGA-----GTGCC-ACTTCCCCA- 1187
Db 3361 CAACAATGCCATGAAGGGGGAGTAGATGATGAATGACCTCTCTGCTTACATAACCAT 3420
QY 1188 ---CC--CGGGAAG--GCTGC--GCCAC-CA-----CCA----- 1213
Db 3421 GGCCTTCTGGAAGTTCACTCCAGCCAGCATCTGTGTCTCCAAAGCCCTGAGCTG 3480
QY 1214 -C-----CA-CC---AACAC-----AACA-----GCAATGGCA-----ACACC-- 1241
Db 3481 CCTGGAGTCATCTCTGGAAGACCATAGAACAGAAATGCCAGCTTTGTGTACACCAA 3540
QY 1242 -----GA---C-A-----GC-----AAC--AATCAGATATACAAA-- 1268
Db 3541 GCTTTGATGGCTATGCTTTTGTCTGTGGGGGAACCAAGATAAGAGAT-GAATCC 3599
QY 1269 TGAA-----AT-----TAGAAGAA-----CAC-----AG-CCTC 1292
Db 3600 TGAAGTCATCTGATGAGNAGCTATAAAGAAAACAACCTCTATCCACTGGAAGACCTC 3659
QY 1293 ATG-----GGA---CAGAA---ATTG-----AGG----- 1311
Db 3660 A-GAAATCCAGGAATCTGAACACCATTTGTACAAACCCAGGCTTCTCTCTGAGTA 3718
QY 1312 GAGGGGA--CAAA----- 1325
Db 3719 GAGATGATGCATATGTGTCTGCTGCTCACTGCCCAGCCAGCCCTCCCTGAG 3778
QY 1326 -AT---ACTTTG-----G-----GGGG-----AAA---AGAGTT-- 1347
Db 3779 GATCTGACTTTGCTCAATGAGCACCATCATGTGGCTCACAAGCAACAGATTCATGTT 3838
QY 1348 ---TT-----AAAAAGAAA-----TTGA-----AAAT----- 1367
Db 3839 GGCCTTCTCTCCACACAGSACACTGTGTGGCCCTTGATGCTCTCTCCAAATATGAGCA 3898
QY 1368 -TGCCCT---G-CAG--TATTTAG--TA--CAAT---GGAGTTTC 1401
Db 3899 GTGACTTTTTCAGAAAGTCAAGAAAACCTATTTGTGTGACTATCCATCTACAGG-G--TC 3954
QY 1402 -TTTTCCCAACG-----GGAAGAAC-----ACAGCA--C-- 1428
Db 3955 ATTTTCCCAAGTTCCAAAGTGG-AGAACAGTAAATCGCTGTACTACAGAGTCCGAT 4013
QY 1429 -ACCCGGC-TT-----GGAC-----CCA-C-----TG-C-----CTGC-- 1455
Db 4014 TACCAGACATCTCTGGGACTATACCATCAGTGTGTGAGGGAAGGATGTGTGTATGCTC 4073
QY 1456 ---ATCGT---CAAC---CTCTTTGTG--CCAG-TGTGGGCA-----AGG 1491
Db 4074 AGACTATCTGAGATACAAATGCAC-TTGGAGAAGCAGCTGTCTGCAATTTGCTATATGG 4132
QY 1492 CT-----CAG--CCTCT--CT-----GCC-----CA 1508
Db 4133 GTACAGACAGTACCTCTTAACCTTGTAAATACCCCAAGGCCAACAGCTTCCAGATCTCA 4192
QY 1509 C-AG-----AGT-----GCC-CCAC-----GTG-----GAAC 1529
Db 4193 CTGAATAATCAGTTACACAGGAGCGGCCAGCTCCCAACATGCTGATGTGTGAAG 4252
QY 1530 ATCTGAGCTGG--CCATCCA--AATTAATCAGTCCA-----TAGAG 1570
Db 4253 ATGCT--ATCTGGTTTATCCCATTTGAACCAA-CAGTGAAGAGCTTTGAAGATTAGAG 4309
QY 1571 -AC-----GAACAGAA-TGAG-----AC-----CTT-----CC 1591


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Db 4310 CACGTCAGCAGAACAGAGCTGAGCACAACATGCTTAATATATTTGGATCAGGTGACC 4369
QY 1592 -----GGCC-----CAAG-----1599
Db 4370 AATCAGACACTGGCCTTCTCCTTCATCAATCAACAGATATCCAGTAGGAACCTGCAG 4429
QY 1600 -----G-----C-----G-----TGSC-----GCTG-----1609
Db 4430 CTGCGCAATGTGAAGTCTATGACTACTATGATGAGACAGATGAATGGCTTTGCTGAATAC 4489
QY 1610 -----CGG--GCAC-----TTTG-----GTAGAC-----1626
Db 4490 AGCAGCCCTGCGCAGCAGACACAAACAAATGTTTGAACCTCTATTTGTAGACAAGGCAT 4549
QY 1627 TG-TG-----CCA--CCA-----C-----GGCG--TGTC-TTG-----TGAA--1652
Db 4550 TGCTGGATCCCGACGCCAGGAACCTTCAAGATGGTGATTTGTGTTGCTCTGAAATA 4609
QY 1653 -----ACGTGAA-----ATAA--AAA-----GAGCAAAAAAAA 1679
Db 4610 CAACTAC-TGAACAAGCTTGATAAATAATGCTAGTCTCTCGAGAAAAAAA 4662

RESULT 19
BC044081
LOCUS
DEFINITION
Xenopus laevis, 5570 bp mRNA linear HTC 19-FEB-2003
IMAGE:4682702, mRNA.
ACCESSION
BC044081
VERSION
BC044081.1 GI:28422174
KEYWORDS
HTC.
SOURCE
Xenopus laevis (African clawed frog)
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
1. (Bases 1 to 5570)
Klein, S. and Strausberg, R.
Submitted (13-JAN-2003) National Institutes of Health, Xenopus Gene
Collection (XGC), National Institute of Child Health and Human
Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
20892-7510, USA
NIH-MGC Project
Contact: XGC help desk
Email: cgapbe@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 94 Row: d Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein
This clone has the following problem: frame shifted.
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/notes="Vector: pcMV-SPORT6"
FEATURES
source

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ORIGIN

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Query Match 41.8%; Score 701.1; DB 11; Length 5570;
Best Local Similarity 39.2%; Pred. No. 0.0043;
Matches 1393; Conservative 0; Mismatches 174; Indels 1985; Gaps 389;

QY 1 GTTGTGTCC-----TTGAGCA--AACAGTGGATTTA--AATCTCT-TGC-AC-----43
Db 1501 GTTGTGCCCCAATAATTTAGCTATTATCCCTGGA--ATGGGAATC-CCTGAGCAACTGAA 1556
QY 44 AA--GCT--TGAGAGC--AACA-----CAA--TCT-----A 66
Db 1557 AATGCTATG-GAGCAGGAACAATGGTAAAGAGAGTCAAGTCTCTGTGAGATGACCA 1615
QY 67 T--CAGG-----AAAGA-----AAGA-----83
Db 1616 TACCAGGGCTTGAAGTGGGGATGGAAGAAGTAATGCAAAAAAGACCAGAGAAGATGCTCTC 1675
QY 84 ---AAAA-----AAACC-----92
Db 1676 AGAAAAAGTTCCCTATGTCTAAACCCATTCGGGTCTAGTTCACAGAGGCATGGATGCAAA 1735
QY 93 -----GAA-----CCTGAC--AA--AAAAGAA-----110
Db 1736 ACAAAGTACCGTAATGCCACCGTCAGAGAGAGTCTCTGACCTTAGAGAGAGAAATGT 1795
QY 111 --GA--AAAAGAGAAGAA--A-----AAAAT--CATGA-----AA--AC 141
Db 1796 CTGATGAAAAGAGAGAGAACCCAGCAGAGATTTGACAGAGATGGCAGCTTTTACAATATAC 1855
QY 142 C-ATCC-----AGC--C-----AAA-BAT-GCACA-ATTCTATCT--170
Db 1856 CAATCTCAGCTGCTGGAGCAACTAAAGATAGAAAAGATAGCAGAGCAAGCTGAGAC 1915
QY 171 -CTTGGGCAATCTTCA-----CG--GGGCTGG--CTGCTC-TGTG-TCTC-208
Db 1916 ACCTGGGCAA-CTTCAGGGTCTCCATCTCGTTGGG-TGACCTTTCACATGGCCCTCA 1973
QY 209 ---TTCCA-----AGAGTGCCTCGT--GC-----GCA--GGGAGAT--G--CC 241
Db 1974 ACATTCAGGCTTCAGGA-----CC-TAGCCACAGCAAGCAAGATTCACAGAGCCCC 2028
QY 242 ACCTTCCCCAAAGC--T-ATGACAAC--GT-----GAC-----270
Db 2029 ACC--CCCCACAGCAGATGATGTGCAACATGTCTCTGAGAGACAGTTTCTTCCACAAG 2086
QY 271 -----GGTCC-----GG-----CAGGGGAGAG--C 289
Db 2087 ATCTCAAGCAGCCCCAGGTCCACAAAATTTTATGTTTCTGTGTCACAGGGGTGAGGTC 2146
QY 290 GC-----CACCTCAGGTGCA-----CT-----ATG-----A 312
Db 2147 TCAAGAAATGCATCCT--GGTGAAGTAGACTACCAAGTTCTCATGACCAATTTGGTGA 2204
QY 313 CAACCGGGTCACCCGGGTGGC-CTGG-----CTAAA-----CGCAG-----CACC-352
Db 2205 CAA--GGTCCCCAGTAACTCTGGGCCACAAAATCAGTTAGGGCTCAGGGGCCATCT 2261
QY 353 -ATCCT-----CTATGCTGGGAATG-----A--CAAG-----TGTTGCC 383
Db 2262 GGTCTAGACCTATTCAAGGAATGCTCTCTCACCATAGCATGCAAGGGGCACCTGGT-CC 2320
QY 384 T--GGATCCTC-----GGGT-----GGTC-----CTTCTGA 407
Db 2321 TCAAGGA-CTCTTATGGGAGTTACTCCAAGGGAGGTCCGATGCCACATGGACTTTC-GA 2378
QY 408 GCAA--CA--CCC-AAAC-----GCAGTA-----CAGCATC-----GAGA--437
Db 2379 GAAAGCTCAGGCCCTTAATCAAGGTATGGCAATAGTGCATCCAGCA-CAAGACATGAGAG 2437
QY 438 ---TC-----CA-----GAAGTGG-----ATGTG-----TATG--AC--GAGG 464
Db 2438 CCCCTCTGGAGCAATAGTTGGACATGGAAGATATGGGAGCCCTTATGGAATCTGAGAGG 2497

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Db 2498 GCCCTCAGATATGCGAGGACACAGGAATAAGAGAGTCCCTGCGAGCTTAAG---AGACC 2554
QY 501 CAAGA---CCTC---TA-----GGGTCCACCT---CAATTGTG-----CA 531
Db 2555 CAATGATATGCGGGCCCTCAGGATATGAGAGGGGC---CCTGACA---TGCAGGCCCTCA 2611
QY 532 AG-TATC---TCCCAA---A-AT---TG-----TA-GAGATTCTTCA-GATAT 567
Db 2612 AGATATCAGGTTACCAATGAGATATGCGTGTCTCAGGATATGAGAGTCCCTCATGATAT 2671
QY 568 -C---TCCATTA---ATGA---AG-----GGAA-----CA-ATATTAG-- 594
Db 2672 ACCTGTGCC---TCAAGACATGAGGAGTCCCTCTGTTAGGTTGCTCCTCAGATATTAGGG 2730
QY 595 -CCTC-----ACC-----TGC----- 604
Db 2731 GACCTCAGATTTGCGTGGGGCTCAGGATATTAGGGAGCCCATGATATCGTGGACCCC 2790
QY 605 ---ATA-----G---CAACTGGTAGACACAG-CC-----TA---CGG-----TTA 635
Db 2791 AAGATATGAGGGTCCATCTG---ATATCAGAGGCCCCACAGATATGCGGGGGCCCCAAGA 2848
QY 636 CTTG-GA-GACAC---ATCTC-----TCCCA-----AAGCGTTGG--CT-----TTGTG 673
Db 2849 CATGAGAGGACCCCATGATATCAGGGGCCCCACAGATATGCG---TGGCCCTCAGGATATG 2906
QY 674 AGTGAAGAC---GA-ATACTTGG-----AA-----AT----- 696
Db 2907 AGGG---GACCCCGAGATATGATGCGCCTCAGGATACAGAGACCCCGAGACATGCGTG 2964
QY 697 ---TCAGGGCATC-----ACC-----CGGAGCAGTCAAG--GGA- 726
Db 2965 GCCCTCAGG---ATCTTAGGGGACCCCGACAGATGCGTG---GCCTTCAGGATATTAAGAGGAC 3021
QY 727 CTACGAG---TGAGTGG---CC-----TCCA-----ATGACGTGGCCGC- 759
Db 3022 CTATG-GACATGC-GTGGGCCCAAAACATGAGGGGTCCAGGTGACATG-CGTGGCCCCC 3078
QY 760 -----GCC-----CGTGGT---AC-GGA---GAGTAAGTGC----- 784
Db 3079 AAGATATGAGGGGTATGCTGTGATGCGAGGTCCAGAGGATATGAG---AGGTCTCTCTG 3135
QY 785 AC---CGTG-----AA-CTAT-----CCACC-ATA-CAT-TTCAGAAG----- 815
Db 3136 ACATGCGTGTCCACCAAGATATGCGGGACCACTGATATGCGTGTCCACAGATATGCG 3195
QY 816 -----CC-----AAG---GGT---ACAGG---TG-----TCC-----CCGTGG-- 839
Db 3196 GGGGACCTCTGATATGCGTGTGCCACAGATATGCGGGGACCTCTCTGATATGCGTGTGC 3255
QY 840 GACAAAA---GGGGA-CAC-----TGC-----AG---TGTGAG-----CCT- 869
Db 3256 CACAAGATATGCGGGACCACTGATATGCGTGTTCACAGATATGCGAGTCCACCTG 3315
QY 870 -CA-GC-AGTCCCTCAGCAG-AAT-----TCC---A---GTGG---TACAAG- 904
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QY 905 GATGACAA-A---AGA-----CTGA-TTG-----AAGGA-AAGA 932
Db 3371 TATG-CAAGGACCTCCAGATATGCGTGTCCACCTGACTTGGTGTCTCAGGATATG- 3428
QY 933 AAGGGGT---GAAA---GTGGA-AAACAGA-----CCTT----- 959
Db 3429 -AGGGGTCAATCAGAAATGCGTGGACACCCAGATATGCGGGCCCTTCAGGACATAAGAGG 3487
QY 960 ---TCC-----TCTCA-----A-----AACTCAT-----CTT 978
Db 3488 CGGTCCGAGCTTGCAGGTGC-CACCAGACATGCGTGGACCTCATGATTTAAGGGGACCTC 3546

QY 979 CTTCAATGTCTC-TGAACATGAC--TAT--G-GG--AACTACACT-----TGCGTGG-- 1022
Db 3547 CTGAATG---CGTGGACATCAGATATAGAGGTCAAC---CTGAATGCGTGTGTCAT 3599
QY 1023 -----CCT-----CCACACAGCT---G-GGCC----- 1040
Db 3600 CAGGATATGAGGGTTCCTCTGATATGCGCCCTCAAGATATGAGAGGCCCGCAGGAGATG 3659
QY 1041 ---ACACCAA-----TGCCAGCAT--CATGTATTGTG-GTCCAGGCGCGTCTCAG--C 1084
Db 3660 AAGAGACCAAAAGATATGAGAGCATCCCATG--ATATGCGT---GGC-CC-TCAGATAT 3712
QY 1085 GAGG---TG--AG-CA-----AC-----G-GCA-----C-G-TC-GAGGAG--G 1111
Db 3713 GAGGGCATGCGAGACCATGAGCCACAGAAATAAGAGCATCCCTGTCTGAGAAGCCC 3772
QY 1112 GCAGG-CTGCG--TCT-----GG--CTGCTG-----CCTC----- 1136
Db 3773 TCAGGATTTGCCAATCTACAGGATAGTAGGGGACCTCTGACATTTGTTGGCCCCCAGGA 3832
QY 1137 -TT-----CTGGTCTT-----GCACCT----- 1152
Db 3833 TTTAAGAGCCCTCAGCCTGGACTTTTCAAGAGAACTCCCAAGGACCTCATAGCCAGCA 3892
QY 1153 -----GCTTCTCA-----A-ATT--T--TGATG----- 1170
Db 3893 GAACAGGCACGAGCATCTCACCCAGCACAAAGAGGACCATTTACTGGGAGATGGACC 3952
QY 1171 -----T-----GAGTG-----CCTTCCCC--A-CCC-----GG 1192
Db 3953 CAGGCCTTTAAACAGAGTGGAAAGGTTCAGGCCCCACCTCCCTGTATCCCTGGCCTTAG 4012
QY 1193 -----GA-----AAGG-C-TGCCGCCACCA---CCA---CC-ACCA-----ACA- 1222
Db 4013 ATCAGAGATTTCACAGGACGTG--GCCATCAGGTCCAAGCCCTTAACAAAGTGTGACATC 4070
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Db 4071 CGTGTCTCTCAACCATCAGTTAGGCGCAACGAGACCGAAGCGTGAAGCAAGCC-- 4128
QY 1254 TCAG--AT-----AT-----ACAA-A-----TGAAATTT-----AGA- 1281
Db 4129 -CTGACCATGCGCCATTCTATGGCGGACAGAGTGGGTG--ATTCCGAGACACAGAG 4185
QY 1282 -AAC-----ACAG-----CCTCA--TG-----GGACAGAA----- 1303
Db 4186 GACCTTCTGACAGACGGGGCCCTCACCCTGATTTCTCAGAGAGCCAGAGATTTCTCCTC 4245
QY 1304 -----ATTGA-----G-GGAG----- 1315
Db 4246 CAGATGATCGGTATGTTCCAGCGGGCGTGNATTTGATGAGAGGTGGAGTTCTTCCT 4305
QY 1316 ---GGA-ACAA---AGAATATTTGGGGGA-----AA----- 1341
Db 4306 CTCAGGATGACAGTGGAG--ACGT--GGGGGACCTGCTTCACAGTTTCTCTTAACCA 4360
QY 1342 -AGAG-TTTT---A-AAAAGAA---ATTGAAA-----ATTGCCCTT- 1373
Db 4361 CAGAGATTTCCAGACAGAGAGAACAGGATTCAAATCGTGGAGGGTGAAGGCAATC 4420
QY 1374 ---GCAGATATTTA--G-GTA-CA---ATGGA--GTTTTCTTTTCC-----CAAAACGG 1414
Db 4421 AGAGGAGATATAACCGAGNAITCAGAGGATGAGG--TTACGAGGACAAA-GG 4472
QY 1415 GAAGAA---CACAG-----CACA-----CCC----- 1432
Db 4473 GATGAAGCTTTTCAGAGGCTGTGTCACAAAGCGGTGAAGGGGTGGGTCCCGAGGGAGT 4532
QY 1433 ---GGCTTG--GACCCA-----CTG-----CAA---G-CTGCTATG-TGCA 1463
Db 4533 GAAGGGTTTCTTAACCCAGAGGAATTTGGTCTCTGATGACAAATTTTGACTCCAAAGATG-A 4591
QY 1464 ACCTTTTGTGGCAGTG-TG--GGCA-AG-----GCTCAGCCTCTCTGCCACAG-- 1511

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QY      1547 CCCAATTCATCAATCAGTCC-----AT--AGAGA-----CGAACAGA 1579
Db      4701 -CCTAA--CCATCAGTCCCGAGAAATCAAGAGAAGCTGGACCTGATCACTTTCTTACAG- 4756
QY      1580 AT-----GAGACTTCC-----GG-----CCCA--AGC-GTG-GCG----- 1606
Db      4757 -TCCTGCGCGTACATTCCTACTCTCTGATGGTCATTCCTCCAGCCAGCAGGAGCGATCTT 4815
QY      1607 -----CTGC-GGGCACTTTGGTAGAC-TG-----TGCCACCAC-----GG-CGTG-- 1643
Db      4816 CTTCACTCAGGGCA--TG--GACATGGCTTCCTTACCCCCAGCAAAAGGCGCTGGC 4869
QY      1644 ----TG-----TTGTGAAAGCTGA-----A-AT--AAAAAG-AG-----CA-AA 1673
Db      4870 ACGATGGCGCTGCT-ACACCTGACCACAGGAGACATGGACACAGAGGGGGGGCCACCAGAA 4928
QY      1674 -AA-----AAAA 1679
Db      4929 GAACCTGTAAAA 4940

RESULT 20
LOCUS      AY418622
DEFINITION Mus musculus MLL gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION  AY418622
VERSION     AY418622.1 GI:39774582
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 11415)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE        Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE    2 (bases 1 to 11415)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE        Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT      These sequences were made by sequencing genomic exons and ordering
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Best Local Similarity 37.8%; Pred. No. 0.054;
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QY      35 T-----CCTTTGACAA--GCTT--GAGA--GC-----A-AC-----A 59
Db      3867 TGAACCTTCCACAGTTTTGCTTAGAGAGAAATAGCGCCCCCTGGAGGACCACTGGA 3926
QY      60 CAA-----TC-----TAT--CA-----GGAA--AGAA--AG----- 79
Db      3927 AAACCTGTGTGTCGCCGCTGCAAGTTTTGCAATGTGTGTGAAGACACAGCATCAGGCTAC 3986
QY      80 AAGGAA-----AAAA--CCGAA-----CCT--GA-C 101
Db      3987 AAGCAGTTGTGAGTGAACAAAGTGCAGAAACAGCTATCACCCCGAGTGCCTGGGACC 4046
QY      102 AAA-----GAAGAAAAAGAA--GAAGA-----AAAAAAT----- 132
Db      4047 AAACCTACCCCAACCAACCCACGAGAGAAAGAAAGTGTGGATCTGCACCAAGTGTGTCCG 4106
QY      133 CATGAAA-----ACCA-TCCAGCCAAA-----AATGCACAAT--TCT----- 166
Db      4107 C-TGCAAGAGCTGTGGTCTCCACCACTCCAGGCAAAAGGTGGGACGACAGTGTCTCAG 4165
QY      167 ATCTCT-----TGGGC--AA-TCCTT--C--ACGGG-----GCTGGCTGTCT 201
Db      4166 ATTCTCACTGTGCCATGACTGTGCCAAACTCTTTGCTAAAGGGAACCTCTGCTCCTCT 4225
QY      202 GT-----GT-CT-----CTTC-----CAAG-----G-AGTGC----- 221
Db      4226 GTGCAAGTGTCTACGATGACGATCACTACGAGACAGATGATGATGATGATGATGATGATG 4285
QY      222 -CCG-----TGCG-----CAG--C-----G--GAGATG----- 239
Db      4286 ACCGTGGGTCCACTCCAAGTGGCAGAGTCTCTCAGGTACAGAGATGATGATGATGATGATG 4345
QY      240 -----CCACCTT-CCCCAAAGCTATGG-----AC-----AAC-G--TGA-CGG--T 273
Db      4346 TTCTGTCCAACTTGCCAGAAAG-TGTGGCTACAGTGTGTGAACCTCACTGAGCGGCAC 4404
QY      274 CCGGCAG-GGGGAGA--GC-----GC--CA-----CCCT--CAGGT----- 302
Db      4405 CCGCAGAGTGGAGACTGGCCCTGGAGAAAGAGTGTGAGCGGTCCCTCAAGCAGGTCTC 4464
QY      303 ---GCAT-----ATT-----GACAAACGGGTACCCGGGTGGGCTG-GCTAAACCG-CAG 348
Db      4465 ACGGCCCTGTGAATTCTCGGACTACC-AGTCAC-----TTG-CTGGCT--ACCGTCAG 4515
QY      349 -----CACCATCTCT--TA-----TG-----CTG-GGAATG--AC-----AAG-T 377
Db      4516 GCTGCCA--AGCTTCAGACTTAAACCTGAGACTGAGGAAAGCATACCTTCCGAGCT 4573
QY      378 -----GPTGCTGGATCTCGCTGGTCTTCTCTGAG--CAACACCCA-----AAC-GC 422
Db      4574 CCCCAGAGGGGCC-AGACCCTC-C-TGTTCTTACTGAGGTTCAGCAGCAGGATGAACAGC 4630
QY      423 AG-----TACAGTACA-----GATCAGAGAGTGGATGTGTATGACGAGGCG--CCTTAC- 472
Db      4631 AGCCGTTAGA-CCTCGAAGGGGTCAAGAA-GAGAAATG-----GACCAGGGCAGC--TACG 4681
QY      473 -ACCTGCT-----CG-----GTGCAGA-----CAGACACCA-----CCCA 502
Db      4682 TATCTG-TGTTGAGTTGAGGATGATATTGTGAAGATCAITTCAGCAGCCATTAATCA 4740
QY      503 AA--GA-----CCTCTAG-GGT-----CC-ACCTCATTTGTGCAAGTATCTC----- 539
Db      4741 GATGGAGGGCAGCC--AGAGATAAAAAAGCAACACAGCATGCT-CAATCTTCTTCAT 4796
QY      540 -C--CAAAATTGTAGAGA---TTTC-----TTGAG-----ATA-TCTCCATT----- 574
Db      4797 TCGGCAAA--TGGAGCGAGTTTTTCCGTGGTTTCAGTGTCAAAAAGTCTAGATTTTGGGAG 4854
QY      575 ---AATGAAG---GGAACA-----ATATTA-----GCC-TCACCT 602

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Db 4855 CCAATAAAGTATCAAAACAACAGTGGGATGTTACCAACGAGTGGCTTCCGCTTCACTT 4914
Qy 603 G-CATA-----GCA-----ACTGGTAGACAG-----AGCTTAC 630
Db 4915 GACCATTAATTANGTCTAGTGGCAGGAGGAGG-AGAGCAGCCACACTGAGCAGCTCC 4973
Qy 631 GGTACT--TGGAGA--CA--CATCTC--TCCCAAG--CGG-----T 663
Db 4974 --T-CTAATGAAGAAATCATTCAGCTCCAAACCCAAAGAGCCCGGAGACGACT 5029
Qy 664 TG-----GCT-----TTG-----T--GAGT--GAAG 680
Db 5030 CGCCACGCGCTCCACCGCTACACCCCGATCTTGGTACTGATCGGAGTCGAGAAG 5089
Qy 681 ACGAATACTTGA--AAATCA--GGGATC--AC--CCG--G-GAGCA-----717
Db 5090 AC-AGTCC--AGACTGAATCCACCCAGCATCGATGACAAACCGACAGTGTGCACTGT 5146
Qy 718 GTACG-GGGACTACAGTG-CAGTGCCTCCAATGACG-TGSCCG--CGCCGCTGGTAC--770
Db 5147 GTCTGATGTACGGGA-TGACAGTG-CT--AATGATCTGGCCGTTGC--T-GTACAT 5198
Qy 771 -GG-----A-GAGTAAGTTCAC-CGTGAATATCCACCATACATT--TCAGAGCCA 818
Db 5199 TGGCCAAAATGAGT--GGACATGTGAATCTGTC--T--TTGTGCTCAGCAG--A 5246
Qy 819 AGGT--ACAGTG--TCCCG--TGGGACAAA--AGGG--850
Db 5247 AGTGTGGA-AGATGATGACGGATCACTGAAGAATGTG-CATATGGCTGTGATTAGGGC 5304
Qy 851 -A-CA-CTGAG--TGTGAA-----GCCTCA- 871
Db 5305 AAGCAGCTG-AGATGTGAATCTGCCAGAGCAGGAGCCACCGTGGTGTGCTGCCTCAC 5363
Qy 872 -----GCAGTCC-----TCA-----GC--AGAA-----TTCC-- 893
Db 5364 ATCTGCA--CCAGCACTACCATTTTATGTGTCCCGGCCAAGAACTGTGTCTTCTG 5421
Qy 894 -----AGTGTA--CA--A--GGA--TGA-CAAA-----913
Db 5422 GATGATAAAAAAGT-GTATGTGTCAGCGCATCGGATTTGATCAAGGCGAGGTGTTC 5480
Qy 914 --AGACT-GA-TTGAG--GAA-----AGA--AAGG--GGT-----939
Db 5481 TGAGAATGGATTTGAAGTTTTAGAGAGTGTGTGTAGATTTTGAAGGAATCAGCTTGC 5540
Qy 940 --GAAAGT--G--GAA--CA-----CA--GAC 956
Db 5541 CAGGAAGTTCCTTAATGGCTTGAACCAAGAAATATCCATGATAGGCTCAATGAC 5600
Qy 957 --C--TTT-----CCTCTC-----A-AAACTCATCTTC-- 979
Db 5601 AATCGACTGTGTGGGAATCCTGAATGACCTCTGACTGTGAAGATAACTC-T-TTCT 5658
Qy 980 -TT-----CAATG-TCTC--TGAATG-----AC-TATG--GAAA--C-----1009
Db 5659 ATTGGATACAGTGTCTCGGTGTAC-TGGAGCACACAGATGCCCGAAGCGCTGTGT 5717
Qy 1010 -TACACTGC-----GTG--G-CCTC-----CAACAGC- 1034
Db 5718 GTACACATCAAGATCATGGATGCGCGCTCTCTGTGTAGAGCCGGATATCAAC-AGCA 5776
Qy 1035 ----TGGC-C--AC-----ACCAATGCC--AG--CATCATGC--TAT-----1064
Db 5777 CGGTTGAGCAGCATGACATAGACCATTTGCCATAGCCCATCAT-CATTTATATGCA 5835
Qy 1065 T--TG-----GTC-----CAG--GC-----G-----CGGTACG--GA--GG--1088
Db 5836 TCGTGAAGCAGTCAAAAGCAGTGCATTTCTCAGTCTCCGTC-GCCAGATCGGCC 5894
Qy 1089 -----TGACGA-AC--GG-----CAG-----TCG-AGG-----AGG-----1111

Db 5895 TCATTCA-CAGACCTCAGGCTCCTGTTATTATATCATGTATCATCTCGAAGGTCCTAGGATTC 5953
Qy 1112 G-----CAGGCT--GC-----GT-----CTGGCTGC-----TGCC-----1134
Db 5954 GAACACCCA-GCTACTCGCTACACAGAGTCCCTTGGCTGGCCCAATTGGCTTTCGCA 6012
Qy 1135 -----TCTTCT 1140
Db 6013 GGAAGTCTACCCCAACCACTACGAAATCGTCACAGTGGTGACCCGTTACTGTCTTCT 6072
Qy 1141 GGTCTT-----GCA--C-CT--GCTTCTCA--AATT-----TTG-----1167
Db 6073 GGTCTTGGAGCAATGGCTCTAGCGTACAGTACTTCTTCTGTGTACCCCTGCGGTCC 6132
Qy 1168 -----ATGTG--AGTG-----CCA-----C 1180
Db 6133 AAGCTCGCATATGCTCCAGTGAGACGGGAGCGCTTACTCCAGGAGTAGTGTTC 6192
Qy 1181 T---TCCCCACC--GGGA-----A-----AGGC--TGCC-----1203
Db 6193 TCAGTCCCGAGCTTGGAGCTGCCAGATCTCTAGGCGCAGTGCCAAAGCATCGGATCGA 6252
Qy 1204 -----GC-----CA-----C-CA-----CCACCAC--CAA--CA 1222
Db 6253 GGAGGCTGTGAGTTCAGTCAAGTCTAATCTCGGCAACAGGCTCCCCCTTCAAGCTCA 6312
Qy 1223 CA-----ACAG-----CA-----ATGG-----1234
Db 6313 CAGAGCAGTGGAGGCTCCAAACCAAGTCTGATCTGATGGGTCTGTCACCTCGGAGTG 6372
Qy 1235 -----CA-AC-----ACC-----G--AC 1244
Db 6373 AAGCGGTGAGTGTTCAGACTTGGTACCCAAAGGCTCCTTAGTAAAGGAGAGAAAAC 6432
Qy 1245 AG-----CAA-----CAGAT--AT-----ATA-CAAA-----TGAAT- 1274
Db 6433 AGAATCTCAAGTTCAGAGCAGATGATCTGCATAGCAGCTTACCTGGAATC 6492
Qy 1275 --TAGAA--GA-AACACA-----GC--CTCATGG-G--AC--AG--AAAT 1305
Db 5493 CCTA-AACTGACACACAGGTTTATAAGCAACTCTTGAGAACTAAACATTAGCAAT 6551
Qy 1306 TTGAGGGAG--G--GGA-----ACA-----AAGATA-----1328
Db 5552 T--GGCAGTTTGTGTAACCTCTACAGTGCCCTTTTCTTAAGGATACAGTCTCTTA 6608
Qy 1329 -----CT--TTGGGGG--AAA-----AGAG-----TT--1347
Db 5609 CCCACAGCTTCACTTGGGGCCAAAGAGTGCACAGACCAAGCATGGATCTTCCCA 6668
Qy 1348 T--TAAA-----AAA-GAA-AT--TG-----AAAA--TTG-----CCT--T 1373
Db 6669 GTCAAGAGCCCTCTCCAAATGAAGATGTTGAATCAAAACCTTGAAGCTCCCTGGTAT 6728
Qy 1374 G-----CAG--AT--ATT-----TAGG-----TA-----C- 1389
Db 6729 GGGCCACAGCCATCCATCTACATGAACATAGGCTTAGTCTAGAGACAGAGACA 6788
Qy --390--AATGG-----AGTTTTCT-----TT-----TTC-----1407
Db 6789 GAAAGGAAAAAGTCTTCTAAAGAGACTTGCAGAAAGACATCCAGTAATCTTACTT 6848
Qy 1408 -----CAACG--GGAAG--AAC--ACAGC-----1426
Db 6849 GGAACCTGGCAGGTGACACCGGTGAGAGAGAAACCTTAAGCCAGAGTTTGTGTATGA 6908
Qy 1427 -----ACACCGG--CTTGG--AC--CCACTGCA--GCTGCATC-----G- 1459
Db 6909 GGTGTGACTCTGGGTTCTTGGGCAACGACCA-TGTAATAATGTTTTCATCTGAGAAGA 6967
Qy 1460 -TG-----CAA-----CCTCTTT--G-GTGCC--AG-----T-----GTG--G 1484
Db 6968 TTGGAGATAAAGTCTTCTTTCAGGAGTCCCTTAAAGGTCATCCACACAGTGAAG 7027

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QY 1485 G-----CAAGG-----GCTC-----AG-----CCTCT----- 1501
Db 7028 GATCTTCCAAAGGAGTTACAGGCACCCCGAAGTGCTCGTCAAGTGACACCTCTGAAGA 7087
QY 1502 -----CTG-----CC-----CAC-----AGAGTG-----CCCC---C 1520
Db 7088 TGAAGGTGAGAAATCAATCCAAACACCCAGAAAGAGAGTGCCCTGGCTCCCGGCAC 7147
QY 1521 AC-----GTG-----GA-ACATTC-----ATCCCA-AT--TCAATCAGT----- 1562
Db 7148 ACATAGAGTCAGTGTCGCCAGCAGAGCCAGTCTCAGCTCCAGAGCCCGAGAGCTGCC 7207
QY 1545 -----GTG-----ATCCCA-AT--TCAATCAGT----- 1562
Db 7208 CAGGAGTTCAGCGGAGCCCAACAAATACCTTATCCCAAGATCCTCAA--AGTAACTA 7265
QY 1563 CCA-----T--AGAGAC-GAACAGAA--TGA-GACCTTCC-----GG-CCCAAGC----- 1600
Db 7266 CCAGAACTTCCAGA-ACAGGACAGAAACCTGATGA--TTCCAGATGGCCCCCAAGCCTCA 7322
QY 1601 -----GT-----GGGC--TG--CGGCACTTTGG--TAG 1624
Db 7323 GGAGGATGCTCTTTAAAGCGGTACCCCGCGCGAGTGCCCGGCAC--GGTCTA-- 7378
QY 1625 AC-TGT-----GC-CA--CCAC-----GGCGT--GTGTT--GTGAA-----A--- 1653
Db 7379 ACATGTTCTTTGGGCTCACCCCACTGTATGGAGTCAGGTCTTACGGTGAAGACATTC 7438
QY 1654 CGT-----GAAAT-----AAAA--GAGCAAAA-----AAAA 1679
Db 7439 CGTCTACAGCAATCCACTGGGAAAAGCGAGGAAAGAGATCAGCAGAA 7488

RESULT 21
AY408639 4754 bp DNA linear GSS 15-DEC-2003
LOCUS Homo sapiens UNC13 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY408639
VERSION AY408639.1 GI:39764610
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4754)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..4754
/organism="Homo sapiens"
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/db_xref="taxon:9606"
<1..>4754
/gene="UNC13"
/locus_tag="HCM3291"

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ORIGIN

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Query Match 41.7%; Score 699.9; DB 29; Length 4754;
Best Local Similarity 39.0%; Pred. No. 0.0027;
Matches 1414; Conservative 0; Mismatches 171; Indels 2045; Gaps 407;

QY 1 GT--TGTC--TC-----CT--TCAGC-AA--AA-----CAGT-----G-----GATT 28
Db 772 GTAATGTGAGTCAAGGAAGCTCTCAGCTAAGTGAAGTACAGCAGTATCAGCAACAGA-T 830
QY 29 TA--A--ATC-----TC-----CTTGACA-AGCT--TGAGAGCAACACAT 63
Db 831 GACGACCATCGGAGACGGACTCGATTCACTTCTTGC-CACAGCTCT-----CACAGC 881
QY 64 CTAT--CAGGAAGA-----AAGAA-----AGAA-AA--AAACC--GAACCTGACA 102
Db 882 CTGTCCAG--AGATGGCCAGCAGGTTTGTGAGAACAAAGAGAACCCCTTGGAGTGACA 938
QY 103 ---AA--AAGAAG-----A---AA---AAGAAGAAAAAAT--CATGAAA 139
Db 939 GGTCAAGCAGAGAAGGAGGAGCATGTGAACCCAGGAGATGAAGAAGATGCCA--CAA 996
QY 140 ---ACCATCC-----A-----GC--CAAAAATG--CACAATT--CTA--TC----- 169
Db 997 CCCACCTCCCCAGATCTGTGCTGCAGAAA--GACCAC--TTCTAGTCCCAGAGAGA 1053
QY 170 ---TCTTGGCA-----ATCTTCAC-----G--GGGC--TGGCT--G 197
Db 1054 GTTTCTCTGAGGAGATGTCATCTTCCACATTTACCAAGCCAGACATTTGGATCCGAG 1113
QY 198 C--TCT--GT--GTCTC-----TTCCA-AGGA--GTG--CCC----- 223
Db 1114 CAGT--TACCAGGTTCCAGTCCAGTCCAGAGATCCAGATGATGGTACCCCTCTCTG 1172
QY 224 ---GTG-----CG-----CAG-CGGAG-----ATGCCA-----CC----- 244
Db 1173 CCTCAGTGGCTCCCGAAGCCAGCGAGGGCTCTATGGCATTTGACAGCATGCCAGAT 1232
QY 245 TTCCCCA-----AAGCTA-TG-----GACAACTG-----AC-GGTC-----CGGC 278
Db 1233 TTACGCAGAAAGAACCCCTGAGGCTTAATCTACCCATTTCGTGCACCACTCCT 1409
QY 329 ---GTGGCCTGG-----CTA-----AAC--GC-----A---GCA--CCAT 354
Db 1410 CATAACTTTGAGTCTGGAGCGGCACCTACCCCAACCTACTGTATGATGTGAAGGCC-T 1468
QY 355 CCTCT-----AT--GCTG--G-GAAT--GA--CAAGTG----- 378
Db 1469 GCTCTGGGCAATTCGCCGAGGCGATGCTGCAGCAATGTGGAGTCAAGTGCCATGA 1528
QY 379 ---GTCCCTGGATC--CTC--GCGTG--GTCCCT-----TCT-----GAGC--- 409
Db 1529 GAAGTCCAGGATCTCTCAATGC-TGACTG-CCTGCAGCGGCTGCAGAAAAGAGCTGT 1586
QY 410 -AAC-----ACCCA-AAC-----GC-----AGTACAGATCGAG 436
Db 1587 AAACATGGAGCTGAGGACCGGACCCAGAACATTTATCATGSCCATGAAGCCGATGAAG 1646
QY 437 ATCC-AGAACG---T-----G-GATGTGTATGACG--A---GGGCC--CTT-AC----- 472
Db 1647 ATCCGAGAGGAAATAAGCCAGAGATCT-T-TGAAGTTATCCGGAGCGTCTTCACAGTGA 1704
QY 473 AC-----CTGCTC-GGTGCAG-----ACAG--A-CA-----AC-----CACG- 500
Db 1705 ACAAGCTGCCATGTGCACAGATGAAGAGAGTGAAGCAGAGTGTACTGTGATGGCACT 1764

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QY	501	-----CA---AAG---ACC---T-CT-----AGGG-----	515
DB	1765	CCAAATGGTCAGCCAGATCACCACTACTGTGGTGTGCCAGGGCCTACAAGCCAGG	1824
QY	516	-----TCCA-----CCT---C---ATTGTGCAAGT-----ATCT-----C---539	
DB	1825	ACAAACAGGATCCAGTGACCCCTTACGTGACTGTGCAAGTCAGCAAACTAAGAAGCGTA	1884
QY	540	CCAA-----AAT---TGT---A-GAGA---TT---TCTTCAG-----563	
DB	1885	CCAAGACCACTTTTGGAAACTTGAATCTGTGTTGGAGGAGAGTTCATTTTGGATGCC	1944
QY	564	ATATCTC-----CAITAA-----TG-AAGGG-----AA---CAA588	
DB	1945	ACACTCTCTGACCGCATTAAGTGCCTGTATGGGATGAGGATGATGATCAATCAAGTCAA	2004
QY	589	TATT---AGCCTCACCTGCATAGCAA---CTGGT-----AGACCA-----GA624	
DB	2005	GAGTAAGCAACGCCT---AAAGCGAGTCTGATGATTTCTTGGCCAAACCATCATGTGA	2062
QY	625	G-----CCTA-----CG-----GT-----T---ACTTGG-----AGACA645	
DB	2063	GGTTCGACCCCTTAAGTGCAGATGGACGCTGTGTACAACTTGGAGAAGGACAGACAA	2122
QY	646	---CA---TCTC-----TCC---CAAAGCGGT---TGSCITT---GTGAGTGA---678	
DB	2123	ATCAGCCGTCTCAGGGGCTATCCGACTACAAATCAGTGTGAGATCAAGGGGAG-GAGA	2181
QY	679	---AG-----ACG---A-ATACTTG-----GAA-----694	
DB	2182	AAGTAGCCCCATACACAGTCGAGTATATATGCTCCATGAGATCTTTTCCATTACCTCA	2241
QY	695	---ATTGAGGCA-----T---CA-CCCGGAGCAGTC-AGGGAC-----727	
DB	2242	CAGACATTCAGGGCAGTGGAGGATCCGATCCCTGAAGC---TCGAGGACAGATGCCTG	2299
QY	728	---TAC---GAGTG---CAG-----TGCC-----742	
DB	2300	GAAGGTGTACTTTGA-TGAGACAGCCCAAGAAATTGGATGAATTTGCCATCGTTATG	2358
QY	743	---TCCA-----ATGAGC---TG-G-----CC-----GC759	
DB	2359	GCATTGAGTCATATATCAGGCCATGACCACTTTGCATTTTATCATCCAAGTACATGT	2418
QY	760	GCCCGTGGT-----A-C-G-GA-GAG---TA---AAGGTACCG-TGAACTAT-796	
DB	2419	GTCC-TGGTGTGCCAGCAGTGATGAGCACCTTACTGGCCACACATCAAGCCT--ACTTG	2475
QY	797	---CCAC-CA-----TAC-----A---TTT-CAG-----812	
DB	2476	CCACACAACTGCTCTACCAATGTCTGTGATCTGATCGCTTTGACGCTCCAATTG	2535
QY	813	---AAG-----CCA-----AGG---G-----822	
DB	2536	GGAAGAGAGATTGTAAAACTGTCGACAGCTACACAACCTCACTGAGATCGACCTCT	2595
QY	823	---TACAGG---TGTCCTCG-TGGGA---C-AAAAGG-----GGAC-----A-CTG856	
DB	2596	CTACATACAGGAATAATTTCCCTGCTGGGAGTCTGACGGTTCAGGACTTTAAAATCCA	2655
QY	857	CAGTG-----TGA-AGC-----C-TCAGCA---GT-----C---CC879	
DB	2656	CAGTGGATTGCTGACCAGCATTTCTTCAGATGAAGGTACAGACTGCAAGGCC	2715
QY	880	CTC-----AG-CAGAAATTCG-TGGTACAAGGA-----TGACAAAGACTGATTGAA---925	
DB	2716	CTCAAGAGCCAG---CCAGGTGGTA-AAGGATTGTGTG---AAGGCTGTGTGAATC	2767
QY	926	---GGA-----AAGAA-----AG-----G-----GGTGAA942	
DB	2768	CACATATGATATATCTTCAACACTGCCAGCACTTATACGCCCCAGTACCACTGAA	2827

QY	943	-----AGTGGAA-AA-----CAG-----ACCT-----TTCTCT-----	963
Db	2828	GCAGGAGCTACCTCCAGAGGAAACAAGGGCCCGAGCAITTCGGAAACCTGATTTCTGGCCCAA	2887
QY	964	-CTCA--AAACTCATC-----TT-CTTCA-A--TGTCTC	990
Db	2888	GCTCATCACACTCATCGTGTCAATCATAGAGGAAGATAAGAAATTCCTACACACTGT-TC	2946
QY	991	TGAAC-----A--TGACTATGGGACTA--CA-CWTGC-----GTGG	1022
Db	2947	TGAACCAAGTTTCTCAGAGTGAATGTGGAA--AAGTCAGC--GCAGAAGTGAATGTGG	3002
QY	1023	CCT-----CCAA-----CA-----AGC-TG-----GGCCAC-----	1042
Db	3003	CAITTTGTTTCCCAAGACATGAATATGCAITGGAGGAGCATGAGAAAGACCACCTGTGT	3062
QY	1043	-----ACCA-ATG--CCAGCA--TCA-----T-GCT-----	1062
Db	3063	AAAAGTGTGTACTACATGAACCTGCACCTTCAAGGTGAAGTGGTCCACAAATGAATACGTG	3122
QY	1063	-----ATTTG-----GTCC-----AGGCC--GT--CAGGGAGG--TGAACA--AC	1096
Db	3123	CGGATCTGCCTGTCTCTCCAGGGCGAGTGCTTGAGTACCAGCGTGGTTTGACGAGTTC	3182
QY	1097	G-GC-AC--GTC-----GAG--GAGG--G--CAGG-----CTGGGT-----CTG	1125
Db	3183	GTGCTTACAAATGGCTTGGATGAGATGAGGATGTATCCTCGAAATCTCTGCTGGGGCCCTG	3242
QY	1126	G-----CTGC-----TGC-CTCTT-----CTGGTCT	1145
Db	3243	GAAAGAGATGAAGAGATGGATTCAGACAGACATCAGAGATGCACCTTTCTCTGCTCT	3302
QY	1146	-----TGCACTGT-CTTCTCA-----AAT-----TTTGA-----TGTGAG	1174
Db	3303	GTGGTGA--TGTCTTACACAACTCAATCAGAGCTTTTGAGATCATCCGGAAGCTG-GAA	3359
QY	1175	TGC-----CA-CTTCCC-----ACC--CGGAAA	1196
Db	3360	TGCCAGACCCAGCATCTCTTGGCCATCATAGGAGGTTTGTAAAGACCATCGGAAG	3419
QY	1197	G-GCTGCGCG-----CA-CCA-C-----CA-----CCA-CAAA--CACAA-----	1225
Db	3420	GTGCTGATGAGTATGCAGACATCTTGTCAAGGACTTCCAGCTTATGCAAAAGGAG	3479
QY	1226	-----CAGCA-----ATGGCAACCG-ACAGCAACCAA--T-CAGATATATACAA	1267
Db	3480	AAACTGCCCTGCATCCTGATG--AAACAAGTGCAGCACTGAGGCTCCAGCTGGAGA-AA	3536
QY	1268	ATGAAAT-----AG--AAGAAC--AC-----AGCCTCATGGGACAGAAAT	1305
Db	3537	ATG-----TTTGAGGCCATGGAGCAGAGAGCTTGAACCTTGAAGCTGCA--GACAG--	3587
QY	1306	TTGAGGAG-----GG-GAACAAAGAATAC--TT-TGG-----GG-----GG	1338
Db	3588	CTGAAGAGCTGCAGGTGA--ACTGAAATACGGTCTTGGATGAGTCAAGTGTGTTGG	3646
QY	1339	AAAAGAGTTTAAAGAAGAA--ATTGA-----AAATTGCTTGAGATAT	1381
Db	3647	-AAACAGTTT--CCAGGTACGATTTGATGATGTGTTTCGACAAATGCC-----GACAT	3697
QY	1382	-T--TAGGT-----AC-----AATGAGTTTCTTTTCCCAACG-----	1413
Db	3698	CCTGGGCCAGGTTCCGGGACAGGGAATGA--TCT-----CCAGAGCCAGGGCCTCA	3749
QY	1414	-----GGAAGACACAGCACAC-CCGG--CT--TGGAC--CCACTGCAAGCTGCAT	1457
Db	3750	GCGGCTCAGATGCAATAGCGTACTCCGGCTCTCATGSACTTC--CTGGATG--GCAA	3805
QY	1458	CGTGCAACCTCTTTGGTGCCA-----GTGTGGCAAG--GGCTC-----CT-----	1499
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QY	1500	---CTCTGCC-----CAC-----AGAG-----TGCCCCAC--GT	1524

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Db      3861 GAGCTCTGGGCGTGGTGTGATGAACACAAATGGAGAGGATGATTGTTCTGCCCACTCACT 3920
QY      1525 G-----GA-----AC-----AT-----T-CT-----GGAGCTG-GGCATC--CCAAA 1552
Db      3921 GACCAGAGGGGACCCAGCTGATCTTCACTGCTGCTGCCAAGGAGCTGAGCCATCTTTCCAAA 3980
QY      1553 TTCA---ATCAGTCCA---TA-GAGACG-AAACA-GAA-----TG-A 1583
Db      3981 CTCAGGATCA---CATGTCAGAGAGGAACACCGATCTCACTCCAAAGCAGTGTGCA 4037
QY      1584 GACCTT-----CC-GG---CC-CAAGC-----GTGGC-----GCTG 1609
Db      4038 GTCCTTGACCTCGCCCTGGACACCATCAAGCAATCTCCATGAGGAGCAATGGCTG 4097
QY      1610 -----C-GG-----GCA-----CTTTG-----G 1621
Db      4098 AAGAAAACCTTCCTGGAGAGAGGCCAGATGCGAGTCTTACGCTATGCTGTCTCTG 4157
QY      1622 T-----AGAC-----TGTC-----ACGTGAA-----ATAAAA 1666
Db      4218 TCTGCTGGAGCATCTCTGTGGAGAGAGTCTCTATTACGCTGGACTGTTTACACACCT 4277
QY      1667 -----GAGCA-AA-----AAA-----AAA 1679
Db      4278 GGTACTGGGAGACACAGGTACACAGTGAAA 4307

RESULT 22
AK044634
LOCUS
DEFINITION
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930028N13 product:ankyrin 2, neuronal long splice form
homolog [Homo sapiens], full insert sequence.
ACCESSION
AK044634
VERSION
AK044634.1 GI:26336658
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci,P. and Hayashizaki,Y.
4035 bp mRNA linear HTC 20-SEP-2003
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
95279253
PUBMED
10349636
REFERENCE
2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
20499374
MEDLINE
11042159
PUBMED
11042159
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3 Shibata,K., Itoh,M., Aizawa,K., Nagao,K., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,U., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
20530913
MEDLINE
11076861
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REFERENCE
4

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AUTHORS TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

FEATURES source

CDS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 4035)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

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ORIGIN

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DB 510 GGA--ATACTGAAGGGGCAATTGACATCAATACCTGCAATCAGA--ATGAGCTCAAT 564
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DB 743 AGTCGAGAAATGCTTCACTCTCTTTGTACATGCTGCCAGGAGAAAT-CACATTTGATGT 801
QY 164 -T---CTATCT-CT-----TGG-GC-AA-----T-CTTC-AC--GG--GG----- 190
DB 802 GTAAATATTTGTAGAAATGAGCTAACAGAGTACTGCTACAGAGAGCGCTTTACT 861
QY 191 -----CTGGCTG--CT-----CTGTG-----T-CTCTT----- 210
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QY 211 -----CCAA-GGA--GT-----GCCGTGC-----GCAG--CGG--AGATGCCAC 243
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QY 244 -----CTTC-----CCAAAGCT-ATGGACAA--C-G-TGAC 270
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QY 344 -----CG-----CAG-----CACC-----CACC----- 356
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DB 1337 CCTTGTCTGGCAGGACCAAGATGGGCTGTCCCGCTTACATGGCTGCGAGGGGAC- 1395
QY 414 CCC-----AA--AC-G--CAGTACA-----GC--ATCGA-GA--TCCAGAAC 445
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Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
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splice form homolog (Homo sapiens), full insert sequence.

AK036018
AK036018.1 GI:26084967
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
2049374
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3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
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AUTHORS

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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the

Functional annotation of a full-length mouse cDNA collection

JOURNAL

REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

JOURNAL

REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/

FEATURES

Source

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misc_feature

ORIGIN

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Best Local Similarity 37.3%; Pred. No. 0.0036;
Matches 1417; Conservative 0; Mismatches 180; Indels 2201; Gaps 390;

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QY 20 CA-----GTGGATTAAATCT-----CCTTG-CA-CAA-----GC-TTCAGAGCA- 56
Db 327 CAAAGTGGTGA--ATATCTGAAGGGGCATGTGACATCACTGCAATCAGA--AT 381
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QY 132 TC-ATG-----AAAA--C-CA-TC-----CA-----G-CCA-AAAATGCAC 160
Db 560 TCAATCCCAAGTGCAGAAATGGCTTCACTCCTTTGTACATGGCTGCCAGGAGAAAT-CAC 618
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QY 235 AGATGCCAC-----CTTC-----CCCAAGCT-ATGAGCAA-C 265
Db 798 AGATGACACCAAGTCCGCGCCCTCTCTGTTCAAGATGATCAACGCTGATGTACAATC 857
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QY 321 TCAC--CCGG--TGG-----CC-----TGGCT--AAAC----- 343
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Db 1094 CACCATTCACTGTGCTGCGGAGTGGGCAATGATCAAGTGTGAGAGTCTGTTGGAAC 1153
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Db 1154 GGAAGGCTCCCTTGTGTCGCGAGGACCAAGATGGGTGTCCCGCTTACATGGCTGCGC 1213
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Db 1214 AGGGGAC-CACGTGGAATGTGTAAGCAGCCTGTCCAATACAGGCGCTGTGATGAC 1272
QY 438 -TCCAGAACGTGGATGTGA--TGACGAGGCGCTT-A-----CAC-CTG-----C 478
Db 1273 GTC---ACCTGGAT---TACCTGAC---GGCTTTTATGTTGTCACACATGTGGGAC 1323
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Db 1324 TACCGTGTAAACAAACTCTCTGCTGACACAGAGAGCAACCCGAGCAAGAGCCCTGAAT 1383
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Db 2028 TTCCACACTACTGAACATATGGGCGGAGACTAACACTGTGACAAAGAGGGGTCACTCC 2087
QY 853 ACTGCAGTGTGAGCCTCA-----GCA-----GTCCCTCAGCAGAAATTTCCA 894
Db 2088 ACTGCA-TCTG--GCCTCACAAGAGGGGCCACACAGATGTCACTT-TGC---TTC-- 2137
QY 895 GTGTAC-AAGG-----ATGACAA--AAGACTG-----A--T 921
Db 2138 -TGG-ACAAAGGACCAATATCCACATGTCAACCAAGAGTGGACTCATCTTACACCT 2195
QY 922 TG-----AAGGAAGA-AAGGGGTGAAGT--GGA-----GTCCCTCAGCAGAAATTTCCA 957
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Db 3139 AACAAATGCCCCCATGTTGGAGAGAGAGCCCTGGCCAGCGCTGATTTGAAGTCCGACC 3198
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Db 3199 TTCCGGAGCTCAGTTCTTTGGGCGCGTGATCGTGGAGATCCCTCACTTGGCGCTCTTCG 3258
QY 1321 ---AAGAATA--CT-TTGG-----GGGA-----AAAGAG-- 1345
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QY 1584 --GA-----CCTTCC-----G-----GCC-----CA 1597
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RESULT 24
LOCUS AK087828
DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330026B02 product:hypothetical von Willebrand factor type A domain containing protein, full insert sequence.
ACCESSION AK087828
VERSION AK087828.1 GI:26104533
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
REFERENCE 2 10349636
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Kazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

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TITLE RIKEN integrated sequence analysis (RISA) system--384-format
JOURNAL sequencing pipeline with 384 multicapillary sequencer
MEDLINE Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 20530913
REFERENCE 11076861
AUTHORS 4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4728)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES
source
location/Qualifiers
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misc_feature
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ORIGIN
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Best Local Similarity 37.0%; Pred. No. 0.0028;
Matches 1433; Conservative 0; Mismatches 149; Indels 2291; Gaps 416;
QY 1 GTTGTG---TCCTTCAGC-----AAAA--CAG-TGATTT-----AA--A- 32
Db 267 GTTGGGATTC--TCACCTACACCTGAAATGCTGCTGTGCTGCTGCAATGAT 325
QY 33 ---TCTCC-----T-TGCA-CAAGCTT-----GAG-A-GCA-AC----- 58

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Db	445	ACAAGATGATCAGAGCCTCCCATAGAGGCCACAAAGTACCGCTGGCCCTGGGCCAGT	Db	1499	GTTCCTGAAGAACTGCGGAACCAATCACACACGGTCTCTGTCTTCTCAGAAGCGAC	1558
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QY 1662 A-----AA---AAGA-GCAA-----AAAAAA 1679
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RESULT 25

AK090138

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

AK090138 10481 bp mRNA linear
Mus musculus 7 days embryo nullipotent stem cell CRL-2070 NE cDNA,
RIKEN full-length enriched library, clone:G431005B01 product:gene
el protein, full insert sequence.
AK090138
AK090138.1 GI:26354968
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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prepare full-length cDNA libraries for rapid discovery of new genes
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
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RIKEN integrated sequence analysis (RISA) system--384-format

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 11076861

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The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 695-690 (2001)

JOURNAL REFERENCE AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
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 Nature 420, 563-573 (2002)

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 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saibara, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submision

JOURNAL REFERENCE AUTHORS

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
 URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: <http://genome.gsc.riken.go.jp/>
 URL: <http://fantom.gsc.riken.go.jp/>
 Location/Qualifiers

FEATURES

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CDS

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ORIGIN

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Best Local Similarity 36.6%; Pred. No. 0.047;
Matches 1447; Conservative 0; Mismatches 166; Indels 2342; Gaps 415;

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QY 28 -TT--AAAT-----CTC---CTTG-----CACAAAG-- 47
Db 5664 GTTCAGAAATGGCTAAAGGGCTGCATCGAGGAGCTCATGCTTGGGCTTCTC-CAAGCCC 5722
QY 48 -----T-----TG-----AGAG-----CAACAC----- 60
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QY 61 --A-ATCTATCAG--GAAA-----GA-AA--A-GAA--A-GAA--AAA-AA-- 90
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QY 91 -----CCGAA-----C-----CT-GA-----CAAA-----AAAG-----A--- 109
Db 5843 GAGTGCCTAAAGGCTGAGTTGCTAGATGCCAAGTGGCTGCGCTGCGAAGAGCAGATGG 5902
QY 110 AGA-----AAAA--GAAGA-----A-----GAA-----AAAAAATC 133
Db 5903 AGAGCTATTGCCAGCTCGGAAATATTGAGGAGCTCTAGCCCTCTTTTGGACGCAAAA--C 5960
QY 134 A-TGAAAC--CATCAGC-----AAAA-----CAAA-----A-----TGCA 159
Db 5961 ATTGAATCTATCATCAGCGCTCTCGTCGTCTCTATGCGCAACACACCCATCGCCCGTCA 6020
QY 160 -----CAATT-----CT--A--TCT-----CT--TGS-----GCA-----ATC--TTCAC 186
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Db 6200 TCTGTTCCGATCAGAGACTAT-CCACGGTACCTGTTTGAGATCCGGGACTGGCGGCTAA 6258
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Db 6259 TGGTGCACCTTGGGGCAGCTGAGC-AGAGTGGCCAGCCATGCTCCCGTGCAGCTCAGATC 6317
QY 275 CGGCA-----GGGG-----GAGAG-----C-GCCACC-CTCAGG 301
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Db 6378 TTTTACATGACTTCCACTCGGAATCTTCCAGTACACAGTGTGTGGGCCCCATGTTGG 6437
QY 320 G-TC-----ACCC-----GG-----GTGG-CC--TGCTAA-----AC 343
Db 6438 GATCCAGCCTGGACACTGATGTCAGTGTGTGAGCTCTTGACTAAGCCCTCAGCTGAC 6497
QY 344 CGCAG-CACC-----AT-----CC-----TCT-----ATGCTGGGAATGAC 373
Db 6498 CCAGGCCACTTTTGCCCTGGTGGGATAAGAGCCGTCTTCTGTTCATG--GGGACTGGC 6555
QY 374 AAGTGG--TG-----CCTGATC-CTCGC-----GTGGT--CCT--T----- 403
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QY 404 CTGAGCAACCCAAAC--GCAGTACAG-CA-----TC-----GA-----GATC-- 439
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QY 440 -----CAGA--ACGTGGATGT-----GTATGACGAGGGC- 466
Db 6673 TTGTGTTCAGGGGACCTGGATGTCAAGTGAAGACAGCTTCTAAGTATGACGACTGCT 6732
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Db 6733 GCTTCCTT-CACCTGCTGACCTC--TGATGACACTGGACCTACAGTGGCTGTGCCAG 6789
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QY 1527 AACATCTGTGAG-----CTGG-----CCATCCCAA---TTCAATCAG---TC 1563
Db 9145 AACACT-TTGAGTAATGTGGTGGCTCTCACCATC---AGTGTCCACCGGTCTTC 9200
QY 1564 CATAGA-GA-----CGAAC--AGA--ATGA-GACCTTCG-- 1592
Db 9201 CATAGAATGATGGGCTTTTCTTCTCTGTCGAAATGTAGAAGATGATGAGTT--GGTG 9258
QY 1593 -----GCCCAAGCTGGCG-CTGGCGG-----CACTT----- 1618
Db 9259 ATGAAGAGGATAGTCCAAC-TGGTGACTCTGGAATACCACTTGTAAAGCTCGCCAG 9317
QY 1619 -TGGTAG--AC---TG-TGC--CAACAC-----GGCGTG-----T- 1644
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RESULT 26
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AK054393
AK054393.1 GI:26096352
HTC: CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1
Carninci, P., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
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3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3971)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S.,

Db 2334 GCAACGATCCAGCCACAGTCAGTGTGCTGAGGAGAAACACCCCTTGGCATATGGCGA 2275
QY T--TACTT--GGA-----GACACATCTCT--CC-----CAA--AGC----- 660
Db 2274 TAGTACTTCTGATAGTACGAGCAGTGTCTGGAACCTGGATGACAGAGGACATATGTG 2215
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Db 2214 GAAAAACAGAAACATGTTGTGTGCTGGGACCTGTGCTGTGATCTGGGAGACAGACTTACT 2155
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Db 2154 TCGAGCCACAGTCAGTCACCATGACACCCATGAGCCCAACATGAGCCCTTATCACTACTAG 2095
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Db 2094 GAAATTAGATCGTCCACAGAGGGGTGAACAACCTACTCTTGGGCCCACTTCTATGGGTTT 2035
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Db 1802 CGCAGAGMACATGAGGACATCAGAGGAGACCCAGTGGGATCTAGGCTGCAGCA-T 1744
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QY 918 TGA-----TTGA-----AGG--AAAGAAAGGGGTGAAGTGGAAAA 951
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Db 1343 AAAGGGCAGG--GCCTCACTGTGAAGCGCAGGAACCTCGTGAAGCTTCTGCAGGCG 1286
QY 1138 -----TCTGGTCT-----TGCACTGTCTT-----CAAAAT----- 1163

Db 1285 GGCAGAAACTCAGTCTGTGTGTGACCTGCTCTAAACAGTGTGTGATAGCAATGAA 1226
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Db 1225 GTGTCCAGATCTGTGTATCCATTTGTGTC--CTGCATTTTCATGCCATCAAGGCCAGCCA 1167
QY 1188 -----C-----CCGGHAA--G-GCTGCC-----GCC-----A-----CCA-CCA 1213
Db 1166 AAGGTAAATCTTTGTATCCGAGAAACGTGCT--CCTGGAAGCCCGGGAGGATGGTCCATCCA 1108
QY 1214 C-CACCAAC--ACAACAGCA-----ATGG-C-----AAC--ACCGA--C-A-GC----- 1247
Db 1107 CTGACCAACGAA--AGCATGTTGATGGTCTTTGAGATCGGGCCGATGCTGATGCATTT 1050
QY 1248 -----AACCA--ATCAG-----ATAT-----ATACA-----A- 1267
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QY 1268 -----AT-GAAA-----TT-AGAG--AAACA-----CA 1287
Db 989 GCTGTGCTATGGAACGCTTCATACAGGTTGAGGAGTCCATACACACATGCAGCAGCA 930
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QY 1395 A-----GT-TT--TCTTTTCCC-----AAAC-----GGGAAGAACACAGCACACCCGG 1434
Db 694 AATAGGTTGTGATGTC-CTTCCAGCTATAAATCATTAGG-----ACAGC--CAGCAG 644
QY 1435 --CTTGACCCACTGCAA--GCTG--CATGTCGA--ACCTCTTTGGT-----CC 1477
Db 543 AACTT-----CCCCAGAGAGGATGGCCACC--GCACACACTTTTGTGAAGACGTTCC 589
QY 1478 -AGTGTGGCAAGGGC-----TCAG--CC--T--C-----TCTG--CCACAGAGT 1514
Db 588 GAGCGGCACAAGGTCAAGGATCATCAGGCCCATATCCAGGATTCCTGAGAGCCACATAGT 529
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QY 1535 --GGAGCT-----GG-----CCATC--CCAAATTCATCAG--TCCA--T-- 1566
Db 470 AGGAGCTGCACTGACCGCAGGATGACCGCACTCTCC-----TC--TCTGTATCCAGCTG 417
QY 1567 -AGAGACGA-----ACAG--AAT--GAGACT--TC-----CGGC 1595
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Db 357 CACCATAATCACAGCCAGTGTCCATCTCAGCTTGCAGCTTGGCATAAAAGTTACTC 298
QY 1628 -----GTCCCAACCAC--GGC-GTGTG-----TTGTGAAA--CGTGAATAA----- 1663
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QY 1664 -----AAAGAG 1669
Db 238 GTGTCCAGTCCCAAGAG 221

Db	813	GCAAGGTCAGAAAGAGGGACA-CGTACAGAGGAGCCCTCAAGAACGGGAGGCCCT	871
QY	308	ATTG-ACA-ACC-GGG-TCA-CCCGG	329
Db	872	AGTGACAGGTCAACCCAGAGGGGCTCGCTCAGGGCCCTCTCAGGACCATCCAGACT	931
QY	330	T-GGCTG-GCT-AA-ACC-GGAGCACCATCT-CTATGCT-GGGAAT	370
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QY	371	-----GAC-AAG-TGGT-----	418
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QY	390	-----CTCG-C-GTGG-----TC-C-TTCTGA	407
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QY	408	-----GCA-ACA-----C-----CCAA-----	418
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QY	419	AC-ACAG-TC-AGC-AAC-ATC-GA-ACCT	435
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QY	539	-----C-CCA-AAAT-ATG-AG-ATTTCTTCAG-----ATAT-567	
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QY	568	CTCCAT-----TAATGAAGGAAACAT-ATT-AGCC-----TCACCTGC-604	
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QY	605	AT-----AG-----C-----AACTG-GTAGACCAG-AG-CCTA-C-GGTTA-635	
Db	1584	ATCGGTCACTGAAGTCTGTCCGGTGAACAGCAGTAG-CAGAAAGCCAGCTG-1638	
QY	636	CTTGAG-ACACAT-CT-CT-C-CCA-AAGC-GG-TTGGC-TT-TGTG-----673	
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QY	699	AGG-----GCA-TCACC-----G-GGAGCAGTCAG-----GG-GACTA-729	
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QY	730	CGA-----GTGAGTGC-TC-ATGAC-----GTG-----754	
Db	1818	GGAGCTGTGAGTGGCTTTTCAAGATGACTCTCTCTCTTTTACTTCCAGTGAACAC	1877
QY	755	-----GCCGCG-CCGTGGT-----AC-GGA-----G-AGTAAAG-----GTCA-785	
Db	1878	TGATGTCTGTGCCCGCTTCCCTGATCCATCACTGAGAGAACGAAGTAGAGAAACGTGTAA	1937
QY	786	CC-----G-T-GAA-CTATC-C-ACCAT-----803	
Db	938	CCAGCAACAGACTCAGAACTATCTCTACCATGGGCCCAACCGGAGTCGGACGCAAGAA	1997
QY	804	-----ACAT-----TTCAAGAGCAAGG-G-----822	
Db	1998	TACTCTTACGTATGACATCTGTATTAATTAACAGCTTTCTG-GCCAAGAGATTC	2055
QY	823	TACA-----GG-TGTCCCGTGGGA-CAAA-----AGGGGA-----851	
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QY	852	---CAC---TGC---AGT---G-TGAAGCTCAGCA-GT---876	
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QY	877	---CCCCTC-AG---CAGA---ATTCAGTG-GTA---CAA---GG-905	
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QY	906	ATGACA---AA-----AGA-----AT-----TGAAG---926	
Db	2232	CTGTCACTGGAAACCCCATTCAGAACCAACCTGTTGGATATGATTAATCAATGAAGTTTC	2291
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QY	1050	-----CCAG-----CA-TCA-----T-GCT---A-TTTGG-TCCAG-----1073	
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Db	2826	CCAGGTCTGATGTCTCAGAGCCATCCACCGTTAGCCTTAATGGCACATG-TT-TCAA	2883
QY	1162	-----A-----TTTGTATG-----TCAGTGCCA-----CTTC-----1183	
Db	2884	GGCGAGCTTTTGTATGACACAGGAGGACCAAGGTGTCTTCTGTGTGGCAGAACT	2943
QY	1184	-----C-CCA-----CCC-GGG---AAAG-----G-1198	
Db	2944	GGAGCGATCCAAAAGAGCCCGAGGTCCCAAAAGAGTGTCTTCTCAGTGGACAG	3003

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QY 1199 C-TGCGC-----CAC-CACC-----ACC-ACCAAC-A--CAACAGCA 1231
Db 3004 CATGCTGAGGTAGTACTGACCTCAAGAGAAACCGACTGACTTACGCCCATCGA 3063
QY 1232 TGG-----CAACACC-----GAC-----A-GC-----AACC- 1252
Db 3064 TGGCTGTCAACCCCAACAGAGAAATGGACCTGCTGGAGGCATTTAACCACTCCAGGG 3123
QY 1253 A--TCAG--AT--ATAT-----AC--AA-ATGAATTAGA 1278
Db 3124 ACCTCAGGTATGCTGATCCCTCTTGGCTGGCGGTGGACTTAACTG--ACTGGA 3181
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Db 3182 GGAAC-CA-CCTTTCTCTGACATGCACTGGAATCCTCACTTGAGACCAAGCTT 3239
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QY 1335 -GGGA-A--AAGAG--TTTT-----AAAAAGAAA--TTG--AAAA- 1366
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QY 1367 -----TT-----GC-----CTGC-----AGAT-- 1379
Db 3360 AGTCCTTTCTGGATCCGAAGGACCTGTCAACCAAGCTCACTGGCTGACCTCAAGATCC 3419
QY 1380 -----ATTAG-----GT-A-----CA-A--TGGAGT----- 1397
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QY 1419 --AACA--CAG-----CA--CACCGGCTTG-----G--ACCCACTG 1447
Db 3540 GTTAAACAACACCTAGTACTAGTCA-----GCTTGTGAATGTGGCCATAGAACCCATTG 3595
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Db 3596 GTTATTTCAAGATTAGCTGCGCATGTTAGTGCATGCTGTATCCAGCAAGAAGATGA 3655
QY 1465 -----CCTCTTGG-----TG-----CC-----AGTG-----TGGGC 1486
Db 3656 GAGTCTCACTTGGCCTGTGTAGACTCTTCTCAAAACAACCAACAAAGTCTCTGG-- 3713
QY 1487 AAGGCTCAGCC-----TC--T-CTGCCA-CA-----GA 1512
Db 3714 AAGG--CAGCCATGTAGTCTTCCATCTTCCCGACACCTGAAGGCTGAGTGGGATGTGA 3770
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Db 3771 GTTAGAGGCCAGTTTATGCCACAGAGT--ACATTTACGCCAGCCTGGGCTACGAATG 3827
QY 1547 ---CC-----CAATTC-ATCAGT-----CCATAG 1568
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QY 1569 A-----GACGAACAG--AA-----TGAGACCT--TCCG--GCC-----CA 1597
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QY 1598 AGC-----GTGGC-----GC-----TGCGGCATTTTGGTAGACTGTGCCACACGG--C 1640
Db 3945 AGCATAGTGACATGCTTAGATGCTGGCATTTT-GTAGGCAAGGCAAGA-GGATCTC 4002
QY 1641 GTGT-----GT-----TGTGAAC-GTGA-----AATAA-----AAAGA 1668
Db 4003 GAGTCTAAGGTTAGCTCGTAAACAGTGAAGTCTTTTAGCAGCCTTAATTAATGAAGA 4062
QY 1669 -----G-CAAAA-----AAA 1678

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Db 4063 CCTGTGTTGTCAAAACAGCCTCAAA 4086

RESULT 28

AY402248

LOCUS

DEFINITION

AY402248

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

ORIGIN

Query Match

Best Local Similarity

Matches 1401; Conservative

0; Mismatches 160; Indels 2056; Gaps 403;

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Db 1333 GTTGATGTTCTATAGCATCGGATTCGGAATTTTGTAAAGTTTCGAGCCTTTTGA 1392

QY 30 -----AAA-----TCTCC-----TTGC--ACAAG-CTTG--AG-- 52

Db 1393 GTTCTTGCAAAAGTTTTCGAGATTTCTCCGACAGGTTGAGATGACCTTGTACAGTAC 1452

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QY 121 A-----AGAAAAAATCA-----TG-AAAAACA-----TCCAG--CCAA-----AA 154

Db 1570 ACTTATGTCAGAGAGAAAT-ATTGTGCCAAACAAAGGTTCCAGAGACGATACCGAA 1628

QY 155 ---ATG-----CACA-AT-----TCTATC--T-CTT---GGG----- 176

Db 1629 GGTGATGATTCTCATCAGATGGAAGTC-ATCAGATGCTTTCAGGGATCCTCTATAA 1697

AY402248 9022 bp DNA linear GSS 15-DEC-2003
Mus musculus COL12A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

AY402248 GI:39758234

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 9022)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 9022)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

1..9022

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

<1..>9022

/gene="COL12A1"

/locus_tag="HCM1160"

QY 177 ---CA-----ATCTT---CA---CG-----GG---GCTG---GCTGCT--- 199
Db 1688 AACTCAGGAATCCGACGCTGGAGATCTTCGAGTCGGTGTAAAGGACGCTGTGC---GCTCA 1746
QY 200 ---CTG---TG---TCTCTTCCAG---GAGTGCC---CGTG---CGCAGCGGA----- 235
Db 1747 GAACTGGAGCCATTGCTCTCTCTCC---TGCTGAGACCCACGCTGTTTCAAGTGGAGGATTT 1805
QY 236 -GATGCC-----ACC---TT---C---CCCAAAG-----CT-----ATGGA---CA 263
Db 1806 TGATSCCTTTTCAGAGATATCATTTGAACCTCACAGTCCATCTCTCTTAGAATTTGAGCA 1865
QY 264 ACGTGACGCTCGGAG-----GGGAGAG-----CG---CCACC----- 295
Db 1866 A---GA---GT---TGGCAGCTATAAGAAAGAAAGCTTTACGTTCCACCAAGAGATCTGAGGTT 1919
QY 296 ---CTCAGG---TGC---ACTA---TTGACAA---CCG---GGTACCCGGGTGCTGCTGCTAA 341
Db 1920 TACTCAGGTAAGTCTAATAGTTT---CAAGCTGAAATGCTCTCC-----T---CCTGG---AG 1969
QY 342 AC-----CGCAGCAC---CATCTCTA-----TGC---TGG---GA---ATGA---CA 374
Db 1970 ACAATGTCTTTTCGATATCACGTACATAC---AAGGATGCTAATGCTGATGATGAGTCA 2026
QY 375 -AGTGGT---GCCTGGATCCTC---GC---GTGGTCTCTTCTGAGCAACCCC----- 416
Db 2027 CAGTGGTGGAGCC---AGCCTCAGCACTAGT---GTTGTTCT---CAACAACTGAGGCCA 2079
QY 417 -AAACGCGAGT-----ACGATCTGAG---ATCCAGAACGTTGAT---GTG--- 454
Db 2080 GAAACCTGTACTTGGTGAATGTGACAGC---CGAGTAT---GAGGAC---GGCTTCAGTGTTC 2134
QY 455 -TATGAC-----GAGG---GCCC-----TT---AC---ACCTGCTCGGTG 484
Db 2135 CTATACTGGGAGGAGACCACTGCAGAGTAAAGGAGTTCCAGAAACCTG---AAGGTG 2193
QY 485 -CAG-----ACAGACA-----ACC---ACCMAAGACCTCTAGG----- 515
Db 2194 ACAGATGAGACTACGGACAGTTTAAACTTACCTGGTCCC---AAG---CTCCAGGGAGAGTC 2250
QY 516 -----TC-----C---ACC---TCAATGT-----GCA-----AGTAT 536
Db 2251 TTAAGTATCGGATTAGATACAGACCAAGTTTC---TGGTGGAGAAAGCAAGAGTGAGTA--- 2308
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Db 2309 C---CCAGCCAAT---CAGAGGAGGAAACA---CTGGAGA---ATCTGAGCCCGACACAAA 2361
QY 573 TTAATGAA-----GGGA---AC---AATATTAGCTC---ACCTGCAT----- 606
Db 2362 T---ATGAATATCTGTGATTTGCTGAATATT---CCTGGGACCTGGATCTCCACTGACAGG 2417
QY 607 -----AGCAACTG-----G---TAGA-----CC---AGAG---CCTACG---GTTACTTGA---G--- 642
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QY 643 AC---ACATCTCTCCCAAGC---G---GTTGGCTTTGTGAGT-----GAA-----GACG--- 683
Db 2476 ACAGCAT-----CAACGCTGAAGTTGTC---TTG---GAGTAGGGCACCAGAAAGGTGAAGC 2527
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QY 724 -----GG-----ACTAC-----GAG-----TG-----CAG---TGC 741
Db 2580 TGTGAGAGGAGATACAACTACTACCTACCTGTTGAGGAATTTGAAGGAAGGACACAGTATGA 2639
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RESULT 29
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DEFINITION
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factor type A domain containing protein, full insert sequence.
AK086942
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
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Fujisake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
REFERENCE
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 12043379
REFERENCE
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL:<http://genome.gsc.riken.go.jp/>
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source

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Db 972 CCACCATGCCACTCCAGCAGTGAAGACAGCGAAGATGATGTTTCCAGTAGGCCG 1031
QY 386 GATC-----CTCG-C-GTGG-----TC--C-TT 403
Db 1032 GGTCCCCACTTCTTTGACTCGACTGTGACTCAAGAGAGGGAGCGCTTCAGCAT 1091
QY 404 CTGA-----GCA--ACA-----C-----CCAA-----418
Db 1092 CTGACCAGAGTGTGCAGACAGATGCTGCTGCTGCTTCAAGAGGGAGAT 1151
QY 419 -----AC--GCAG-----TA-----CAGC--ATC--GA-----435
Db 1152 CCTCTGACCAGCAGCCCGACGCTGCAAACTTAACAACAGCTGAAACAAAGAGGGTA 1211
QY 436 -----GA--TCCAG-----AA-CGTG-GA--TG-----452
Db 1212 CCCTGGCTGCAGTGAACATCCAGCTCTCCCTGATAGGGGTGAGAAGTTGCTTAAGCAAA 1271
QY 453 -----TGATAGC-----AG-----GGCCCT-T-----AC--ACCT-- 476
Db 1272 TCCAGGCTTTGGAGGAGCGCACTCAGTGTCTTGGCTCTCTCCCCAGCAAGAGCACTAAG 1331

QY 477 -----GCTGGTG--CAGA-CAGA-CAAC--CACCCAAAGA-----CC 508
Db 1332 AGAAGTGCAGCGTCTAG-GAACCAAGAGCAGAGCAACATCA-CCAAAGCTGCTGCTGCCCC 1389
QY 509 TCT--A--GGGT-----CCA-----CCTCAT--TG--TCAAG-TATCT 538
Db 1390 TCTCCACTTGTGTACCTCCCCAGGCCCTTCCAGGCCCTCATCCAGCTGCAAGCTCTCT 1449
QY 539 -----C-CCA--AAATT-----GTAG--AG--ATTTCTTCAG-----563
Db 1450 AGGACTAAAGCGCAGCGCCGAGGAACTCTGTAGGGGAGCCAGCAGTGC-TGAGGAGGCC 1508
QY 564 ATAT-----CTCCAT-----TAATGAAGGGAACAAT-----ATT--AGCC-----TCAC 600
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QY 601 CTGCAT-----AG-----C-----AACTG--GTAGACCAG-AG-CCTA-C-G 631
Db 1568 CTGCATCGTCACTGAAGTCTTGTCCGGGTGAACAGCAGTAG--CAGAAGACCCAGCTG 1625
QY 632 GTTACTTGGAG--ACACAT-CT-CT-C-CCA-AAAGC-GG--TTGGC--TT--TGTG-- 673
Db 1626 G---CTTGAAGTCCCTTGTACTGCAACAGAGCAGGCAITTAGCTGTATCTGTGGA 1682
QY 674 ---AGT--GAAG-AC-----GA--ATA---CTT-GGA--ATTG 698
Db 1683 GGGAAAGTCAGAGCCACAGGAGGATCTGTGGGATGATATGGGCTTAGGAAGACTC 1742
QY 699 ---AGG--GCA-TCACCC-----G--GGAGCAGTCAG-----GG-G 725
Db 1743 TGACATGATTGCATCTATCTTAACCAAGAGATCAG-CAGAAAGCAGAGAAAGGAG 1801
QY 726 ACTA-CGA--GTGCAGTGCC--TCC---AATGAC-----GTG-- 754
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QY 927 -----GA-----AAGA--AAGG-----GG-----938
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QY 969 A--ACTATC--TTCTCAAT--GT--CTCTG--AACA--TGACT--ATG-- 1004
DB 2397 AAGAC--CAGCTGATTC--CACTGTAAACCTCTGTGTAGCACTGCTGCAGCTAGATGCC 2453
QY 1005 --GG--AA--CT--ACA--CTTGC-- 1018
DB 2454 AGCTGACCGGTTAAGCTTTCTGAGGACGAGCGGCCGTTTATGACATCTTTCTTGCAA 2513
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QY 1148 --CAC--CTG--CTT--CTCA-- 1160
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QY 1208 --CCA--CCA--CCA--CCA--CA--CA--CA--CA-- 1224
DB 2927 GAACGTGAGGCGGATCCAAAAGGCCAGGCTCCCAAGAGAGTGTCATTTGTCTCTCAGTGG 2986
QY 1225 A--CAGCAATG--GCA--AC--ACCGACAG-- 1246
DB 2987 ACCAGC--ATGCTGAGGTAGTAGTCACTGTCACCTCAAGAGAACCGACTGACTTACGCCAC 3045
QY 1247 --CAA--CCAATCAGA--T--ATATA-- 1264
DB 3046 CATCGATGGCTCTGTCAACCCCAACAGAGAAATGGACCTGTGGAGGCAITTTACCACTC 3105
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DB 3106 CCAGGACCTCAGTCAATGTGATCTCCCTTGGCTGGGGTGTGTGGACTTACCTGAC 3165
QY 1277 --GAAGAAACACAGCCT--CATG--GG--AC--AGA--AA 1304
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QY 1305 --TT--TGA--GG--GAG--GG--GAACAAGA--ATAC--TTTG-- 1333
DB 3224 GCTTGTGACCGGATTTACCGAGTAGGACAGAGAAGGATGTGTGTCATACACAGGTTTGTG 3283
QY 1334 --G--GGGA--A--AAGG--TTTT--AAAAAGAAA--TTG--A 1363
DB 3284 TGTGAGGGGACATGGGAGAGAGATCTTACAGCTCCAGAGAAAAGAAAGATTGGCA 3343
QY 1364 AAA--TT--CTTGC-- 1377
DB 3344 AAACAGGTCTTTCTGGATCCGAGGACCTGTACCAAGTCTACACTGGCTGACCTCAAG 3403
QY 1378 AT--ATTAG--GT--A--CA--A--TGGAGT-- 1397
DB 3404 ATCCTCTTTGGCATCTAGTCTGCTGGAGTGATGCTTTTCCATGATCTGGAGTC 3463
QY 1398 --TTT--CTT--TTCC--C--AA--ACGGG--A 1416

DB 3464 TTAGATTTCACTCTACTCGAAGTGAGGCTTGTCTCTAGTAGGAATTGAGATGGGTTA 3523
QY 1417 --AG--AACA--CAG--CA--CACCGGCTTG--G--ACCC 1443
DB 3524 CCAGGTTAACAAACACAGTTAGTCACTCA--GCTTGTGTAATGTGGGCCATAGAAACCC 3579
QY 1444 ACTG--C--AAGC--TGCAT--C--GT--GCAA-- 1464
DB 3580 ATTGTTATTTTCAAGATTAAGCCTGGCATGTAGTGCATGCTGTAAATCCAGCAAGAATA 3639
QY 1465 --CCTCTTTGG--TG--CC--AGTG--T 1482
DB 3640 TGGAGAGTCCACITTTGGCCTGTGTAGACTCTTTCTCAAAACAAACCAAAAGTGTCT 3699
QY 1483 GGGCAAGGCTCAGCC--TC--T--CTGCCA--CA-- 1510
DB 3700 GG--AAGG--CAGCCATGTAGTCCATACITTTCCAGCACCTGMAAAGGCTGAGTGGGAT 3754
QY 1511 --GAGT--GCC--CCCAC--GTGGAACA--TTCTGG--AG--CTGGCC-- 1544
DB 3755 GTGAGTTAGGCGCCAGTTTATGCCACAGAGT--ACATTTTCAAGCCAGCCTGGGCTACAG 3811
QY 1545 --AT--CC--CAAA--TTCAATCAGT--CC 1564
DB 3812 AATCAGACCGTGTCTTAGAAAAACAAAGTAAACACAGTGTGAGCTTTGGCGTTGGATGCC 3871
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DB 3872 --TGAAGCTGAGTCTGGAAGAACTGTGTAAGTGTCTGGGTGTGA--TGCTCAGGGAGCCAT 3928
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QY 1665 AAGA--G--CAAAA--AAA 1678
DB 4047 AAGACCTCTCTGTCAAAACAGCCTCAAA 4074

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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 14:04:04 ; Search time 4221.99 Seconds
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1035	100.0	1679	6	AX358872	AX358872 Sequence
2	1035	100.0	1679	6	AX362365	AX362365 Sequence
3	1035	100.0	1679	6	AX403748	AX403748 Sequence
4	1035	100.0	1679	6	AX454470	AX454470 Sequence
5	1035	100.0	1679	6	AX464242	AX464242 Sequence
6	1035	100.0	1679	6	AX490948	AX490948 Sequence
7	1035	100.0	1679	6	AX358331	AX358331 Homo sapi
8	979.3	94.6	1839	9	AX665342	AX665342 Sequence
9	973.9	94.6	1839	9	AF126426	AF126426 Homo sapi
10	973.9	94.1	1068	6	AX665344	AX665344 Sequence
11	970.3	93.7	1104	6	AX665346	AX665346 Sequence
12	966.7	93.4	1140	6	AX665348	AX665348 Sequence
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14	833.7	80.6	2040	10	RNU16845	RNU16845 Rattus norv
15	829	80.1	1615	10	BC023307	BC023307 Mus muscu
16	814.4	78.7	1410	10	AF282980	AF282980 Mus muscu
17	690	66.7	1257	5	GGCEPUI	Z72497 G.gallus mR
18	681.3	65.8	1638	12	AF271233	AF271233 Synthetic
19	673	65.0	1035	5	AB011810	AB011810 Gallus ga
20	669.6	64.0	1058	5	AF292935	AF292935 Gallus ga
21	651.9	63.0	1013	5	AF292936	AF292936 Gallus ga
22	636.9	61.5	6380	9	HSM805672	BX537377 Homo sapi
23	633.8	61.2	1478	9	HUMORCAM	L34774 Human (clon
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25	632.4	61.1	3216	5	GGCEPUS	AU225897 Gallus ga
26	629.5	60.8	2593	4	BTBOCAM	X12672 Bovine mRNA
27	628.7	60.7	2935	12	AF271618	AF271618 Synthetic
28	619.1	59.8	2179	10	RATCALMB	M88710 Rattus norv
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30	616.2	59.5	3069	10	RATCALMA	M88709 Rattus norv
31	613.5	59.3	1533	5	FFNINH55A	Y08170 Gallus gall
32	606	58.6	1556	5	AF292934	AF292934 Gallus ga
33	535.3	51.7	20731	9	AP004721	AP004721 Homo sapi
34	535.3	51.7	40387	9	AP005155	AP005155 Homo sapi
35	490.8	47.4	1107	5	GGLAMPG9	Z94718 G.gallus mR
36	490.4	47.4	1194	5	GGLAMPG11	Z94719 G.gallus mR
37	489.9	47.3	1238	6	AR030575	AR030575 Sequence
38	489.9	47.3	1238	6	AR220258	AR220258 Sequence
39	489.5	47.3	1238	10	RNU31554	U31554 Rattus norv
40	489.5	47.3	1158	5	GGLAMPG19	Z94720 G.gallus mR
41	489.5	47.3	239249	2	AC102028	AC102028 Mus muscu
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43	483	46.7	1640	9	BC033803	BC033803 Homo sapi
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47	481	46.5	191071	9	AP004248	AP004248 Homo sapi
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49	476.8	46.1	1017	9	HSU41901	U41901 Human limbl
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	72	451.9	43.7	170302	9	HS0402821	AL049553 Human DNA
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	76	451.4	43.6	8405	10	AP221622	AP221622 Rattus no
	77	451	43.6	228501	10	AC094784	AC094784 Rattus no
	78	450.8	43.6	2684	10	HAMHGC0B	M12705 Syrian hams
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	80	450.3	43.5	5117	6	BD158655	BD158655 Primer fo
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	82	450.3	43.5	183252	2	AC023637	AC023637 Homo sapi
	83	450.2	43.5	129389	9	HS526114	Z82214 Human DNA s
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	88	450.1	43.5	4510	9	MACAPOA	J04635 Rhesus monk
	89	450.1	43.5	7368	9	HSU55208	U55208 Human myosi
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	91	450	43.5	186792	2	AC116523	AC116523 Mus muscu
	92	449.9	43.5	348517	1	BX248354	BX248354 Corynebac
	93	449.4	43.4	8461	10	AB035201	AB035201 Rattus no
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	95	449.4	43.4	259563	9	AC126930	AC126930 Mus muscu
	96	449.3	43.4	163475	2	AC092619	AC092619 Homo sapi
	97	449.2	43.4	6268	6	AX098230	AX098230 Sequence
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VERSION					
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REFERENCE	1				
AUTHORS	Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL	Patent: WO 0193983-A 125 13-DEC-2001; Genentech Inc. (US)				
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DEFINITION Sequence 125 from Patent WO0208288.
ACCESSION AX362365
VERSION AX362365.1 GI:18694640
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 125 31-JAN-2002;
Genentech, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 134 ATGAAACCATCCAGCAAAATGACAAATCTATCTCTGGCAATCTTCAAGGGCTG 193
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DB 194 GCTGCTGTGTCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 253
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DB 314 AACCGGGTCAACCGGGTGGCTGCTAAACCGCAGCACCCTCTATGCTGGGAATGAC 373
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DEFINITION AX403748
ACCESSION AX403748
VERSION AX403748.1 GI:21437184
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ashkenazi, A., Baker, K., Botstein, D., Desnoyers, L., Eaton, D.L.,
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P., Gurney, A., Kljavin, I.J., Mather, J.,
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,
Williams, P.M., Wood, W.I. and Zhang, Z.
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JOURNAL Patent: WO 0077037-A 103 21-DEC-2000;
Genentech Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 3.6e-06;
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VERSION
KEYWORDS
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Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Goddard, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,

Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.

Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 55 31-JAN-2002;

JOURNAL

Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 1035; DB 6; Length 1679;
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 ACCESSION AX464242
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 Genentech Inc. (US)
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 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
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 DEFINITION Sequence 55 from Patent WO0200690.
 ACCESSION AX490948
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 Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.L.
 and Ye, W.
 Compositions and methods for the diagnosis and treatment of
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 Patent: WO 0200690-A 55 03-JAN-2002;
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DEFINITION Sequence 100 from Patent WO03002765.
ACCESSION AX665342
VERSION AX665342.1 GI:29290464
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
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AUTHORS Sellar,G.C. and Gabra,H.
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JOURNAL Cancer Research Technology Limited (GB)
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AUTHORS	Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
TITLE	Cloning and identification of human neurotrophin full length cDNA
JOURNAL	Unpublished
REFERENCE	
AUTHORS	Li,G., Jin,J., Tan,X., Hu,S., Yuan,J. and Qiang,B.
TITLE	Direct Submission
JOURNAL	Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
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VERSION AX665344.1 GI:29290465
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REFERENCE
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 102 09-JAN-2003;
Cancer Research Technology Limited (GB)
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DEFINITION Sequence 104 from Patent WO03002765.
ACCESSION AX665346
VERSION AX665346.1 GI:29290466
KEYWORDS
SOURCE Homo sapiens (human)
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AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
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Cancer Research Technology Limited (GB)
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AX665348.1 GI:29290467
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AUTHORS Sellar, G.C. and Gabra, H.
TITLE Cancer
JOURNAL Cancer Research Technology Limited (GB)
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REFERENCE Struyk,A.F., Canoll,P.D., Wolfgang,M.J., Rosen,C.L., D'Eustachio,P.
AUTHORS and Salzer,J.B.
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TITLE Cloning of neurotrophin defines a new subfamily of differentially
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JOURNAL expressed neural cell adhesion molecules
MEDLINE J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
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AUTHORS Salzer,J.B.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
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QY 993 GCTGCTGCTCTCTGCTGCTTCTGACCTGCTTCTCAAAATTTGA 1035
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LOCUS Mus musculus neurotrimin, mRNA (cDNA clone MGC:30504
IMAGE:4480983), complete cds.
ACCESSION BC023307.1 GI:23958300
VERSION MGC.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM
REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1615)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smalls, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
PUBMED
2 (bases 1 to 1615)
Strausberg, R.
Direct Submission

JOURNAL

REMARK
COMMENT

Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, R.G., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 41 Row: h Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 26986610.

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 QY 213 CAGCACCATCTCTATGCTGGGAATGACAAGTGGTGGCTGGATCCTGGCTGGCTCTTCT 272
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 DB 316 GAGTAACACCCAGACCCAGTACAGCATTTGATGATCCAGATGTTGATGATGATGAGG 375
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 DB 376 CCCTTATACCTGCTCGGTGACAGACAGACACCAACCTCTAGGGTCCACCTCAT 435
 QY 393 TGTGCAAGTATCTCCAAAATTTGAGAGATTTCTTCAGATATCTCCATTAATGAAGGAA 452
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 QY 453 CAATATTAGCTCAGCTGCATAGCACTGCTAGACAGACCTCTAGGGTCCACCTCAT 512
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RESULT 16
 AF282980
 LOCUS AF282980 1410 bp mRNA linear ROD 01-FEB-2001
 DEFINITION Mus musculus neurotrophin mRNA, complete cds.
 ACCESSION AF282980
 VERSION AF282980.1 GI:12642539
 KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE

1 (bases 1 to 1410)
 Kim, T.H., Choi, S.C., Kim, J., Jeon, J.W., Kim, K.D. and Lee, S.H.
 Cloning and expression of mouse neurotrophin gene in the developing
 nervous system

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1410)
 Kim, T.H., Choi, S.C., Kim, J., Jeon, J.W., Kim, K.D. and Lee, S.H.

AUTHORS

Direct Submission

TITLE

Submitted (27-JUN-2000) Graduate School of Biotechnology, Korea

JOURNAL

University, 1-5-ka Anam-dong Sungbuk-ku, Seoul 136-701, Korea

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 78.7%; Score 814.4; DB 10; Length 1410;
 Best Local Similarity 85.6%; Pred. No. 0.013;
 Matches 897; Conservative 0; Mismatches 113; Indels 38; Gaps 11;

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LOCUS G.gallus mRNA for CEPU-1.
DEFINITION G.gallus mRNA for CEPU-1.
ACCESSION Z72497
VERSION Z72497.1 GI:1325950
KEYWORDS Brain; CEPU-1; glycoprotein; GPI-anchor protein.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS Spatmann,F. and Brummendorf,T.
TITLE CEPU-1, a novel immunoglobulin superfamily molecule, is expressed
by developing cerebellar Purkinje cells
J. Neurosci. 16 (5), 1770-1779 (1996)
JOURNAL 96370549
MEDLINE 877445
PUBMED 877445
REFERENCE
AUTHORS Brummendorf,T.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-1996) Brummendorf T., Max-Planck-Institute for
Developmental Biology, Molecular Biology, Spemannstrasse 35,
Tuebingen, Germany, 72076
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LOCUS AF292935 1058 bp mRNA linear VRT 24-AUG-2000
DEFINITION Gallus gallus CEPU-Se alpha 2 isoform (CEPU-Se) mRNA, complete cds.
ACCESSION AF292935
VERSION AF292935.1 GI:9887384
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1058)
Lodge,A.P., McNamee,C.J., Howard,M.R., Reed,J.E. and Moss,D.J.
Characterisation of CEPU-Se, a secreted isoform of the Iglon family
protein CEPU-1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1058)
Lodge,A.P. and Moss,D.J.
Direct Submission
AUTHORS
TITLE
JOURNAL
JOURNAL Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The
University of Liverpool, Ashton Street, Liverpool, Merseyside L69
3GE, UK
FEATURES
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DB 105 GCGCGACTCT-CTCTTCCAAAGAGTGCCCGTGGCAGCGAGAGTCCACCTTCCCCA 163
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DB 164 AAGCTATGGACAACAGTGCAGCTCCGCGAAGGGAGAGTCCACCTCAGGTGCTCCGTGG 223
QY 179 ACAACCGGGTACCGGGTGCGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATG 238
DB 224 ACAACCGGGTACCGGGTGCGCTGGCTAAACCGCAGCAGATCTCTATGCTGGGAATG 283
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QY 299 TCGAGATCCAGACGTGGATGTGATGACG-AGGGCCCTTACACTGCTCGGTGCAGACA 357
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Query Match 64.7%; Score 669.6; DB 5; Length 1058;
Best Local Similarity 77.1%; Pred. No. 2.5;
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DB 105 GCGCGACTCT-CTCTTCCAAAGAGTGCCCGTGGCAGCGAGAGTCCACCTTCCCCA 163
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DB 164 AAGCTATGGACAACAGTGCAGCTCCGCGAAGGGAGAGTCCACCTCAGGTGCTCCGTGG 223
QY 179 ACAACCGGGTACCGGGTGCGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATG 238
DB 224 ACAACCGGGTACCGGGTGCGCTGGCTAAACCGCAGCAGATCTCTATGCTGGGAATG 283
QY 239 ACAAGTGTGCTGTGATCTCTCGGTGGTCTTCTTGGCAACACCCAAACGAGTACAGCA 298
DB 284 ACAAGTGTGCTGTGATCTCTCGGTGGTCTTCTTGGCAACACCCAAACGAGTACAGCA 343
QY 299 TCGAGATCCAGACGTGGATGTGATGACG-AGGGCCCTTACACTGCTCGGTGCAGACA 357
DB 344 TCCAGATCCAGACGTGGACGTGTACGATGAAGGGCCC-TACACTGCTCGGTGCAGACA 402

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RESULT 21
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LOCUS
DEFINITION Gallus gallus CEPU-Se alpha 1 isoform (CEPU-Se) mRNA, complete cds.
ACCESSION AF292936
VERSION AF292936.1 GI:9887386
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1013)
Lodge,A.P. and Moss,D.J.
Characterisation of CEPU-Se, a secreted isoform of the Iglon family
protein CEPU-1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1013)
Lodge,A.P. and Moss,D.J.
Direct Submission
AUTHORS
TITLE
JOURNAL
JOURNAL Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The
University of Liverpool, Ashton Street, Liverpool, Merseyside L69
3GE, UK
Location/Qualifiers

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659 ACTACCCACCGTACATCTCGGATGCGAAGAGCACCGGTGTGCCGGTGGGCGACGAAGGG-- 716
 719 CA--CTGCAGTGTGAAGCCCTCAGCAGTCCCGCTCAGCAGAAATTCACAGTGGTACAGGATGA 776
 717 CATCCTGATGTGAAGCCCTCCGCTGTGCCTCTGCTGACTTTCAGTGGTACAAAGACGA 775
 777 CAAAAGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCCTCAA 836
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 957 GAGCAACGGCAC-----GTCAGGA--GGG--CAGG--CTGCGT--CTGCTGCTG--CCT 1002
 937 GAGCA--GCATGAGGGTCTGGGATGGGAGCCCGGCACAGCTTAAC--GG--AG--TGACCA 990
 1003 CTTCGTGCTCTTGC--ACCTGC 1021
 991 CCACGTG---TGCAAGACGTGC 1008

RESULT 22
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 LOCUS Homo sapiens mRNA; cDNA DKFP686H1949 (from clone DKFP686H1949);
 DEFINITION complete cds.
 ACCESSION BX537377.1 GI:31873255
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (base 1 to 6380)
 AUTHORS Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
 Fobo,G., Han,M. and Wiemann,S.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuhberg, GERMANY
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
 consortium of AGOWA (Berlin/Germany) within the cDNA sequencing
 consortium of the German Genome Project.
 This clone (DKFP686H1949) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
 information about the clone and the sequencing project is available
 at http://mips.gsf.de/proj/cDNA/.
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gene
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Best Local Similarity 71.4%; Pred. No. 46;
Matches 820; Conservative 0; Mismatches 159; Indels 169; Gaps 71;

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DB 173 ACAACTGCCCTGCTCT-----TCATCCAGAGGTGCCCGTGGCAGCGAGATGCCACT 227
QY 113 TCCCAAGCATATGACACACGTGACGCTCCGCGAGGGGAGAGGCCACCTCAGGTGCA 172
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DB 288 CCATAGATTGACCGGGTAAACCGGGTGGCTGGCTTAACCGGAGCACCATCTCTACGCTG 347
QY 233 GGAATGACAGTGGTGGCTGGATCTCGCTGGTCTCTCTTCTGAGCAA--CACCCAAAGCA 290
DB 348 GGAATGACAGTGGTGGTGGATCTCGCTGGTCTCTCTTCTGATCATCTGGTCAATACAC 405
QY 291 GTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACTGCTCGGT 350
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DB 466 GCAGACAGACATCATCCCAA--ACGTCCCGGTTTCACTTAATAGTCAAGTCTCTCTC 524
QY 409 AAA--ATTGTAGAGATTCT--TCAGATATCTCCATTAATGAAGGAA--CAATATTAGCC 463
DB 525 AGATCAT---GA-ATATCTCTCAGACATCACTGTGAATG--AGGAAGCAGTGTGACCC 578
QY 464 TCACCTG---CATAGCACTGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTC 520
DB 579 T--GCTGTGTC--TTGCTATTGGCAGCAGACAGCACTGTGACATGGAGACAC--CTGTC 633
QY 521 ---CCA--AAG--CGGTTGGCTTCTGTAGTGAAGCAATCTTGGAAAT--TCAGGGCAT 572
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QY 573 CACCCGGGAGCAGTCCAGGAGCTACGAGTGCAGTGCCTCCATGACGTGGCGCGCCCGT 632
DB 691 CAAGCGAGACAGTCCCGGGAGTACGAATGCAGCGCGTTGAACGATGTGCTGCGCCGA 750
QY 633 GTATCGGAGAGTAAAGGTCAACGCTGAATATCCACATATTTTCAAGAGCAAGGGTAC 692
DB 751 TGTGCGGAAAGTAAATACCTGTAAACTATCTCCTCCTATATCTCAAAAGCCAA--GAAC 808
QY 693 A--GGTGTCCCGTGGGACAAAGGAGCA--CTGCAG--TGGAAGCCTCAGCAGTCCCC 747
DB 809 ACTGGTGTTCAGTCCGTGAGAGGG--CATCTGT--AGCTGGAAGCCTCTGCACTGCC- 864
QY 748 TCA--GCAGAAATTCAGTGGTACAAAGGATGACAA--A-----AG--ACTGAT--T-GAAGGA 795
DB 865 -CATGGCTGAATTCAGTGGTTCAGGAAGA-AACAGGTTAGCCACTGGTGTGATGA 922
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QY 913 AATGCCAGCATCATGCTATT---TGFTCCAGGCGCCTCAGCGA--GGTG--AGCAA--CGG 965
DB 1031 AATGCCAGCATCA--C-ATTGTATGGCCCTGGAGCAGCTCATGATGGTGTGA--AACTCGG 1085
QY 966 CACGTCCAGGAGGCA--GGC-TGCGTCTGGCT-----G-----CT--GCC-----TCTT 1005
DB 1086 C-C-TCCA-CA--GCATCTGGCTGTCTCTGGCTATCAGGACCTCTTAGCCACTTCTT 1140
QY 1006 -----CT-GTCTTT---GCA-----CCTGCTTCT-CAAT----- 1030
DB 1141 CATCAAGTTTGTATAAGAAATCCTAGTCTCTGAGCAACGCTGCTTCTCCATATCACA 1200
QY 1031 ---TTTGA 1035
DB 1201 GACTTTAA 1208

RESULT 23
LOCUS HUMOBAM 1478 bp mRNA linear PRI 21-JUL-1994
DEFINITION Human (clone PHOM) opioid-binding cell adhesion molecule mRNA,
complete cds.
ACCESSION L34774.1 GI:514373
VERSION L34774.1
KEYWORDS opioid-binding cell adhesion molecule.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1478)
AUTHORS Shark, K.B. and Lee, N.M.
TITLE Cloning, sequencing and localization to chromosome 11 of a cDNA
encoding a human opioid-binding cell adhesion molecule (OBAM)
JOURNAL Unpublished (1994)
COMMENT Original source text: Homo sapiens (library: Stratagene brain)
occipital cortex cDNA to mRNA.
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ORIGIN

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Best Local Similarity 70.0%; Pred. No. 14;
Matches 817; Conservative 0; Mismatches 145; Indels 205; Gaps 77;

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QY 43 ----GCAATCT--TCAGGGGCTGGCTGCTCTGTGCTCTT-----CCA-AGGAGTGGCGGT 92
Db 97 TCGTG---TCTCTCA-----GGCTG--CTGT-TC-CTTGTACCCACAGGAGTGGCGGT 142
QY 93 GGGCAGCGAGATGCCACCTTCCCCAAAGCTATGACAACTGACCGGTCCGGCAGGGGGA 152
Db 143 GCGCAGCGAGATGCCACCTTCCCCAAAGCTATGACAACTGACCGGTCCGGCAGGGGGA 202
QY 153 GAGCGCACCTCAGGTGACATATTGACAAACCGGGTCAACCGGGTGGCTGGCTGCTGCTAAACCG 212
Db 203 GAGCGCACCTCAGGTGACATATTGACAAACCGGGTGGCTGGCTGCTGCTGCTAAACCG 262
QY 213 CAGCACCATCTCTATGCTGGGAATGACAAAGTGGCTGGATCCTCGGCTGGCTCTTCT 272
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QY 331 GGCCTTACACCTGCTGGTGGAGAGACAGACACCA--CCCAAGACCTCTAGGGTCCACCT 389
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Db 495 G-AGGAAAGCAGTGTGACCT--GCTGTGTC--TTGCTATTGGCAGACAGACCACTCT 550
QY 501 TACTTGGAGACATCTCTC--CCA--AAG--CGGTTGGCTTTGTGAGTGAAGACGAT 553
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QY 613 AATGAGTGGCGCGCGCTGGTGGAGAGTAAAGGTCAACCTGAACTATCCACCATAC 672
Db 666 AACGATGTGCTGCGCGCGCTGGTGGAGAGTAAAGGTCAACCTGAACTATCCCTCCCTAT 725
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Db 838 TAGCCACTGCTGGATGAATG--AGGATTGAAA-----ACAA-AGGCCGATGTCCACT 890
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RESULT 24
AX665340
LOCUS AX665340 3110 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 98 from Patent WO03002765.
ACCESSION AX665340
VERSION AX665340.1 GI:29290463
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 98 09-JAN-2003;
Cancer Research Technology Limited (GB)
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Query Match 61.2%; Score 633.8; DB 6; Length 3110;
Best Local Similarity 70.0%; Pred. No. 27;
Matches 817; Conservative 0; Mismatches 145; Indels 205; Gaps 77;
QY 3 GA-AA-----ACC--ATCCAGCC--AAAAATGCACAATCTATCTCTTGG 42
Db 47 GAGAAATGGGGTCTGTGGGTACTGTTCTCTGCGCTGGAAAGTGC-----CTCGTGG 96
QY 43 ---GCAATCT--TCACGGGCTGGCTGCTGTGCTCTT-----CCA-AGGAGTGGCGGT 92
Db 97 TCGTG--TCTCTCA-----GGCTG--CTGT-TC-CTTGTACCAAGAGTGGCGGT 142
QY 93 GCGCAGCGAGATGCCACCTTCCCCAAAGCTATGACAACTGACCGGTCCGGCAGGGGGA 152
Db 143 GCGCAGCGAGATGCCACCTTCCCCAAAGCTATGACAACTGACCGGTCCGGCAGGGGGA 202
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QY 950 GCGA-GGTG-AGCAA--CGGCACCTCGAGAGGCA--GGC-TGCGTCTGGCT-----G 996
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QY 997 ---CT--GCC---TCTT-----CT-GTCTT---GCA-- 1016
Db 1056 ACCCTCTAGCCCACTTCTCATCAAGTTTGTAGAAATCTTAGTCTCTGAGCAAC 1115
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Db 1116 GCCTGCTTCTCATATCACAGACTTTAA 1142

RESULT 25
LOCUS GCCEPUS 3216 bp DNA linear VRT 17-AUG-1999
DEFINITION Gallus gallus CEPU gene.
ACCESSION AJ225897
VERSION AJ225897.1 GI:2897596
KEYWORDS CEPU gene; neural secreted glycoprotein.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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REFERENCE
1 Kim,D.S., Rhee,T.H., Moss,D.J. and Kim,J.Y.
cDNA cloning of the CEPU, a secreted type of neural glycoprotein
belonging to the immunoglobulin-like oploid binding cell adhesion
molecule (OBAM) subfamily
Mol. Cells 9 (3), 270-276 (1999)
99347334
MEDLINE
PUBMED 10420985
REFERENCE
2. (bases 1 to 3216)
Kim,D.
Direct Submission
Submitted (16-FEB-1998) Pukyong National University, Microbiology,
599-1 Daeyeon-3dong, Nam-gu, Pusan 608-737, KOREA (ROK)
LOCATION/Qualifiers
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source
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mRNA

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ORIGIN

Query Match 61.1%; Score 632.4; DB 5; Length 3216;

Best Local Similarity 48.3%; Pred. No. 29;

Matches 871; Conservative 0; Mismatches 155; Indels 776; Gaps 68;

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QY 148 GGGGAGAGCGGCCACCTCTCAGGTGCACTATTGACAAACGGGTGACCCGGGTGGCTGGCTA 207
Db 460 GGGGAGAGTGGCAACGCTCAGGTGCTCCGTGGACAACCGCGTCAACCGCGTGGCTG 519
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Db 520 AACCGAGAGCATCTCTTATGCGGCAATGACAAGTGGTGGTGGACCGGAGGTGGTG 579
QY 268 CTTCTGAGCAACACCCAAACGAGTACAGATCCAGATCCAGATCCAGATCCAGATCCAGAT 639
Db 580 CTCTGGCAACACCAAAACCCAGTACAGATCCAGATCCAGATCCAGATCCAGATCCAGAT 639
QY 328 G-AGGCGCTTACCTCTCGGTGGAGACAGACACACCCAAAGACTCTTAGGGTCCA 386
Db 640 GAAGGGCCC-TACACCTGCTCGGTGGAGACAGACATCAACCCCAAGACTCTCGGTGCA 698
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Db 699 CTTCTATGCAAGTATCTCCCAAAATTGTA--GAGATTCTTTCAGATATCTCCATTAAT 444
QY 445 GAAG--GGAACAATATTAGCCTCACCTGATAGCACTGCTAGACAGAGCGCTACGGTTA 502
Db 757 GAAGTGG--CAACGTGACGCTCACCTGATAGCAACCGGAGGCGGAGACCCCAATCA 814
QY 503 CTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTTGTAGTGAAGACGAATATCTTGGAAA 562
Db 815 CTTGGAGACACATCTCTCCCAAGCGTGTGGCTTTTGTAGTGAAGACGAATATCTTGGAAA 874
QY 563 TTCA-GGGCATCAACCGGAGAGAGTCAAGGGAGTACAGTGTGAGTGTGCTTCCCAATGACGTG 621
Db 875 -TCACAGGCATCACGAGGGAGAGTTCGGGCGAGTACAGTGTGAGTGTGCTTCCCAACGAGTG 933
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QY 646 -----A-----AGG-----TCACC----- 654
Db 994 GGGACAGCCAGGGCCACATTGTCACCCCGAGGGGATGCACCGTTACCTGCCCTTGG 1053
QY 655 -----GTG----- 657
Db 1054 TCCACACCCAGCCTGGCAGCAGCAGGTTTCCAAAGCAGGTGGTCTTGGCCCTTTATT 1113
QY 658 -----AA----- 663
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QY 664 CCACC-----ATA----- 671
Db 1174 CAACCTGAGTTTCTGCTGTGCTGATGCTGTGCTGATAACCTCAGGGGAGAGGG 1233
QY 672 -----CATTT----- 676
Db 1234 AAGTGAGCAGTAACAGGCAATTTCTCGTTTGAATAAATAAAGAGAGAGAGGAAG 1293
QY 677 -----CAGAAG----- 682
Db 1294 AAAGCAGCACTGTTGTGCTCATAGACAGAGTGAAGACCCTCCAAACCCCCAGACTC 1353
QY 683 -----CAAG-----GGT----- 690
Db 1354 CACTGTGGCCACCCCTGGAGCTTCCGGGCATCAGGAGAGCCCAAGAGTGTGCTGCTTG 1413
QY 691 ---A--CA-----GT-----GTCCT----- 701
Db 1414 GAGGATGAGGATGTGGTTGGGTGCCCCCATCTCTCAGCCCTTTCGGACAGCAGACA 1473
QY 702 -----CG-----TGGG-- 707
Db 1474 AGAGCTGAGGAGCTGGGCAATAGCTCGAGATGATTTTCTCCTTCTTGATGGGA 1533
QY 708 -ACAAAAG----- 715
Db 1534 AAGAAAGGAGAGAGAGGTGGGAGGACCAACCCCGAGCTCGTCTCCACAGACCCA 1593
QY 716 -----GGA-----CAC-----T-----GCA-----G 726
Db 1594 CGGTACATCTCGATGCGAAGACCCCGTGTGCGGTGGGCGAGAGGGCATCTGTATG 1653
QY 727 TGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAAAGACTG 786
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QY 945 CG--TCAGC-----GAGGTAGCA--AC-G-GCAGTCGAGGAG--GGAGGCT---CGC 988
Db 1894 CGGCACGCTTAACCGGA--GTGACCAACCACTGTGCAAGACGTGCACTGGAAAGCTGGGCT 1952
QY 989 TCTGG-CTGCTGC-----CTC-----TTCT-----GGTC-----T 1012
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QY 1034 GA 1035
Db 2073 GA 2074

RESULT 26
BTOBCAM
LOCUS      Bovine mRNA for opioind binding protein/cell adhesion molecule
DEFINITION
ACCESSION  X12672.1 GI:585
VERSION    X12672.1
KEYWORDS   cell adhesion molecule; glycoprotein; immunoglobulin superfamily;
           membrane protein; opioind binding protein.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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REFERENCE  1 (bases 1 to 2593)
            Schofield, P.R., McFarland, K.C., Hayflick, J.S., Wilcox, J.N.,
            Cho, T.M., Roy, S., Lee, N.M., Loh, H.H. and Seeburg, P.H.
            Molecular characterization of a new immunoglobulin superfamily
            protein with potential roles in opioind binding and cell contact
            EMBO J. 8 (2), 489-495 (1989)
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED     89251576
          2721489
AUTHORS
REFERENCE  2 (bases 1 to 2593)
            Schofield, P.R.
DIRECT SUBMISSION
JOURNAL
COMMENT    Submitted (23-AUG-1988) Schofield P.R.
FEATURES   Data kindly reviewed (19-may-1989) by Schofield P.R.
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Best Local Similarity 70.5%; Pred. No. 27;
Matches 802; Conservative 0; Mismatches 161; Indels 174; Gaps 61;
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QY 234 GAATGACAAGTGGTCCCTGGAATCTCTGCGTGGTCTCTGAGCAACCCAAACGCACTA 293
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QY 294 CAGCATCAGATCAGAAAGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCA 353
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QY 354 GACAGAACACCAACAGACCTCTAGGTCACCTCATTTGCAAGTATCTCCAAAT 413
Db 1138 GACGACAAACCAACAGACCTCCGGTCCACCTCATCTGTCAGGTCCCTCCCAAT 1197
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Db 1198 CATG-A-ACATCTCTCAGATGTCACTGATGAGGGAGC-----AGGTCACCTG 1249
QY 471 C-----ATAGCACTGTGACGAGAGCTTACGTTACTTGGAGACATCTCTC---CC 522
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QY 523 A--AAG--CGGTTGGCTTTGAGTGAAGAGCAATCTTGGAAT--TCAGGGCATCACCC 577
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QY 578 GGGAGAGTCAGGGAACCTAGAGTGCAGTGCCTCCAATGACGTGGCGCGCCCTG--GT 635
Db 1365 GTGACCACTCGGAGATGATGAGTGCAGCGCTTGAATGATGTTGCTGC--CCC-TGACGT 1422
QY 636 ACGGAGATGAAGTCAACCTGACCTTCACTATCCACATATTCAGAACGAGGTGACAGG 695
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QY 696 TGTCCCGTGGGACAAAGGGGACA-CTGCAG-TGTGAAGCTTCAGAGTCCCTCTCA--G 751
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QY 752 CAGAAATCCAGTGTGATCAAGGATGACAAAGACTG--A-----TTGAAGGAAGAAAG 802
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RESULT 27

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LOCUS      2935 bp DNA linear SYN 21-MAY-2001
DEFINITION Synthetic construct secretory IgCEPUS-GFP fusion protein
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ACCESSION  AF271618
VERSION     AF271618.1 GI:14161270
KEYWORDS    .
SOURCE      synthetic construct
            artificial construct
            sequences
ORIGIN      1 (bases 1 to 2935)
            Kim,D.-S. and Moss,D.J.
            Neuronal-specific secretory IgCEPUS-GFP fusion protein expression
            in transfected cells
REFERENCE   2 (bases 1 to 2935)
            Direct Submission
            Kim,D.-S. and Moss,D.J.
            Submitted (24-MAY-2000) College of Natural Resources and Life
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promoter

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ORIGIN

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Best Local Similarity 47.6%; Pred. No. 31;
Matches 871; Conservative 0; Mismatches 143; Indels 815; Gaps 75;

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Db 705 ACCCGCTCTCATGGGTGATCTTTCGCGGGATGGCGCACTCC--TCTCTTCAAGAGATG 763
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Db 764 CCGTGGCAGCGGAGATGCCACTTCCCAAGCTTATGCAACAGCTGACGCTGCGGCGAA 823
QY 148 GGGGAGAGCGCAACCCCTCAGGTGCACTATTGCAACCGGGTCAACCGGGTGCCTGGCTA 207
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Db 824 GGGAGAGTGTCCACGCTCAGTGTCCGTGACAAACCGCGTACCCCGGTGGCGTGGCTG 883
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Db 944 CTCCTGGCCAAACACCCAAACGAGTACAGCATCCAGATCCAGAACGTTGATGTATGAC 1003
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Qy 655 -----GTG----- 657
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Qy 658 -----AA-----ATAT 663
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Db 1838 AGAGCTGACAGAGTGGGCAATAGCTCGGAGATGATTTTCTCTCTCTGAGATGGGA 1897
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Qy 1021 CTT-----CT-----GAAATTTGA 1035
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RESULT 28

RATCALMB

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

CDS

RATCALMB 2179 bp mRNA linear ROD 27-APR-1993
Rattus norvegicus cell adhesion-like molecule mRNA, complete cds.

M88710.1 GI:203247

cell adhesion-like molecule; opiod binding protein.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;

Rattus.

1 (bases 1 to 2179)

Lippman,D.A., Lee,N.M. and Loh,H.H.

Opiod-binding cell adhesion molecule (OBCAM)-related clones from a

rat brain cDNA library

Gene 117 92347701

1339369

Original source text: Rattus norvegicus (strain Simonsen ICR) brain

cDNA to mRNA.

Location/Qualifiers

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ORIGIN

Query Match 59.8%; Score 619.1; DB 10; Length 2179;
Best Local Similarity 70.8%; Pred. No. 34;
Matches 809; Conservative 0; Mismatches 169; Indels 165; Gaps 72;

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QY 40 -TGGGCA-ATCTTTCAC-----GG--G-GC-----TGG--C-TG-CTCTG-----TGCT 74
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Db 1333 TGA 1335

RESULT 29
LOCUS RATCALMC 2337 bp mRNA linear ROD 08-MAY-1993
DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete cds.
ACCESSION M88711
VERSION M88711.1 GI:203249
KEYWORDS cell adhesion-like molecule; opioid binding protein.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2337)
Lippman,D.A., Lee,N.M. and Loh,H.H.
Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
rat brain cDNA library
Gene 117 (2), 249-254 (1992)
MEDLINE 92347701
PUBMED 1339369
COMMENT Original source text: Rattus norvegicus brain cDNA to mRNA.
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RESULT 30

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RATCALMA
LOCUS 3069 bp mRNA linear ROD 08-MAY-1993
DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete cds.
ACCESSION M88709
VERSION M88709.1 GI:203245
KEYWORDS cell adhesion-like molecule; oploid binding protein.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1. (bases 1 to 3069)
Lippman,D.A., Lee,N.M. and Loh,H.H.
Oploid-binding cell adhesion molecule (OBCAM)-related clones from a
rat brain cDNA library
Gene 117 (2), 249-254 (1992)
JOURNAL 92347701
MEDLINE 1339369
PUBMED
COMMENT: Original source text: Rattus norvegicus (strain Simonsen ICR)
(library: UZ) brain cDNA to mRNA.
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ORIGIN
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Best Local Similarity 72.8%; Pred. No. 52;
Matches 794; Conservative 0; Mismatches 176; Indels 120; Gaps 63;
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QY 56 -GGCTG-GCTGCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGAGATGCCACCTT 113
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QY 114 CCCCAAGCTATGACAAACGTCGCTCCGAGGGGAGAGCGCCACCTTCAGTGTCAC 173
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QY 174 TATTGACAAACGGGTTCACCGGTGGCTGGCTTAACCGCAGCAGCATCTCTATGCTGG 233
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QY 234 GAATGACAAAGTGGTGGCTGGATCTCGCTGGTGC--CTTCTGAGCAACACCCAAACGAC 291
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Job time : 4251.99 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 15:40:25 ; Search time 495.763 Seconds

(without alignments)
9496.706 Million cell updates/sec

Title: US-10-017-084A-522_COPY_134_1168

Perfect score: 1035

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Scoring table: IDENTITY_NUC

Gapop 1.0 , Gapext 0.1

Searched: 2960401 seqs, 2274450654 residues

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1035	100.0	1679	9	US-09-999-832A-522	Sequence 522, App
5	1035	100.0	1679	10	US-09-978-189-522	Sequence 522, App
6	1035	100.0	1679	10	US-09-978-608A-522	Sequence 522, App
7	1035	100.0	1679	10	US-09-978-585A-522	Sequence 522, App
8	1035	100.0	1679	10	US-09-978-191A-522	Sequence 522, App
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42	1035	100.0	1679	13	US-10-140-024-375	Sequence 375, App
43	1035	100.0	1679	13	US-10-013-917A-522	Sequence 522, App
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66	1035	100.0	1679	13	US-10-172-039A-522	Sequence 522, App
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73	1035	100.0	1679	15	US-10-140-470-375	Sequence 375, App
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 89 1035 100.0 1679 15 US-10-066-193-103 Sequence 103, App
 90 1035 100.0 1679 15 US-10-230-338-125 Sequence 125, App
 91 1035 100.0 1679 15 US-10-142-419-375 Sequence 375, App
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 94 1035 100.0 1679 15 US-10-123-262-375 Sequence 375, App
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 99 1035 100.0 1679 15 US-10-167-749-522 Sequence 522, App
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ALIGNMENTS

RESULT 1

US-09-978-295A-522
 ; Sequence 522, Application US/09978295A
 ; Patent No. US20020156006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.
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 ; APPLICANT: Godowski, Paul J.
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 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C11
 ; CURRENT APPLICATION NUMBER: US/09/978,295A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/318585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/085697									
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QY	61	GCTGCTCTGTGTCCTTTCCAAAGGAGTGCCCGTGCAGCGGAGATGCCACTTCTCCCCAAA	120						
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DB	254	GCTATGACAAACGPGACGGTCCGGCAGGGGGAGAGGCCACCTCAGGTGCACTATTGAC	313						
QY	181	AACCGGCTCACCGGGTGGCTGCTTAAACCGCAGACCACTCTCTATGCTGTGGGAATGAC	240						
DB	314	AACCGGCTCACCGGGTGGCTGCTTAAACCGCAGACCACTCTCTATGCTGTGGGAATGAC	373						
QY	241	AAGTGGTGCTTGGATCTCTCGGTGGTCCTTCTTGAGCAACCCAAACGCAGTACAGCATC	300						
DB	374	AAGTGGTGCTTGGATCTCTCGGTGGTCCTTCTTGAGCAACCCAAACGCAGTACAGCATC	433						
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DB	434	GAGATCCAGAACGTTGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACGAC	493						
QY	361	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTTGTAGAG	420						
DB	494	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTTGTAGAG	553						
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DB	554	ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCAGCTGCATAGCAACT	613						
QY	481	GGTAGACAGAGCCTACGGTTACTTTGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG	540						
DB	614	GGTAGACAGAGCCTACGGTTACTTTGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG	673						
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DB	674	AGTGAAGACGAATACTTTGGAAATTCAGGGCAATCACCCGGAGCAGTCAGGGGACTACGAG	733						
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DB	734	TGCAGTGCCTCCAATGACGTGGCGCGCCGTGGTACGGAGGTAAAGGTACCGGTGAAC	793						
QY	661	TATCCACCATACATTTTCAGAAAGCCAAAGGTACAGGTGTCCCGCTGGACAAAAGGGGACA	720						
DB	794	TATCCACCATACATTTTCAGAAAGCCAAAGGTACAGGTGTCCCGCTGGACAAAAGGGGACA	853						
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DB	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA	913						
QY	781	AGACTGATTGAAGGAAAGAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAAATC	840						
DB	914	AGACTGATTGAAGGAAAGAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAAATC	973						
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DB	1094	AACGGCACGTCGAGGAGGGCAGGCTCGCTGCTGCTCTCTCTTCTGTCTTTCACCTTG	1153						

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Db 1154 CTTCTCAAAATTGGA 1168

RESULT 2

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; Sequence 522, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PLC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322

APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PLC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1035; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCCAAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGGTG 60
DB 134 ATGAAACCATCCAGCCAAAATGACAAATCTATCTCTTGGGCAATCTTACGGGGGTG 193
QY 61 GTCGCTCTGTGCTCTTCCAAAGAGTCCCGTGGCGAGGAGATGCCACCTTCCCAA 120
DB 194 GTCGCTCTGTGCTCTTCCAAAGAGTCCCGTGGCGAGGAGATGCCACCTTCCCAA 253
QY 121 GCTATGGACAAAGTGCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATTTGAC 180
DB 254 GCTATGGACAAAGTGCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATTTGAC 313
QY 181 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
DB 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
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QY 301 GAGATCCAGAAAGTGGATGTGTATGACGAGGGCCCTTACACTCTGCTCGGTGAGACAGAC 360
DB 434 GAGATCCAGAAAGTGGATGTGTATGACGAGGGCCCTTACACTCTGCTCGGTGAGACAGAC 493
QY 361 AACACCCCAAGAGACCTCTAGGGTCCACCTCATTTGCGAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACACCCCAAGAGACCTCTAGGGTCCACCTCATTTGCGAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCCTGCATACCAACT 480
DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCCTGCATACCAACT 613
QY 481 GGTAGACAGAGACCTTACCGTTTACTTTGGAGACACATCTCTCCCAAAAGCGGTTGGCTTGTG 540
DB 614 GGTAGACAGAGACCTTACCGTTTACTTTGGAGACACATCTCTCCCAAAAGCGGTTGGCTTGTG 673
QY 541 AGTGAAGACGAATATCTTGGAAATTCAGGGGCATCACCCGGGAGCAGTCAAGGGGACTTACGAG 600
DB 674 AGTGAAGACGAATATCTTGGAAATTCAGGGGCATCACCCGGGAGCAGTCAAGGGGACTTACGAG 733
QY 601 TGCAGTGCCTCCAAATGACGTGGCCGCCCGCTGGTACGAGAGATAAAGGTCAACGTGAAC 660
DB 734 TGCAGTGCCTCCAAATGACGTGGCCGCCCGCTGGTACGAGAGATAAAGGTCAACGTGAAC 793
QY 661 TATCCACCATACATTTTCAAGAGCCAGGGTACAGGTGTCCCGCTGGGACAAAGGGGACA 720
DB 794 TATCCACCATACATTTTCAAGAGCCAGGGTACAGGTGTCCCGCTGGGACAAAGGGGACA 853
QY 721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTGTACAGGATGACAAA 780
DB 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGAGTGTGTACAGGATGACAAA 913
QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAACACAGACCTTTCTCTCAAACTC 840
DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAACACAGACCTTTCTCTCAAACTC 973
QY 841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACATACACTTGGGTGGCCCTCCACAG 900
DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACATACACTTGGGTGGCCCTCCACAG 1033
QY 901 CTGGGCCACACCAATGCCCAGCATCATGTATTGTGTCAGGCGCGCTCAGCGAGGTGAGC 960
DB 1034 CTGGGCCACACCAATGCCCAGCATCATGTATTGTGTCAGGCGCGCTCAGCGAGGTGAGC 1093
QY 961 AACGGCAGCTCAGAGAGGCGAGGCTGCGTCTGGGTGCTGCTCTTCTGCTTGTGCTGACCTG 1020
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QY 1021 CTCTCTCAAAATTTTGA 1035
DB 1154 CTCTCTCAAAATTTTGA 1168

RESULT 4
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; Sequence 522, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414

1	APPLICANT: Williams, P. Mickey
2	APPLICANT: Wood, William I.
3	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
4	TITLE OF INVENTION: Acids Encoding the Same
5	FILE REFERENCE: P2630P1C7
6	CURRENT APPLICATION NUMBER: US/09/978,189
7	CURRENT FILING DATE: 2001-10-15
8	PRIOR APPLICATION NUMBER: 09/918585
9	PRIOR FILING DATE: 2001-07-30
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72	PRIOR APPLICATION NUMBER: 60/0801070
73	PRIOR FILING DATE: 1998-04-08


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! ORGANISM: Homo sapiens
US-09-978-585A-522

Query Match      100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCAATCCAGCCAAATATCTATCTCTTGGGCAATCTTACGGGGCTG 60
DB 134 ATGAAACCAATCCAGCCAAATATCTATCTCTTGGGCAATCTTACGGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAGAGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGTCTCTTCCAGAGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGACAACTGACGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 180
DB 254 GCTATGACAACTGACGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 313
QY 181 AACCGGGTCAACCGGGTGGCTTAAACCGGAGAGCGAGATGCCACCTTCCCAAA 240
DB 314 AACCGGGTCAACCGGGTGGCTTAAACCGGAGAGCGAGATGCCACCTTCCCAAA 373
QY 241 AAGTGGTCCCTGATCTCTGAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 300
DB 374 AAGTGGTCCCTGATCTCTGAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 433
QY 301 GAGATCCAGAACGTTGATGAGAGGCGCTTACACCTGCTCGGTCGAGACGAC 360
DB 434 GAGATCCAGAACGTTGATGAGAGGCGCTTACACCTGCTCGGTCGAGACGAC 493
QY 361 AACCCAAAGACCTCTAGGCTCCACCTATTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACCCAAAGACCTCTAGGCTCCACCTATTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTCAGATCTCTTAAAGGAGCAATATTAGCTTACCTGCTACCTGATGCACT 480
DB 554 ATTCTTCAGATCTCTTAAAGGAGCAATATTAGCTTACCTGCTACCTGATGCACT 613
QY 481 GGTAGACGAGGCTACGTTACTTTGAGAGACATCTCTCCAAAGCGTTGCTTTGTG 540
DB 614 GGTAGACGAGGCTACGTTACTTTGAGAGACATCTCTCCAAAGCGTTGCTTTGTG 673
QY 541 AGTGAAGCAAAATCTTGGAAATTCAGGGATCACCCGGGAGAGTACGGGGCTACGAG 600
DB 674 AGTGAAGCAAAATCTTGGAAATTCAGGGATCACCCGGGAGAGTACGGGGCTACGAG 733
QY 601 TGCACTGCTCCATGACGTTGCGCGCGCTGTTAGCGAGAGTAAAGGTACCGTGAAC 660
DB 734 TGCACTGCTCCATGACGTTGCGCGCGCTGTTAGCGAGAGTAAAGGTACCGTGAAC 793
QY 661 TATCCACATACATTTTCAAGAGCAAGGTTACAGGTTCCCGTGGGACAAAGGGGACA 720
DB 794 TATCCACATACATTTTCAAGAGCAAGGTTACAGGTTCCCGTGGGACAAAGGGGACA 853
QY 721 CTGCACTGTTGAGCTTCCAGTCCCTTACAGAGATTCAGTGGTTTCAAGAGTACAAA 780
DB 854 CTGCACTGTTGAGCTTCCAGTCCCTTACAGAGATTCAGTGGTTTCAAGAGTACAAA 913
QY 781 AGACTGATTGAAGGAAAGAGGTTGAAAGTGAAGACAGCTTTCCTCTCAAACTC 840
DB 914 AGACTGATTGAAGGAAAGAGGTTGAAAGTGAAGACAGCTTTCCTCTCAAACTC 973
QY 841 ATCTTCTCAATGCTCTGAACATGATATGGAACTTACACTTTCGCTGGCTTCCAAAG 900
DB 974 ATCTTCTCAATGCTCTGAACATGATATGGAACTTACACTTTCGCTGGCTTCCAAAG 1033
QY 901 CTGGGCCACCAATGCGAGTATGATTTGGTCCAGCGCGCTGACGAGGTTGAGC 960
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QY 961 AACGGCAGCTGAGGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
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US-09-978-585A-522
; Sequence 522, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-978-585A-522

Query Match      100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCAATCCAGCCAAATATCTATCTCTTGGGCAATCTTACGGGGCTG 60
DB 134 ATGAAACCAATCCAGCCAAATATCTATCTCTTGGGCAATCTTACGGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAGAGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGTCTCTTCCAGAGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGACAACTGACGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 180
DB 254 GCTATGACAACTGACGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 313
QY 181 AACCGGGTCAACCGGGTGGCTTAAACCGGAGAGCGAGATGCCACCTTCCCAAA 240
DB 314 AACCGGGTCAACCGGGTGGCTTAAACCGGAGAGCGAGATGCCACCTTCCCAAA 373
QY 241 AAGTGGTCCCTGATCTCTGAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 300
DB 374 AAGTGGTCCCTGATCTCTGAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 433
QY 301 GAGATCCAGAACGTTGATGAGAGGCGCTTACACCTGCTCGGTCGAGACGAC 360
DB 434 GAGATCCAGAACGTTGATGAGAGGCGCTTACACCTGCTCGGTCGAGACGAC 493
QY 361 AACCCAAAGACCTCTAGGCTCCACCTATTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACCCAAAGACCTCTAGGCTCCACCTATTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTCAGATCTCTTAAAGGAGCAATATTAGCTTACCTGCTACCTGATGCACT 480
DB 554 ATTCTTCAGATCTCTTAAAGGAGCAATATTAGCTTACCTGCTACCTGATGCACT 613
QY 481 GGTAGACGAGGCTACGTTACTTTGAGAGACATCTCTCCAAAGCGTTGCTTTGTG 540
DB 614 GGTAGACGAGGCTACGTTACTTTGAGAGACATCTCTCCAAAGCGTTGCTTTGTG 673
QY 541 AGTGAAGCAAAATCTTGGAAATTCAGGGATCACCCGGGAGAGTACGGGGCTACGAG 600
DB 674 AGTGAAGCAAAATCTTGGAAATTCAGGGATCACCCGGGAGAGTACGGGGCTACGAG 733
QY 601 TGCACTGCTCCATGACGTTGCGCGCGCTGTTAGCGAGAGTAAAGGTACCGTGAAC 660
DB 734 TGCACTGCTCCATGACGTTGCGCGCGCTGTTAGCGAGAGTAAAGGTACCGTGAAC 793
QY 661 TATCCACATACATTTTCAAGAGCAAGGTTACAGGTTCCCGTGGGACAAAGGGGACA 720
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DB 854 CTGCACTGTTGAGCTTCCAGTCCCTTACAGAGATTCAGTGGTTTCAAGAGTACAAA 913
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DB 914 AGACTGATTGAAGGAAAGAGGTTGAAAGTGAAGACAGCTTTCCTCTCAAACTC 973
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QY 961 AACGGCAGCTGAGGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
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Db	434	GAGATCCAGAAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCACACAGAC	493
Qy	361	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTTGTAGAG	420
Db	494	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTTGTAGAG	553
Qy	421	ATTTCCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCTACCTGCATAGCAACT	480
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Qy	481	GGTAGACGAGACCTACGGTTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG	540
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Qy	541	AGTGAAGACGAATACTTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGATACGAG	600
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Db	794	TATCCACCATACATTTCCAGAGCCCAAGGATACAGTGTCCCCGTGGGACAAAGGGGACA	853
Qy	721	CTGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAA	780
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Qy	781	AGACTGATTGAAGGAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAAAATC	840
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Qy	901	CTGGGCCACACCAATGCCAGCATCATGCTATTGGTCCAGGCGCCGTCAAGGAGGTGAGC	960
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Qy	1021	CTTCTCAAAATTTGA	1035
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RESULT 8

RESCHI 8
US-09-978-191A-522

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: Sequence 522. Application US/09978191A

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GENERAL INFORMATION:

APPLICANT: Ashkenazi Avi

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P

APPLICANT: Baker Kevin P.
APPLICANT: Botstein David

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

APPLICANT: Desnoyers, Esten Desno

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoli

; APPLICANT: Filvaroff, Eli

APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mar

1	APPLICANT:	Godowski, Paul J.
2	APPLICANT:	Grimaldi, J. Christopher
3	APPLICANT:	Gurney, Austin L.
4	APPLICANT:	Hillan, Kenneth J.
5	APPLICANT:	Kiljavin, Ivar J.
6	APPLICANT:	Kuo, Sophia S.
7	APPLICANT:	Napier, Mary A.
8	APPLICANT:	Pan, James;
9	APPLICANT:	Paoni, Nicholas F.
10	APPLICANT:	Roy, Margaret Ann
11	APPLICANT:	Shelton, David L.
12	APPLICANT:	Stewart, Timothy A.
13	APPLICANT:	Tumas, Daniel
14	APPLICANT:	Williams, P. Mickey
15	APPLICANT:	Wood, William I.
16	TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
17	TITLE OF INVENTION:	Acids Encoding the Same
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Qy 121 GCTATGGACAACGTGACCGTCCGGCAGGGGAGAGCCCACTCAGGTGCACTATTGAC 180

Db 254 GCTATGGACAACGTGACCGTCCGGCAGGGGAGAGCCCACTCAGGTGCACTATTGAC 313

Qy 181 AACCGGGTCACCGGGTGGCTGGCTTAACCCGAGACCATCTCTATCTCTGGGATGAC 240

Db 314 AACCGGGTCACCGGGTGGCTGGCTTAACCCGAGACCATCTCTATCTCTGGGATGAC 373

Qy 241 AAGTGTGCTCGGATCCTCGCGTGGTCTTTCAGCAACACCCAAACGAGTACAGCATC 300

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Db 134 ATGAAAACCATCCAGCCAAAATGCAATTTCTTCTGGGCAATCTTACGGGGCTG 193
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QY 121 GCTATGGAACAAGTACGCTCCGGGAGGAGGAGGAGCCACCTTCAAGTGTACTTATGAC 180
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; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCCAAATAATGCAATTTCTATCTCTTGGCAATCTTTCAGGGGCTG 60
Db 134 ATGAAACCATCCAGCCAAATAATGCAATTTCTATCTCTTGGCAATCTTTCAGGGGCTG 193
QY 61 GCTGCTCTGTGTCTCTTCCAAAGGAGTGCCGCGCAGCGGAGATGCCACCTTCCCAA 120
Db 194 GCTGCTCTGTGTCTCTTCCAAAGGAGTGCCGCGCAGCGGAGATGCCACCTTCCCAA 253
QY 121 GCTATGGACAAAGTACGCTTCCGCGAGGGGAGAGCGCCACCTCAGGTGCAATTGAC 180
Db 254 GCTATGGACAAAGTACGCTTCCGCGAGGGGAGAGCGCCACCTCAGGTGCAATTGAC 313
QY 181 AACCGGGTCAACCGGGTGGCTTAAACCGCAGCACCATCTCTATCTGCGGAATGAC 240
Db 314 AACCGGGTCAACCGGGTGGCTTAAACCGCAGCACCATCTCTATCTGCGGAATGAC 373
QY 241 AAGTGTGCTGGATCCTCGCGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
Db 374 AAGTGTGCTGGATCCTCGCGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 301 GAGATCCAGAAAGTGTATGATGACGAGGGCCCTTACCTGTCTCGGTGACAGACAG 360
Db 434 GAGATCCAGAAAGTGTATGATGACGAGGGCCCTTACCTGTCTCGGTGACAGACAG 493
QY 361 AACCAACCCAAAGACCTTAGGGTCCACCTCATTTGTCAGAGTATCTCCAAAATTGTAG 420
Db 494 AACCAACCCAAAGACCTTAGGGTCCACCTCATTTGTCAGAGTATCTCCAAAATTGTAG 553
QY 421 ATTTCTTCAGATATCTCCATTTAATGAAGGAAACAATATTAGCCTCACCTGCTAGCAACT 480
Db 554 ATTTCTTCAGATATCTCCATTTAATGAAGGAAACAATATTAGCCTCACCTGCTAGCAACT 613
QY 481 GGTAGACAGAGCTAGGTTACTTGGAGACACATCTCTCCAAAGCGGTGCTTTGTG 540
Db 614 GGTAGACAGAGCTAGGTTACTTGGAGACACATCTCTCCAAAGCGGTGCTTTGTG 673
QY 541 AGTGAAGACGAATACCTTGGAAATTTACGGGCATCACCCGGGAGCAGTCAGGGGACTAG 600
Db 674 AGTGAAGACGAATACCTTGGAAATTTACGGGCATCACCCGGGAGCAGTCAGGGGACTAG 733
QY 601 TGCAGTGCCTCCAAATGACGTCGGCCGCGCGGTGTAGCGAGAGTAAGGTACCGTGAAC 660
Db 734 TGCAGTGCCTCCAAATGACGTCGGCCGCGCGGTGTAGCGAGAGTAAGGTACCGTGAAC 793
QY 661 TATCCACCATACATTTTCAGAGCCAAAGGTTACAGGTGTCTCCCGTGGGACAAAGGGGACA 720
Db 794 TATCCACCATACATTTTCAGAGCCAAAGGTTACAGGTGTCTCCCGTGGGACAAAGGGGACA 853
QY 721 CTCAGTGTGAGCCCTCAGCAGTCCCTCAGCAGAGATTTCCAGTGTGTACAGGATGACAA 780
Db 854 CTCAGTGTGAGCCCTCAGCAGTCCCTCAGCAGAGATTTCCAGTGTGTACAGGATGACAA 913
QY 781 AGACTGATTGAAGAAAGAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAACTC 840
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QY 841 ATCTTTCTTCAATGCTCTGAAACATGACTATGGAACTACACTTGGTGGCCCTCCAAACAG 900
Db 974 ATCTTTCTTCAATGCTCTGAAACATGACTATGGAACTACACTTGGTGGCCCTCCAAACAG 1033
QY 901 CTGGGCGACACCAATGCCAGCATCATGCTATTGTTGGTCCAGGGCGGCTCAGCGAGGTGAGC 960
Db 1034 CTGGGCGACACCAATGCCAGCATCATGCTATTGTTGGTCCAGGGCGGCTCAGCGAGGTGAGC 1093
QY 961 AACGGCAGCTCAGAGGCGAGGCTGCGTCTGGCTGCTGCTCTCTTCTGCTTTCGACCTG 1020
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QY 1021 CTCTCTCAAAATTTGA 1035
Db 1154 CTCTCTCAAAATTTGA 1168

RESULT 11
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; Sequence 522, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Sheiton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PLC65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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63 PRIOR FILING DATE: 1998-05-15
64 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCCAGCAAAATGCAAAATCTATCTCTTTGGGCAATCTTTCACGGGGCTG 60
Db 134 ATGAAACCATCCAGCAAAATGCAAAATCTATCTCTTTGGGCAATCTTTCACGGGGCTG 193

Qy	61	GCTGCTCTGTGCTCTCTTCCAAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA	120
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Qy	121	GCTATGGACAAACGTCAGCGGTCCGGCAGGGGGAGAGCCACCCCTCAGGTGCACTATTGAC	180
Db	254	GCTATGGACAAACGTCAGCGGTCCGGCAGGGGGAGAGCCACCCCTCAGGTGCACTATTGAC	313
Qy	181	AACCGGGTCAACCGGGTGGCTGGCTTAAACCGGAGCACCATCTCTATGCTGGGAATGAC	240
Db	314	AACCGGGTCAACCGGGTGGCTGGCTTAAACCGGAGCACCATCTCTATGCTGGGAATGAC	373
Qy	241	AGTGTGCTGCTGATCCTCGGTGCTCTTCTGAGCAACACCCACAGCAGGTACAGATC	300
Db	374	AGTGTGCTGCTGATCCTCGGTGCTCTTCTGAGCAACACCCACAGCAGGTACAGATC	433
Qy	301	GAGATCCAGAACGTCGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGAGACAGAC	360
Db	434	GAGATCCAGAACGTCGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGAGACAGAC	493
Qy	361	AACCAACCAAGACCTCTAGGTGCTCACCCTCATTTGCAAGTATCTCCCAAAATTTAGAG	420
Db	494	AACCAACCAAGACCTCTAGGTGCTCACCCTCATTTGCAAGTATCTCCCAAAATTTAGAG	553
Qy	421	ATTCTCTCAGATATCTCCATTAATGAAGGAAACATATTAGCTCACCCTGCATAGCACT	480
Db	554	ATTCTCTCAGATATCTCCATTAATGAAGGAAACATATTAGCTCACCCTGCATAGCACT	613
Qy	481	GCTAGACAGAGCCTACGGTTACTTTGGAGACATCTCTCCCAAGCGGTGGCTTTGTG	540
Db	614	GCTAGACAGAGCCTACGGTTACTTTGGAGACATCTCTCCCAAGCGGTGGCTTTGTG	673
Qy	541	AGTGAAGACGAATACCTTGAATTCAGGGCATCACCCGGAGCAGTCAGGGGATACAG	600
Db	674	AGTGAAGACGAATACCTTGAATTCAGGGCATCACCCGGAGCAGTCAGGGGATACAG	733
Qy	601	TGAGTGCCTCCAAATGACGTCGGCGCGCGGTGACGAGAGTAAAGTCAACCGTGAAC	660
Db	734	TGAGTGCCTCCAAATGACGTCGGCGCGCGGTGACGAGAGTAAAGTCAACCGTGAAC	793
Qy	661	TATCCACCATATATTTCAAGCCAAAGGTAAGGTATCCCGTGGGACAAAGGGGACA	720
Db	794	TATCCACCATATATTTCAAGCCAAAGGTAAGGTATCCCGTGGGACAAAGGGGACA	853
Qy	721	CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTACAGGATGACAA	780
Db	854	CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTACAGGATGACAA	913
Qy	781	AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAAAAGAGACCTTTCTCTCAAACTC	840
Db	914	AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAAAAGAGACCTTTCTCTCAAACTC	973
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Db	974	ATCTTCTTCAATGTCTCTGAAATGATGGAATACATTTGGTGGCTTCAACAG	1033
Qy	901	CTGGGCAACCAATGCCAGCATCATGCTATTGTTGGTCAAGGCGCGTCAAGCGAGTGC	960
Db	1034	CTGGGCAACCAATGCCAGCATCATGCTATTGTTGGTCAAGGCGCGTCAAGCGAGTGC	1093
Qy	961	AACGGCAGCTCGAGGAGGCGAGGTGCGGTCTGGCTGCTGCTCTTTGCTTGCACCTG	1020
Db	1094	AACGGCAGCTCGAGGAGGCGAGGTGCGGTCTGGCTGCTGCTCTTTGCTTGCACCTG	1153
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Db	1154	CTTCTCAAAATTTGA	1168

RESULT 13
US-09-978-824-522
; Sequence 522, Application US/09978824
; Publication No. US2003005216A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC14
CURRENT APPLICATION NUMBER: US/09/978,824
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/083392
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PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545


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; PRIOR FILING DATE: 1998-04-29
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3,6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCCAGCAAAATGCAAAATCTCTTGGCAATCTTCACGGGCTG 60
Db 134 ATGAAACCATCCAGCAAAATGCAAAATCTCTTGGCAATCTTCACGGGCTG 193
Qy 61 GCTGCTGTGTCTCTTCCAAAGAGTGCCCGTGCGCAGCGGAGATGCCACTTCCCAAA 120
Db 194 GCTGCTGTGTCTCTTCCAAAGAGTGCCCGTGCGCAGCGGAGATGCCACTTCCCAAA 253
Qy 121 GCTATGACACAGTGACGGTCCGCGAGGGGAGCGCCACTCTCAGTGCACATTTGAC 180
Db 254 GCTATGACACAGTGACGGTCCGCGAGGGGAGCGCCACTCTCAGTGCACATTTGAC 313
Qy 181 AACCGGCTCACCCGGGTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
Db 314 AACCGGCTCACCCGGGTGGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373

241 AAGTGTGCTCGATCTCGCTGTGCTCTTCTGAGCAACACCCAAACGAGTACAGATC 300
Db 374 AAGTGTGCTCGATCTCGCTGTGCTCTTCTGAGCAACACCCAAACGAGTACAGATC 433
Qy 301 GAGATCCAGAACGCTGGATGTATGAGAGGGGCCCTTACACCTGCTGGTGCAGACAGAC 360
Db 434 GAGATCCAGAACGCTGGATGTATGAGAGGGGCCCTTACACCTGCTGGTGCAGACAGAC 493
Qy 361 AACCAACCCAAAGACCTCTAGGCTCCACCTCATTTGTCAGAGTATCTCCAAATTTAGAG 420
Db 494 AACCAACCCAAAGACCTCTAGGCTCCACCTCATTTGTCAGAGTATCTCCAAATTTAGAG 553
Qy 421 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTCACCTCATAGCAACT 480
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTCACCTCATAGCAACT 613
Qy 481 GGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGGGTGGCTTTGTG 540
Db 614 GGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGGGTGGCTTTGTG 673
Qy 541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCGGGGAGCAGTCAGGGGACTAGGAG 600
Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCGGGGAGCAGTCAGGGGACTAGGAG 733
Qy 601 TGCAGTGCCTCCAAATGACGTGGCGCGCGCTGTGTACGGAGAGTAAAGGTCAACGTGAAC 660
Db 734 TGCAGTGCCTCCAAATGACGTGGCGCGCTGTGTACGGAGAGTAAAGGTCAACGTGAAC 793
Qy 721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGAGTACAA 780
Db 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGAGTACAA 913
Qy 781 AGACTGATTGAAGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTCTCTCAAAATC 840
Db 914 AGACTGATTGAAGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTCTCTCAAAATC 973
Qy 841 ATCTTCTTCAATGTCTCTGAACATGATGTGGAACTACACTTGGCTGGCTTCAACAG 900
Db 974 ATCTTCTTCAATGTCTCTGAACATGATGTGGAACTACACTTGGCTGGCTTCAACAG 1033
Qy 901 CTGGGCCACACCAATGCGACATCATGTCTATTTGGTCCAGGCGCCCTCAGCAGAGTGAGC 960
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Qy 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

RESULT 14
US-09-918-585A-522
; Sequence 522, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
```

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumaas, Daniel
APPLICANT: Williams, P. Wickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C1
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2003-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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RESULT 15
US-09-978-423A-522
; Sequence 522, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

```

: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2630PIC21
: CURRENT APPLICATION NUMBER: US/09/978,423A
: PRIOR FILING DATE: 2002-05-16
: PRIOR APPLICATION NUMBER: 09/918595
: PRIOR FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
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Query Match 100.08; Score 1035; DB 10; Length 1679;

Best Local Similarity 100.08; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 GCTGCTGTGCTCTTCCAAAGAGTGCCCGTGGCAGCGGAGATGCCACCTTCCCAAA 120
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 QY 314 AACCGGTGACCCGGGTGGCTGTGATGACAGCGCCCTTACACCTGCTCTATGCTGGGAATGAC 373
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 QY 241 AAGTGTGCTGGATCTCGGTGGTCTTCTGAGCAACCCAAACGCGATGACGATC 300
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 QY 374 AAGTGTGCTGGATCTCGGTGGTCTTCTGAGCAACCCAAACGCGATGACGATC 433
 DB |||||
 QY 301 GAGATCCAGAACGTTGATGATGACAGCGCCCTTACACCTGCTCGGTGACAGAC 360
 DB |||||
 QY 434 GAGATCCAGAACGTTGATGATGACAGCGCCCTTACACCTGCTCGGTGACAGAC 493
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 QY 361 AACACCCAAAGACCTTAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
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 QY 494 AACACCCAAAGACCTTAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
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 QY 421 ATTCTTTCAGATCTCCATTAATGAGGAAACAATATTAGCTCCTCAGTGCATGACACT 480
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 QY 554 ATTCTTTCAGATCTCCATTAATGAGGAAACAATATTAGCTCCTCAGTGCATGACACT 613
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 QY 481 GGTAGACAGAGCCTTAGGTTACTTGGAGACATCTCTCCCAAGGGTGTGCTTGTG 540
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 QY 541 AGTGAAGACGAATCTTTGAAATTCAGGGCATCACCGGGAGAGTCAAGGGGACTACGAG 600
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 QY 674 AGTGAAGACGAATCTTTGAAATTCAGGGCATCACCGGGAGAGTCAAGGGGACTACGAG 733
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QY 601 TGCAGTGCCTCCAATGAGTGGCGCGCCCGTGTGACGAGAGTAAAGGTCAACCGTGAAC 660
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 QY 734 TGCAGTGCCTCCAATGAGTGGCGCGCCCGTGTGACGAGAGTAAAGGTCAACCGTGAAC 793
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RESULT 16

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 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
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 ; APPLICANT: Grimaldi, J. Christopher
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 ; APPLICANT: Kljavin, Ivar J.
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PIC6
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 1035; DB 10; Length 1679;
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Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61  GCTGCTGTGTCTCTTCCAAAGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 120
Db      194 GCTGCTGTGTCTCTTCCAAAGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCAAA 253

QY      121 GCTATGACAACTGTGACGGTCCGACGGGGAGAGCCACCTTCAGGTGCATATTGAC 180
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QY      181 AACCGGTTCACCCGGGTGGCTGTCTAAACCGAGAGCCATCTCTATGTCTGGAATGAC 240
Db      314 AACCGGTTCACCCGGGTGGCTGTCTAAACCGAGCACCTTCCTATGTCTGGAATGAC 373

QY      241 AAGTGGTGCCTTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC 300
Db      374 AAGTGGTGCCTTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAACGAGTACAGCATC 433

QY      301 GAGATCCAGAACGTGGATGTATGACAGGGCCCTTACCTGTCTCGGTGCAGACAGAC 360
Db      434 GAGATCCAGAACGTGGATGTATGACAGGGCCCTTACACCTGTCTCGGTGCAGACAGAC 493

QY      361 AACCAACCAAGACCTCTAGGCTCCACTCATCTGCAAGTATCTCCCAAAATGTAGAG 420
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QY      421 ATTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACCTGCATAGCAACT 480
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QY      481 GGTAGACAGAGCTAGGTACTTGTGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
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QY      541 AGTGAAGCAAAATACCTTGGAAATTCAGGCGATACCCGGGAGAGTCCAGGGGACTAGAG 600
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QY      601 TGCAGTCCCTCAATGACGTGGGCGCGCCCGTGTACGGAGAGTAAAGGTCAACCGTGAAC 660
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/918585
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72 PRIOR APPLICATION NUMBER: 60/082796
73 PRIOR FILING DATE: 1998-04-23

1 PRIOR APPLICATION NUMBER: 60/083336
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3 PRIOR APPLICATION NUMBER: 60/083322
4 PRIOR FILING DATE: 1998-04-28
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6 PRIOR FILING DATE: 1998-04-29
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8 PRIOR FILING DATE: 1998-04-29
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60 PRIOR FILING DATE: 1998-05-15
61 PRIOR APPLICATION NUMBER: 60/085573
62 PRIOR FILING DATE: 1998-05-15
63 PRIOR APPLICATION NUMBER: 60/085704
64 PRIOR FILING DATE: 1998-05-15
65 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCCAAAATGCAATTCATCTCTTGGCAATCTTCACGGGGCTG 60

DB 134 ATGAAACCATCCAGCCAAAATGCAATTCATCTCTTGGCAATCTTCACGGGGCTG 193

QY 61 GCTGCTGTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGAGATGCGACCTTCCCCAAA 120
Db 194 GCTGCTGTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGAGATGCGACCTTCCCCAAA 253
QY 121 GCTATGGACAAGTGCAGCGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACATTGAC 180
Db 254 GCTATGGACAAGTGCAGCGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACATTGAC 313
QY 181 AACCGGGTCAACCGGGTGCCTGCTAAACCGCAGCACCATCTCTATGCTGCGGAATGAC 240
Db 314 AACCGGGTCAACCGGGTGCCTGCTAAACCGCAGCACCATCTCTATGCTGCGGAATGAC 373
QY 241 AAGTGGTCCCTGGATCTCTCGGTGGTCTCTTGAGCAACACCCAAAGCAGTACAGCATC 300
Db 374 AAGTGGTCCCTGGATCTCTCGGTGGTCTCTTGAGCAACACCCAAAGCAGTACAGCATC 433
QY 301 GAGATCCAGACGCTGATGTGTATGACGAGGGCCCTTACAGTCTGCTGTCGACAGAC 360
Db 434 GAGATCCAGACGCTGATGTGTATGACGAGGGCCCTTACAGTCTGCTGTCGACAGAC 493
QY 361 AACCAACCAAGACCTCTAGGGTCCACCTATTGTGCAAGTATCTCCCAAAATGTAGAG 420
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTATTGTGCAAGTATCTCCCAAAATGTAGAG 553
QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCCTCACCTGCATAGCAACT 480
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCCTCACCTGCATAGCAACT 613
QY 481 GGTAGACAGAGCTCAGGTGTTACTTGGAGACACATCTCTCCAAAGCGGTGGTTTGTG 540
Db 614 GGTAGACAGAGCTCAGGTGTTACTTGGAGACACATCTCTCCAAAGCGGTGGTTTGTG 673
QY 541 AGTGAAGACGAAATCTTGGAAATTCAGGGCATCACCGGGAGAGTCCAGGGGACTACGAG 600
Db 674 AGTGAAGACGAAATCTTGGAAATTCAGGGCATCACCGGGAGAGTCCAGGGGACTACGAG 733
QY 601 TGCAGTCCCTCAATAGTGTGCGCGCGCGTGTACGAGAGTAAAGGTCAACCGTGAAC 660
Db 734 TGCAGTCCCTCAATAGTGTGCGCGCGCGTGTACGAGAGTAAAGGTCAACCGTGAAC 793
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Db 794 TATCCACCATACATTTTCAGAGGCAAGGTACAGTGTCTCCCGTGGGACAAAGGGGACA 853
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Db 854 CTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAAAGGATGACAAA 913
QY 781 AGACTGATTGAAGAAAGAGGGGTGAAAGTGGAAACAGACCTTTCCTCTCAAAACTC 840
Db 914 AGACTGATTGAAGAAAGAGGGGTGAAAGTGGAAACAGACCTTTCCTCTCAAAACTC 973
QY 841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGCCTGGCGCTCCCAACAG 900
Db 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGCCTGGCGCTCCCAACAG 1033
QY 901 CTGGGCCACCAATGCCAGATCATGCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 960
Db 1034 CTGGGCCACCAATGCCAGATCATGCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1093
QY 961 AACGGCAGCTCGAGGGGAGGCTGGCTGTGCTGTGCTGCTCTCTCTGCTGCTGCTGCTG 1020
Db 1094 AACGGCAGCTCGAGGGGAGGCTGGCTGTGCTGTGCTGCTCTCTCTGCTGCTGCTGCTG 1153
QY 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

RESULT 19

US-09-978-187B-522

; Sequence 522, Application US/09978187B

; Publication No. US20030096744A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C5
; CURRENT APPLICATION NUMBER: US/09/978,187B
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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134

183

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181 AACCGGTCAACCGGTGGCTAAACCGCAGCACCTCTATGCTGGGAATGAC 240

Db 314 AACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373

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374	Db	AAGTGGTGCCTGATCCTCGGCTGGTCTCTGTGACAAACCCAAACGCGATACAGCATC	433
301	QY	GAGATCCAGAACGTTGGATGTGTATGACAGAGGCCCTTTACACTGTCTGGTGAGACAGAC	360
434	Db	GAGATCCAGAACGTTGGATGTGTATGACAGAGGCCCTTTACACTGTCTGGTGAGACAGAC	493
361	QY	AACCACCCAAAGACCTCTFAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGG	420
494	Db	AACCACCCAAAGACCTCTFAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGG	553
421	QY	ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT	480
554	Db	ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT	613
481	QY	GGTAGACAGAGCCTFAGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG	540
614	Db	GGTAGACAGAGCCTFAGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG	673
541	QY	AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTTACCAG	600
674	Db	AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTTACCAG	733
601	QY	TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGGTAAAGGTCACCGTGAAC	660
734	Db	TGCAGTGCCTCCAATGACGTGGCCGCGCCCGTGGTACGGAGGTAAAGGTCACCGTGAAC	793
661	QY	TATCCACCATACATTTTCAGAAAGCCAAAGGTCACAGTGTCCCGGTGGGACAAAGGGGACA	720
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721	QY	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCACAGTGGTACAAAGSATGACAAA	780
854	Db	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCACAGTGGTACAAAGSATGACAAA	913
781	QY	AGACTGATTCAAGAAAGAGGGGTCAAGTGTGAAAACAGACACTTTCCTCTCAAAATCTC	840
914	Db	AGACTGATTCAAGAAAGAGGGGTCAAGTGTGAAAACAGACACTTTCCTCTCAAAATCTC	973
841	QY	ATCTTCTTCAATGTCTCTGAACTGACTATATGGGAACTACACTTCGCTGGCTCCAAACAAG	900
974	Db	ATCTTCTTCAATGTCTCTGAACTGACTATATGGGAACTACACTTCGCTGGCTCCAAACAAG	1033
901	QY	CTGGGCCACACCAATGCCAGCATCATGCTATTGGTCCAGCGCCGTCAGCGAGGTGAGC	960
1034	Db	CTGGGCCACACCAATGCCAGCATCATGCTATTGGTCCAGCGCCGTCAGCGAGGTGAGC	1093
961	QY	AACGGCACGTCGAGGAGGCGAGGCTGGTCTGGCTGCTGCTCTTCTGCTTCTGCACTG	1020
1094	Db	AACGGCACGTCGAGGAGGCGAGGCTGGTCTGGCTGCTGCTCTTCTGCTTCTGCACTG	1153
1021	QY	CTTCTCAAAATTTTGA	1035
1154	Db	CTTCTCAAAATTTTGA	1168

RESULT 20

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US-09-978-643A-522
; Sequence 522, Application US/0978643A
; Publication No. US20030104998A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Destroyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

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;; PRIOR APPLICATION NUMBER: 60/083322
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;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCAATCCAGCAAAATGCAAAATCTATCTCTTGGGCAATCTTACGGGCTG 60
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Db	134	ATGAAACCAATCCAGCAAAATGCAAAATCTATCTCTTGGGCAATCTTACGGGCTG	193
QY	61	GCTGCTCTGTGTCTCTTCCAGAGAGTGCCCGTGGCAGCGGAGATCCACCTTCCCAAA	120
Db	194	GCTGCTCTGTGTCTCTTCCAGAGAGTGCCCGTGGCAGCGGAGATCCACCTTCCCAAA	253
QY	121	GCTATGGACAACGTCAGCGTCCGGCAGGGGAGAGGCCACCTCAGGTGCACTATTGAC	180
Db	254	GCTATGGACAACGTCAGCGTCCGGCAGGGGAGAGGCCACCTCAGGTGCACTATTGAC	313
QY	181	AACCGGTCACCCGGTGGCTTAAACCCGAGCACCATCTCTATCTGGGATGAC	240
Db	314	AACCGGTCACCCGGTGGCTTAAACCCGAGCACCATCTCTATCTGGGATGAC	373
QY	241	AGTGGTGGTGGATCTCTCGGTGCTCTCTGAGGAAACCCAAACGAGTACAGCATC	300
Db	374	AGTGGTGGTGGATCTCTCGGTGCTCTCTGAGGAAACCCAAACGAGTACAGCATC	433
QY	301	GAGATCCAGAACGTCGATGTGTATGACGAGGCGCTTACCTGCTCGGTGCGAGCAGAC	360
Db	434	GAGATCCAGAACGTCGATGTGTATGACGAGGCGCTTACCTGCTCGGTGCGAGCAGAC	493
QY	361	AACCAACCAAGACCTCTAGGCTCCACCTCAATGTGCAAGTATCTCCAAATTTAGAG	420
Db	494	AACCAACCAAGACCTCTAGGCTCCACCTCAATGTGCAAGTATCTCCAAATTTAGAG	553
QY	421	ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCTGCATGCAACT	480
Db	554	ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCTGCATGCAACT	613
QY	481	GGTAGACCAAGCCTTACCGTTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTGTG	540
Db	614	GGTAGACCAAGCCTTACCGTTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTGTG	673
QY	541	AGTGAAGCAATATCTTGGAAATTCAGGGCATACCCGGGAGCAGTCAAGGAGTACGAG	600
Db	674	AGTGAAGCAATATCTTGGAAATTCAGGGCATACCCGGGAGCAGTCAAGGAGTACGAG	733
QY	601	TGCAGTGCCTCCAATGACGTGGCGCGCCGTGTGTAGCGAGTAAAGGTACCGTGAAC	660
Db	734	TGCAGTGCCTCCAATGACGTGGCGCGCCGTGTGTAGCGAGTAAAGGTACCGTGAAC	793
QY	661	TATCCACCATACATTTTCAGAAAGCCAGGTACAGGTGTCCCGTGGGACAAAGGGGACA	720
Db	794	TATCCACCATACATTTTCAGAAAGCCAGGTACAGGTGTCCCGTGGGACAAAGGGGACA	853
QY	721	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAA	780
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAA	913
QY	781	AGACTGATTGAAGGAAAGAGGGTGAAGTGGAAACAGACCTTTCTCTCAAAATCTC	840
Db	914	AGACTGATTGAAGGAAAGAGGGTGAAGTGGAAACAGACCTTTCTCTCAAAATCTC	973
QY	841	ATCTTCTCAATGTCTCTGAACATGACTATGGAACTTACACTTTCGCTGGGCTCCAAAG	900
Db	974	ATCTTCTCAATGTCTCTGAACATGACTATGGAACTTACACTTTCGCTGGGCTCCAAAG	1033
QY	901	CTGGGCAACACCAATGCCAGCATATGCTATTGGTTCAGGCGCGGTCAAGGAGTGAAC	960
Db	1034	CTGGGCAACACCAATGCCAGCATATGCTATTGGTTCAGGCGCGGTCAAGGAGTGAAC	1093
QY	961	AACGGCAGTCGAGGAGGGCAGGCTCGCTGCTGCTGCTCTCTTGGTCTTGGACCTG	1020
Db	1094	AACGGCAGTCGAGGAGGGCAGGCTCGCTGCTGCTGCTCTCTTGGTCTTGGACCTG	1153
QY	1021	CTTCTCAAAATTTGA	1035
Db	1154	CTTCTCAAAATTTGA	1168

RESULT 23
US-09-978-188A-522

Sequence 522, Application US/09978188A
Publication No. US20030139328A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C8
CURRENT APPLICATION NUMBER: US/09/978,188A
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PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/085697

Query Match
Best Local Similarity 100.0%; Score 1035; DB 10; Length 1679;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAACCATCCAGCCAAAATGACAAATCTATCTTGGGCAATCTTACGGGGCTG 60
134 ATGAAACCATCCAGCCAAAATGACAAATCTATCTTGGGCAATCTTACGGGGCTG 193
61 GCTGCTCTGTGCTCTTCCAGGAGTGGCCGTCGCGAGGATGCCACCTTCCCAAA 120
194 GCTGCTCTGTGCTCTTCCAGGAGTGGCCGTCGCGAGGATGCCACCTTCCCAAA 253
121 GCTATGGCAACGTCGAGCGTCCGGCAGGGAGAGCCACCTCAGGTGCACTATTGAC 180
254 GCTATGGCAACGTCGAGCGTCCGGCAGGGAGAGCCACCTCAGGTGCACTATTGAC 313
181 AACCGGGTCACCGGGTGGCTGCTAACCGCAGCACCACTCTATGCTGGGATGAC 240

Db 314 AACCGGGTCACCGGGTGGCTGAGTAAACCGCAGCAACCATCTCTATGCTGGGAATGAC 373
Qy 241 AAGTGTGCTCTGGATCCTCGCGTGGTCTTCTTGAGCAACACCCAAACGAGTACAGATC 300
Db 374 AAGTGTGCTCTGGATCCTCGCGTGGTCTTCTTGAGCAACACCCAAACGAGTACAGATC 433
Qy 301 GAGATCCAGAACGTCGATGTGTATGAGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 360
Db 434 GAGATCCAGAACGTCGATGTGTATGAGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493
Qy 361 AACCAACCAAGACCTCTAGGTCACACCTCATTTGTCAGAGTATCTCCCAAAATTTAGAG 420
Db 494 AACCAACCAAGACCTCTAGGTCACACCTCATTTGTCAGAGTATCTCCCAAAATTTAGAG 553
Qy 421 ATTCTCTCAGATATCTTCCATTAATGAAGGAACAATATTAGCCTCACCTGCAATAGCACT 480
Db 554 ATTCTCTCAGATATCTTCCATTAATGAAGGAACAATATTAGCCTCACCTGCAATAGCACT 613
Qy 481 GGTAGACCAAGACCTTACGTTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
Db 614 GGTAGACCAAGACCTTACGTTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
Qy 541 AGTGAAGACGAATACTTTGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
Db 674 AGTGAAGACGAATACTTTGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
Qy 601 TGCAGTGCCTCAATGACGTCGTCGCCGCCGCTGGTACCGAGAGTAAAGTCAACCGTGAAC 660
Db 734 TGCAGTGCCTCAATGACGTCGTCGCCGCCGCTGGTACCGAGAGTAAAGTCAACCGTGAAC 793
Qy 661 TATCCACCATACATTTTCAGAGCCAGGGTACAGGTGTCGCCGTCGGGACAAAGGGGACA 720
Db 794 TATCCACCATACATTTTCAGAGCCAGGGTACAGGTGTCGCCGTCGGGACAAAGGGGACA 853
Qy 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATCACAAA 780
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATCACAAA 913
Qy 781 AGACTGATGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTTCTCTCAAACTC 840
Db 914 AGACTGATGAAGGAAGAAAGGGGTGAAGTGAAGAAACAGACCTTTCTCTCAAACTC 973
Qy 841 ATCTTCTTCAATGTCTCTGACATGACTATGGGAACTACACTTGGTGGCTCCCAAG 900
Db 974 ATCTTCTTCAATGTCTCTGAAACATGACTATGGGAACTACACTTGGTGGCTCCCAAG 1033
Qy 901 CTGGGCCACACCAATGCCAGATCATGCTATTGGTCCAGGCGCGCTCAGCGAGTGAGC 960
Db 1034 CTGGGCCACACCAATGCCAGATCATGCTATTGGTCCAGGCGCGCTCAGCGAGTGAGC 1093
Qy 961 AACGGCAGTCGAGAGGGCAGGCTGGTCTGGCTGCTGCTCTCTCTGCTTGGACCTG 1020
Db 1094 AACGGCAGTCGAGAGGGCAGGCTGGTCTGGCTGCTGCTCTCTCTGCTTGGACCTG 1153
Qy 1021 CTCTCAAAATTTTGA 1035
Db 1154 CTCTCAAAATTTTGA 1168

RESULT 24
US-09-978-681A-522
; Sequence 522, Application US/09978681A
; Publication No. US20030195148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC18
CURRENT APPLICATION NUMBER: US/09/578.681A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
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 32 PRIOR APPLICATION NUMBER: 60/085689
 33 PRIOR FILING DATE: 1998-05-15
 34 PRIOR APPLICATION NUMBER: 60/085579
 35 PRIOR FILING DATE: 1998-05-15
 36 PRIOR APPLICATION NUMBER: 60/085580
 37 PRIOR FILING DATE: 1998-05-15
 38 PRIOR APPLICATION NUMBER: 60/085573
 39 PRIOR FILING DATE: 1998-05-15
 40 PRIOR APPLICATION NUMBER: 60/085704
 41 PRIOR FILING DATE: 1998-05-15
 42 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3,6e-09;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAAACCATCCAGCCAAATGCAATTTCTTGGGCAATTTTCACGGGGCTG 60
 134 ATGAAACCATCCAGCCAAATGCAATTTCTTGGGCAATTTTCACGGGGCTG 193
 61 GCTGCTCTGTCTCTTCCAGGAGTGCCGTGCGCGAGGAGATGCCATTTCCCAAA 120
 194 GCTGCTCTGTCTCTTCCAGGAGTGCCGTGCGCGAGGAGATGCCATTTCCCAAA 253
 121 GCTATGACAACTGACGGTCCGGAGGGGAGAGCGCCCTCAGTGCACTATTGAC 180
 254 GCTATGACAACTGACGGTCCGGAGGGGAGAGCGCCCTCAGTGCACTATTGAC 313
 181 AACCGGCTACCCGGTGGCTGCTAAACCGAGCACTCTCTATGTGCGGAATGAC 240
 314 AACCGGCTACCCGGTGGCTGCTAAACCGAGCACTCTCTATGTGCGGAATGAC 373
 241 AAGTGGTGCTTGGATCTCTCGGTGGTCTTCTAGAGCAACCCCAACCGAGTACGATC 300
 374 AAGTGGTGCTTGGATCTCTCGGTGGTCTTCTAGAGCAACCCCAACCGAGTACGATC 433
 301 GAGATCAGAACTGGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCGAGACAG 360
 434 GAGATCAGAACTGGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCGAGACAG 493
 361 AACCAACCAAGACCTTAGGGTCCACTATTGTGCAAGTATCTCCCAAAATTTAGAG 420

Db 494 AACCAACCAAGACCTTAGGGTCCACTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
 Qy 421 ATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCTTCACCTGCAATAGCACT 480
 Db 554 ATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCTTCACCTGCAATAGCACT 613
 Qy 481 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTG 540
 Db 614 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTG 673
 Qy 541 AGTGAAGACGAATCTTCGAATTCAGGGCATACCCGGGAGCAGTACGGGAGTACAG 600
 Db 674 AGTGAAGACGAATCTTCGAATTCAGGGCATACCCGGGAGCAGTACGGGAGTACAG 733
 Qy 601 TGCAGTGCTTCCAATGACGTGGCGCGCCGTGGTACGGAGAGTAAAGGTCAACCGTGAAC 660
 Db 734 TGCAGTGCTTCCAATGACGTGGCGCGCCGTGGTACGGAGAGTAAAGGTCAACCGTGAAC 793
 Qy 661 TATCCACCATACATTTGAAAGCCAAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720
 Db 794 TATCCACCATACATTTGAAAGCCAAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
 Qy 721 CTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTCAGAGGATGACAAA 780
 Db 854 CTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTCAGAGGATGACAAA 913
 Qy 781 AGACTGATTGAAGGAAAGAGGGGTGAAAGTGAAGGAAACAGACCTTCTCTCAAACTC 840
 Db 914 AGACTGATTGAAGGAAAGAGGGGTGAAAGTGAAGGAAACAGACCTTCTCTCAAACTC 973
 Qy 841 ATCTTCTTCAATGTCTCTGAACATGATGAGGAACTACACTTGGGCTGCTCCAAAG 900
 Db 974 ATCTTCTTCAATGTCTCTGAACATGATGAGGAACTACACTTGGGCTGCTCCAAAG 1033
 Qy 901 CTGGGCGACACCAATGCCAGCATCATCTATTGCTCCAGGCGCGCTCAGCGAGTGAAC 960
 Db 1034 CTGGGCGACACCAATGCCAGCATCATCTATTGCTCCAGGCGCGCTCAGCGAGTGAAC 1093
 Qy 961 AACGGCACGTGAGAGGGGAGGCTGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 Db 1094 AACGGCACGTGAGAGGGGAGGCTGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
 Qy 1021 CTCTCAAAATTTGA 1035
 Db 1154 CTCTCAAAATTTGA 1168

RESULT 25
 US-09-978-194A-522
 ; Sequence 522, Application US/09978194A
 ; Publication No. US2003019533A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C10
CURRENT APPLICATION NUMBER: US/09/978,194A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCCAAAATTCATCTCTTGGCAATTCATCTTCACGGGGCTG 60

[illegible]

US-09-978-544A-522

Sequence 522, Application US/09978544A
Publication No. US20030199436A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2630P1C13

CURRENT APPLICATION NUMBER: US/09/978,544A

CURRENT FILING DATE: 2002-03-19

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1035; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.6e-09;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCCAAAATGCACAAATCTATCTCTTGGGCAATCTTACGGGGCTG 60
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Db 194 GCTGCTGTGTGTCTTCTTCAAGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAAA 253
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QY 121 GCTATGGACACGTGACCGTCCGCGAGGGGAGAGCGGCAACCTCAGTGCATATTGAC 180
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Db 254 GCTATGGACACGTGACCGTCCGCGAGGGGAGAGCGGCAACCTCAGTGCATATTGAC 313
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QY 181 AACCGGGTCACCCGGGTGCGCTTAAACCGCAGCACCATCTCTATGTCTGGGAATGAC 240
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Db 374 AAGTGGTCTGGATCTCGGTGCTCTTCTGAGCAACCCAAAGCGAGTACAGATC 433
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Db 434 GAGATCCAGAACGTTGATGTATGAGCAGGGGCTTTACACCTGCTCGGTGAGACAGAC 493
QY 361 AACACCCAAAGACCTTAGGTCCACCTCATTTGTCAGATCTCCCAAAATTTAGAG 420
Db 494 AACACCCAAAGACCTTAGGTCCACCTCATTTGTCAGATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCCACCTGCACT 480
Db 554 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCCACCTGCACT 613
QY 481 GTTAGACAGAGCTACGGTTACTTGGAGACATCTCTCCAAAGCGTTGGCTTTGTG 540
Db 614 GTTAGACAGAGCTACGGTTACTTGGAGACATCTCTCCAAAGCGTTGGCTTTGTG 673
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QY 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC19
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Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCCAGCCAAATGCAATTCCTCTCTTGGGCAATCTTCACGGGCTG 60
Db 134 ATGAAACCATCCAGCCAAATGCAATTCCTCTCTTGGGCAATCTTCACGGGCTG 193
Qy 61 GCTGCTCTGTCTCTTCCAAGGAGTGCCCGTGCAGCGGAGATGCCACTTCCCAAA 120
Db 194 GCTGCTCTGTCTCTTCCAAGGAGTGCCCGTGCAGCGGAGATGCCACTTCCCAAA 253
Qy 121 GCTATGACAACTGAGCGGTCCCGGAGGAGCGCCACCTCAGGTGCATATTGAC 180
Db 254 GCTATGACAACTGAGCGGTCCCGGAGGAGCGCCACCTCAGGTGCATATTGAC 313
Qy 181 AACCGGCTCACCCGGGTGGCTCTTAAACCGGAGCAACCATCTCTATGCTGGGAATGAC 240
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Qy 241 AAGTGTGCTGGATCCTCGGTGCTCTTCTGAGCAACCAACCAACGAGTACAGATC 300
Db 374 AAGTGTGCTGGATCCTCGGTGCTCTTCTGAGCAACCAACCAACGAGTACAGATC 433
Qy 301 GAGATCCAGAACGTGATGATGAGGAGGCGCCCTTACCTGCTCGGTGAGAGAC 360
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RESULT 30

RESULT: 30
US-09-978-802A-522

US-09-978-802A-522
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; Sequence 522, APPLICATION US/09
; Publication No. US20030199674A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E

APPLICANT: Goddard, Audrey

APPLICANT: GODOWSKI, PAUL J.

APPLICANT: J. Christonher

APPLICANT: Gurney, Austin J.

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; APPLICANT: Napier, Mary A

1 APPLICANT: Paoni, Nicholas F.
 2 APPLICANT: Roy, Margaret Ann
 3 APPLICANT: Shelton, David L.
 4 APPLICANT: Stewart, Timothy A.
 5 APPLICANT: Tumas, Daniel
 6 APPLICANT: Williams, P. Mickey
 7 APPLICANT: Wood, William I.
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 9 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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 11 TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 1035; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACACCATCCAGCCAAATGCAATTCCTCTTTGGGGAATCTTCACGGGGCTG 60
Db 134 ATGAACACCATCCAGCCAAATGCAATTCCTCTTTGGGGAATCTTCACGGGGCTG 193
QY 61 GCTGCTCTGTGTCTCTTTCCAAAGGAGTGCCCGTGGCAGGCGAGATGCCACTTCCCCAAA 120
Db 194 GCTGCTCTGTGTCTCTTTCCAAAGGAGTGCCCGTGGCAGGCGAGATGCCACTTCCCCAAA 253
QY 121 GCTATGACAAACGTGAGCGGTCCGCGAGGCGAGCGCCACCTCAGGTGCATATTGAC 180
Db 254 GCTATGACAAACGTGAGCGGTCCGCGAGGCGAGCGCCACCTCAGGTGCATATTGAC 313
QY 181 AACCGGCTCACCCGGGTGGCTGCTAAACCGCAGCACCATCTCTTATGCTGGGAATGAC 240
Db 314 AACCGGCTCACCCGGGTGGCTGCTAAACCGCAGCACCATCTCTTATGCTGGGAATGAC 373
QY 241 AAGTGTGCTGATCCTCGGTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
Db 374 AAGTGTGCTGATCCTCGGTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 301 GAGATCCAGAACGTGATGTATGACGAGGCGCTTACCTGCTCGGTGAGACAGAC 360
Db 434 GAGATCCAGAACGTGATGTATGACGAGGCGCTTACCTGCTCGGTGAGACAGAC 493
QY 361 AACCAACCAAGACCTCTAGGCTCCACCTCATTTGTCAGATATCTCCCAAAATTTAGAG 420
Db 494 AACCAACCAAGACCTCTAGGCTCCACCTCATTTGTCAGATATCTCCCAAAATTTAGAG 553
QY 421 ATTTCTTCAGATATCTCCATTAAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 480
Db 554 ATTTCTTCAGATATCTCCATTAAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
QY 481 GGTAGACGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 540
Db 614 GGTAGACGAGCCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 541 AGTGAAGACGAATACTTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
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Db ||||||| 674 AGTGAAGACGAAATCTTGGAAATTCAGGSCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
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Db ||||||| 734 TGCAGTGCCTCCAAATGACGTGGCGCGCCCGTGGTACGGAGATAAAGGTACCGTGAAC 793
Qy ||||||| 661 TATCCACATACATTTCAAGACCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720
Db ||||||| 794 TATCCACCATACATTTCAAGACCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
Qy ||||||| 721 CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGCAATTCAGTGGTACAAGGATGACAAA 780
Db ||||||| 854 CTGCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGCAATTCAGTGGTACAAGGATGACAAA 913
Qy ||||||| 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAAACTC 840
Db ||||||| 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAAACTC 973
Qy ||||||| 841 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGCGTGGCTCCAAACAG 900
Db ||||||| 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGCGTGGCTCCAAACAG 1033
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Db ||||||| 1034 CTGGGCCACACCAATGCAGCATCATGTCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1093
Qy ||||||| 961 AACGGCACGTGAGGAGGGCAGGCTGCGTCTGGCTGCTGCTCTTCTGGTCTTGGCACCTG 1020
Db ||||||| 1094 AACGGCACGTGAGGAGGGCAGGCTGCGTCTGGCTGCTGCTCTTCTGGTCTTGGCACCTG 1153
Qy ||||||| 1021 CTTCTCAAAATTTGA 1035
Db ||||||| 1154 CTTCTCAAAATTTGA 1168

Search completed: May 28, 2004, 21:31:31
Job time : 500.763 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 13:09:09 ; Search time 458.39 Seconds

(without alignments)

9592.021 Million cell updates/sec

Title: US-10-017-084A-522_COPY_134_1168

Perfect score: 1035

Sequence:

1 atgaaaccatccagccaaa.....acctgcttcctcaaatgtga 1035

Scoring table: IDENTITY_NUC

Gapop 1.0 , Gapext 0.1

Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N_Geneseq_29Jan04.*

1: geneseqn1980s.*

2: geneseqn1990s.*

3: geneseqn2000s.*

4: geneseqn2001as.*

5: geneseqn2001bs.*

6: geneseqn2002s.*

7: geneseqn2003as.*

8: geneseqn2003bs.*

9: geneseqn2003cs.*

10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	100.0	1679	2	Aaz34324 Human PRO
2	1035	100.0	1679	3	Aac78590 Human PRO
3	1035	100.0	1679	4	Aac87037 Nucleotid
4	1035	100.0	1679	4	Aas21431 Human cDN
5	1035	100.0	1679	6	ABK33598
6	1035	100.0	1679	6	ABL88099
7	1035	100.0	1679	6	ABL95588
8	1035	100.0	1679	6	ABD24040 Novel hum
9	1035	100.0	1679	7	ACA66903 cDNA enco
10	1035	100.0	1679	7	ACD42387 Novel hum
11	1035	100.0	1679	7	ACD42857 Novel hum
12	1035	100.0	1679	7	ACD68655 Novel hum
13	1035	100.0	1679	7	ACA67181 cDNA enco
14	1035	100.0	1679	7	ACA63892 Novel hum
15	1035	100.0	1679	7	ACA03790 cDNA enco
16	1035	100.0	1679	7	ACA04996 Novel hum
17	1035	100.0	1679	7	ABX89328 Human sec
18	1035	100.0	1679	7	ABX92696 cDNA enco
19	1035	100.0	1679	7	ABX92696 cDNA enco
20	1035	100.0	1679	7	ABX92696 cDNA enco
21	1035	100.0	1679	7	ACA41982 Human sec
22	1035	100.0	1679	7	ACA05026 Novel hum
23	1035	100.0	1679	7	ACA04516 Novel hum
					ACA66437 Human cDN

24	1035	100.0	1679	7	ACA68559	Novel hum
25	1035	100.0	1679	7	ACA04211	Human cDN
26	1035	100.0	1679	8	ACA65657	Human cDN
27	1035	100.0	1679	8	ADA45894	Novel hum
28	1035	100.0	1679	8	ADA76325	Human PRO
29	1035	100.0	1679	8	ABT44288	Human PRO
30	1035	100.0	1679	8	ADA18975	Human PRO
31	1035	100.0	1679	8	ADA61598	Homo sapi
32	1035	100.0	1679	8	ADB19383	Novel hum
33	1035	100.0	1679	8	ADB27924	cDNA enco
34	1035	100.0	1679	8	ADA86403	Novel hum
35	1035	100.0	1679	8	ADB15967	Human PRO
36	1035	100.0	1679	8	ADA47753	Human PRO
37	1035	100.0	1679	8	ADA67548	Human PRO
38	1035	100.0	1679	8	ADB30555	cDNA enco
39	1035	100.0	1679	8	ADA85851	Novel hum
40	1035	100.0	1679	8	ADA97063	Human PRO
41	1035	100.0	1679	8	ADA79367	Human PRO
42	1035	100.0	1679	8	ADA87506	Novel hum
43	1035	100.0	1679	8	ADB16708	Human PRO
44	1035	100.0	1679	8	ADA91800	Novel hum
45	1035	100.0	1679	8	ADB14863	Human PRO
46	1035	100.0	1679	8	ADA25061	Novel hum
47	1035	100.0	1679	8	ADA47275	Human sec
48	1035	100.0	1679	8	ADB18824	Novel hum
49	1035	100.0	1679	8	ADA94039	Human PRO
50	1035	100.0	1679	8	ADB19935	Novel hum
51	1035	100.0	1679	8	ADB13247	Novel hum
52	1035	100.0	1679	8	ACD98611	Novel hum
53	1035	100.0	1679	8	ACD30038	Novel hum
54	1035	100.0	1679	8	ADA12722	Human cDN
55	1035	100.0	1679	8	ADA74501	Human PRO
56	1035	100.0	1679	8	ADB24734	Human PRO
57	1035	100.0	1679	8	ADA82258	Human PRO
58	1035	100.0	1679	8	ADA75221	Human PRO
59	1035	100.0	1679	8	ADA85299	Novel hum
60	1035	100.0	1679	8	ADA84747	Novel hum
61	1035	100.0	1679	8	ADB30003	cDNA enco
62	1035	100.0	1679	8	ADA80531	Human PRO
63	1035	100.0	1679	8	ADA75773	Human PRO
64	1035	100.0	1679	8	ADA46998	Human PRO
65	1035	100.0	1679	8	ADB25294	Human PRO
66	1035	100.0	1679	8	ADA93470	Human PRO
67	1035	100.0	1679	8	ADB26820	cDNA enco
68	1035	100.0	1679	8	ADB31107	cDNA enco
69	1035	100.0	1679	8	ABT44571	Human PRO
70	1035	100.0	1679	8	ADA61035	Homo sapi
71	1035	100.0	1679	8	ADB24182	Human PRO
72	1035	100.0	1679	8	ADA96511	Human PRO
73	1035	100.0	1679	8	ADA81083	Human PRO
74	1035	100.0	1679	8	ADA95959	Human PRO
75	1035	100.0	1679	8	ADB26268	cDNA enco
76	1035	100.0	1679	8	ADB21753	Novel hum
77	1035	100.0	1679	8	ACD82238	Human sec
78	1035	100.0	1679	8	ACD29453	Novel hum
79	1035	100.0	1679	8	ADA77552	Human PRO
80	1035	100.0	1679	8	ADB18272	Human PRO
81	1035	100.0	1679	8	ADA86955	Novel hum
82	1035	100.0	1679	8	ADA88058	Novel hum
83	1035	100.0	1679	8	ADA46446	Novel hum
84	1035	100.0	1679	8	ADB28476	cDNA enco
85	1035	100.0	1679	8	ADB29028	cDNA enco
86	1035	100.0	1679	8	ADA76980	Human PRO
87	1035	100.0	1679	8	ADA88610	Novel hum
88	1035	100.0	1679	8	ADA97615	Human PRO
89	1035	100.0	1679	8	ADB27372	cDNA enco
90	1035	100.0	1679	8	ADB22305	Novel hum
91	1035	100.0	1679	8	ACD30273	Human cDN
92	1035	100.0	1679	8	ABT43944	Human mem
93	1035	100.0	1679	8	ADA66996	Human PRO
94	1035	100.0	1679	8	ADB22857	Human PRO
95	1035	100.0	1679	8	ADB23630	Human PRO
96	1035	100.0	1679	8	ADA92352	Novel hum

97 1035 100.0 1679 8 ADB15415
98 1035 100.0 1679 8 ADB83615
99 1035 100.0 1679 8 ADB80721
100 1035 100.0 1679 8 ADB73262

Adh15415 Human PRO
Adh83615 Novel hum
Adh80721 Novel hum
Adh73262 Novel hum

ALIGNMENTS

RESULT 1
AAZ34324
ID AAZ34324 standard; cDNA; 1679 BP.

XX AAZ34324;

XX 07-DEC-1999 (first entry)

XX Human PRO337 nucleotide sequence.

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein; ss.

XX Homo sapiens.

XX WO9946281-A2.

XX 16-SEP-1999.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1998; 98US-0077450P.

XX 11-MAR-1998; 98US-0077632P.

XX 11-MAR-1998; 98US-0077641P.

XX 11-MAR-1998; 98US-0077649P.

XX 12-MAR-1998; 98US-0077791P.

XX 13-MAR-1998; 98US-0077804P.

XX 17-MAR-1998; 98US-00040220.

XX 20-MAR-1998; 98US-0078886P.

XX 20-MAR-1998; 98US-0078910P.

XX 20-MAR-1998; 98US-0078936P.

XX 20-MAR-1998; 98US-0078939P.

XX 25-MAR-1998; 98US-0079294P.

XX 26-MAR-1998; 98US-0079656P.

XX 27-MAR-1998; 98US-0079663P.

XX 27-MAR-1998; 98US-0079664P.

XX 27-MAR-1998; 98US-0079689P.

XX 27-MAR-1998; 98US-0079728P.

XX 30-MAR-1998; 98US-0079786P.

XX 30-MAR-1998; 98US-0079920P.

XX 31-MAR-1998; 98US-0079923P.

XX 31-MAR-1998; 98US-0080105P.

XX 31-MAR-1998; 98US-0080107P.

XX 31-MAR-1998; 98US-0080165P.

XX 31-MAR-1998; 98US-0080194P.

XX 01-APR-1998; 98US-0080327P.

PR 22-APR-1998; 98US-0082804P.

PR 23-APR-1998; 98US-0082767P.

PR 23-APR-1998; 98US-0082796P.

PR 27-APR-1998; 98US-0083336P.

PR 28-APR-1998; 98US-0083322P.

PR 29-APR-1998; 98US-0083392P.

PR 29-APR-1998; 98US-0083496P.

PR 29-APR-1998; 98US-0083496P.

PR 29-APR-1998; 98US-0083500P.

PR 29-APR-1998; 98US-0083545P.

PR 29-APR-1998; 98US-0083554P.

PR 29-APR-1998; 98US-0083558P.

PR 30-APR-1998; 98US-0083559P.

PR 05-MAY-1998; 98US-0083742P.

PR 06-MAY-1998; 98US-0084366P.

PR 06-MAY-1998; 98US-0084414P.

PR 07-MAY-1998; 98US-0084441P.

PR 07-MAY-1998; 98US-0084598P.

PR 07-MAY-1998; 98US-0084600P.

PR 07-MAY-1998; 98US-0084627P.

PR 07-MAY-1998; 98US-0084637P.

PR 07-MAY-1998; 98US-0084639P.

PR 07-MAY-1998; 98US-0084640P.

PR 13-MAY-1998; 98US-0084643P.

PR 13-MAY-1998; 98US-0085223P.

PR 13-MAY-1998; 98US-0085338P.

PR 15-MAY-1998; 98US-0085339P.

PR 15-MAY-1998; 98US-0085573P.

PR 15-MAY-1998; 98US-0085579P.

PR 15-MAY-1998; 98US-0085580P.

PR 15-MAY-1998; 98US-0085582P.

PR 15-MAY-1998; 98US-0085689P.

PR 15-MAY-1998; 98US-0085697P.

PR 15-MAY-1998; 98US-0085700P.

PR 18-MAY-1998; 98US-0085704P.

PR 22-MAY-1998; 98US-0086023P.

PR 22-MAY-1998; 98US-0086392P.

PR 22-MAY-1998; 98US-0086414P.

PR 22-MAY-1998; 98US-0086430P.

PR 22-MAY-1998; 98US-0086486P.

PR 28-MAY-1998; 98US-0087098P.

PR 28-MAY-1998; 98US-0087108P.

PR 28-MAY-1998; 98US-0087208P.

PR 30-JUL-1998; 98US-0094651P.

PR 11-SEP-1998; 98US-0100038P.

XX (GETH) GENENTECH INC.

XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

XX WPI; 1999-551358/46.

XX P-PSDB; AAY41773.

XX New secreted and transmembrane polypeptides and their polynucleotides,

XX useful for treating blood coagulation disorders, cancers and cellular

XX adhesion disorders.

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Claim 2; Fig 221; 530pp; English.

The Present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 2; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAAACCATCCAGCCAAATGCAATTTCTTCTTGGGCAATTTCTACCGGGCTG 60
Db |||
QY 134 ATGAAACCATCCAGCCAAATGCAATTTCTTCTTGGGCAATTTCTACCGGGCTG 193
Db |||
QY 61 GCTGCTCTGTGCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAA 120
Db |||
QY 194 GCTGCTCTGTGCTCTTCCAAAGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAA 253
Db |||
QY 121 GCTATGACCAAGTGAAGTCCGCGAGCGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
Db |||
QY 254 GCTATGACCAAGTGAAGTCCGCGAGCGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
Db |||
QY 181 AACCGGGTCAACCGGGTCCGCTGCTTAAACCGCAGCAGATCTCTATGCTGGGAATGAC 240
Db |||
QY 314 AACCGGGTCAACCGGGTCCGCTGCTTAAACCGCAGCAGATCTCTATGCTGGGAATGAC 373
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QY 241 AAGTGGTCCCTGGATCCCTCGGCTGCTTCTGAGCAACACCCAAACCGCAGTACAGCATC 300
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QY 301 GAGATCCAGAACGTTGATGAGCAGGGCCCTTACACCTGCTGGTGCAGACAGAC 360
Db |||
QY 434 GAGATCCAGAACGTTGATGAGCAGGGCCCTTACACCTGCTGGTGCAGACAGAC 493
Db |||
QY 361 AACCAACCAAGACCTCTAGGCTCCACCTCTGAGGAGTATCTCCAAATTTGTAGAG 420
Db |||
QY 494 AACCAACCAAGACCTCTAGGCTCCACCTCTGAGGAGTATCTCCAAATTTGTAGAG 553
Db |||
QY 421 ATTCTTCCAGATCTCCATTAATGAAGGGAACATATTAGCCTCAGCTGATAGCAACT 480
Db |||
QY 554 ATTCTTCCAGATCTCCATTAATGAAGGGAACATATTAGCCTCAGCTGATAGCAACT 613
Db |||
QY 481 GGTAGACAGACCTAGCTTACTTTGAGACACATCTCTCCAAAGCGTTGGTTTGTG 540
Db |||
QY 614 GGTAGACAGACCTAGCTTACTTTGAGACACATCTCTCCAAAGCGTTGGTTTGTG 673
Db |||
QY 541 AGTGAAGACCAATATTCTGAAATTCAGGGCATCACCGGGAGCAGTACAGGGGACTACGAG 600
Db |||
QY 674 AGTGAAGACCAATATTCTGAAATTCAGGGCATCACCGGGAGCAGTACAGGGGACTACGAG 733
Db |||
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Db |||
QY 734 TGAGTGCCTCCATAGAGTGGCGCGCCCTCAGCAGATTAAGGTACCGTGAAC 793
Db |||
QY 661 TATCCACCATACATTTTCCAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720
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QY 794 TATCCACCATACATTTTCCAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
Db |||
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Db |||
QY 854 CTCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTTCCAGTGGTACAGGATGACAA 913
Db |||
QY 781 AGACTGATGAAGAAAGAGGGTGAAGTGGAAACAGACCTTTCTCTCTCAAAATC 840
Db |||
QY 914 AGACTGATGAAGAAAGAGGGTGAAGTGGAAACAGACCTTTCTCTCTCAAAATC 973
Db |||
QY 841 ATCTTCTCAATGTCTGTAACATGACTATGGGAATCTACCTTGGTGGCTCCAAAG 900
Db |||
QY 974 ATCTTCTCAATGTCTGTAACATGACTATGGGAATCTACCTTGGTGGCTCCAAAG 1033
Db |||
QY 901 CTGGGCGCACCAATGCGCAGCATCATGCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 960
Db |||
QY 1034 CTGGGCGCACCAATGCGCAGCATCATGCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGC 1093
Db |||
QY 961 AACGGCAGTGCAGAGAGGAGGAGCTGGTGTGCTGTGCTCTTCTGTGCTTGCACCTG 1020
Db |||
QY 1094 AACGGCAGTGCAGAGAGGAGGAGGCTGGTGTGCTGTGCTCTTCTGTGCTTGCACCTG 1153
Db |||
QY 1021 CTCTCTCAATTTTGA 1035
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Db 1154 CTCTCAATTTTGA 1168

RESULT 2

AAC78590
ID AAC78590 standard; cDNA; 1679 BP.

XX AAC78590;

XX 08-FEB-2001 (first entry)

XX Human PRO337 nucleotide sequence SEQ ID NO:522.

XX Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
expressed sequence tag; detection; cancer; ss.

XX Homo sapiens.

XX WO200053756-A2.

XX 14-SEP-2000.

XX 18-FEB-2000; 2000WO-US004341.

XX 08-MAR-1999; 99WO-US005028.

XX 12-MAR-1999; 99US-0123957P.

XX 29-MAR-1999; 99US-0126773P.

XX 21-APR-1999; 99US-0130232P.

XX 28-APR-1999; 99US-0131445P.

XX 14-MAY-1999; 99US-0134287P.

XX 23-JUN-1999; 99US-0141037P.

XX 26-JUL-1999; 99US-0145698P.

XX 29-OCT-1999; 99US-0162506P.

XX 30-NOV-1999; 99WO-US028313.

XX 02-DEC-1999; 99WO-US028551.

XX 16-DEC-1999; 99WO-US028565.

XX 30-DEC-1999; 99WO-US030095.

XX 05-JAN-2000; 99WO-US031243.

XX 06-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Klavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
Stewart TA, Tumas D, Williams PM, Wood WI;

WPI; 2000-611443/58.

P-PSDB; AAB44329.

Novel PRO polypeptides and polynucleotides used in detection methods, to
target bioactive molecules to specific cells, and to modulate cellular
activities.

Claim 2; Fig 221; 636pp; English.

AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
tag) sequences which encode secreted or transmembrane PRO polypeptides.
The PRO polynucleotides and polypeptides have cytosolic activity. The
polynucleotides and polypeptides can be used for detecting the presence
of PRO polypeptides in samples, for linking bioactive molecules to cells
and for modulating biological activities of cells, using the polypeptides
for specific targeting. The polypeptide targeting can be used to kill the
target cells, e.g. for the treatment of cancers. The polypeptide pairs
provide specific targeting of bioactive molecules to cells. AAC78600 to
AAC78897 represent PCR primers and probes used in the isolation of the
PRO polynucleotide sequences

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.08; Score 1035; DB 3; Length 1679;
Best Local Similarity 100.08; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAAACCATCCAGCCAAATGCAATATCTCTTGGGCAATCTTCACGGGGCTG 60
DB 134 ATGAAACCATCCAGCCAAATGCAATATCTCTTGGGCAATCTTCACGGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCAGCGAGATGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCAGCGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGACAAACGTCAGCGTCCGCGAGGGGAGAGCCACCTTCAGTGCATATTGAC 180
DB 254 GCTATGACAAACGTCAGCGTCCGCGAGGGGAGAGCCACCTTCAGTGCATATTGAC 313
QY 181 AACCGGTTCACCCGGGTGGCTTAAACCGCAGCACCATCTCTTATGCTGGGAATGAC 240
DB 314 AACCGGTTCACCCGGGTGGCTTAAACCGCAGCACCATCTCTTATGCTGGGAATGAC 373
QY 241 AAGTGGTGCCTGATCTCCGCTGGTCTTCTGAGCAACACCCAAACGCAATCAGCATC 300
DB 374 AAGTGGTGCCTGATCTCCGCTGGTCTTCTGAGCAACACCCAAACGCAATCAGCATC 433
QY 301 GAGATCCAGAACGTCGATGATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
DB 434 GAGATCCAGAACGTCGATGATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 361 AACCAACCAAGACCTTGAAGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACCAACCAAGACCTTGAAGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTTCAGATATCTCCATTAATGAGGAAACAAATATTAGCTCATCTGCTAGCAACT 480
DB 554 ATTCTTTCAGATATCTCCATTAATGAGGAAACAAATATTAGCTCATCTGCTAGCAACT 613
QY 481 GGTAGACCAAGACCTTACGGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTG 540
DB 614 GGTAGACCAAGACCTTACGGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTG 673
QY 541 AGTGAAGCAATATCTTGAATTTAGGCGATCACCCGGGAGCAGTCAAGGAGTACGAG 600
DB 674 AGTGAAGCAATATCTTGAATTTAGGCGATCACCCGGGAGCAGTCAAGGAGTACGAG 733
QY 601 TGCAGTGCCTCCAAATGACGTGCGCGCCGCTGACGAGGATTAAGGTCAACCGTGAAC 660
DB 734 TGCAGTGCCTCCAAATGACGTGCGCGCCGCTGACGAGGATTAAGGTCAACCGTGAAC 793
QY 661 TATCCACCAATATTTAGAACCCAGGATACAGGTGTCCCGTGGGACAAAGGGGACA 720
DB 794 TATCCACCAATATTTAGAACCCAGGATACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 721 CTGCAAGTGAAGCTTCAGCAGTCCCTTCAGCAGAAATTCAGTGATCAAGGATGACAAA 780
DB 854 CTGCAAGTGAAGCTTCAGCAGTCCCTTCAGCAGAAATTCAGTGATCAAGGATGACAAA 913
QY 781 AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCRAAACTC 840
DB 914 AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCRAAACTC 973
QY 841 ATCTTCTTCAATGTCTTGAACATGACTATGGAACTACACTTGGTGGCTTCCAAACAG 900
DB 974 ATCTTCTTCAATGTCTTGAACATGACTATGGAACTACACTTGGTGGCTTCCAAACAG 1033
QY 901 CTGGGCCACACCAATGCCAGATATGCTATTGTTGTCAGGGCGCTCAGGAGTGAGC 960
DB 1034 CTGGGCCACACCAATGCCAGATATGCTATTGTTGTCAGGGCGCTCAGGAGTGAGC 1093
QY 961 AACGGCAGCTCAGGAGGGCAGGCTGCTGCTGGCTGCTGCTTCTTCTGCTTCCACTG 1020
DB 1094 AACGGCAGCTCAGGAGGGCAGGCTGCTGCTGGCTGCTGCTTCTTCTGCTTCCACTG 1153
```

QY 1021 CTCTCAAAATTTGA 1035
DB 1154 CTCTCAAAATTTGA 1168

RESULT 3
AAC87037

ID AAC87037 standard; cDNA; 1679 BP.

XX AAC87037;

XX 20-APR-2001 (first entry)

XX Nucleotide sequence of human polypeptide PRO337.

Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
ss.

XX Homo sapiens.

XX Key Location/Qualifiers
CDS 134..1168

FT /*tag= a

FT sig_peptide 134..216

FT /*tag= b

XX WO200077037-A2.

XX 21-DEC-2000.

XX 22-MAY-2000; 2000WO-US014042.

XX 15-JUN-1999; 99US-0139695P.

XX 20-JUL-1999; 99US-0145070P.

XX 26-JUL-1999; 99US-0145698P.

XX 17-AUG-1999; 99US-0149396P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1999; 99WO-US028301.

XX 02-DEC-1999; 99WO-US028565.

XX 07-DEC-1999; 99US-0165495P.

XX 05-JAN-2000; 2000WO-US000219.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX 01-MAR-2000; 2000WO-US005601.

XX 20-MAR-2000; 2000WO-US005841.

XX 30-MAR-2000; 2000WO-US007377.

XX 15-MAY-2000; 2000WO-US008439.

XX 17-MAY-2000; 2000WO-US013705.

(GETH) GENENTECH INC.

Askenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Kljavin LJ, Mather JP, Napier MA, Pan J;
Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
Wood WI, Zhang Z;

WPI; 2001-050091/06.

P-PSDB; AAB31204.

Isolated nucleic acid molecule encoding a PRO polypeptide which is a

1 ATGAAACCATCAGCGCAAAAATGACAAATCTATCTCTGGGCAATCTTCAAGGGGTG 60
134 ATGAAACCATCAGCGCAAAAATGACAAATCTATCTCTGGGCAATCTTCAAGGGGTG 193
61 GCTGCTCTGTGTCCTTCCAGAGAGTGCCGTGGCGAGCGGAGATGCCACCTTCCCCAAA 120
194 GCTGCTCTGTGTCCTTCCAGAGAGTGCCGTGGCGAGCGGAGATGCCACCTTCCCCAAA 253
121 GCTATGGACAAGCTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTTCAC 180
254 GCTATGGACAACGCTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTTCAC 313
181 AACCGGGTCACCCGGGTGGCTGGCTAAACCGGAGCAGCATCTCTATGCTGGGAATGAC 240
314 AACCGGGTCACCCGGGTGGCTGGCTAAACCGGAGCAGCATCTCTATGCTGGGAATGAC 373
241 AAGTGGTGCCTGGATCTCGCTGGTCTCTTCTGAGCAACACCCAAACGCGATGACGATC 300
374 AAGTGGTGCCTGGATCTCGCTGGTCTCTTCTGAGCAACACCCAAACGCGATGACGATC 433
301 GAGATCCAGAACGNGGATGTATGACGAGGGCCCTTACCTGCTCGGTGCACAGAC 360
434 GAGATCCAGAACGTTGGATGTATGACGAGGGCCCTTACCTGCTCGGTGCACAGAC 493
361 AACCAACCAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAATTTGTAG 420
494 AACCAACCAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAATTTGTAG 553
421 ATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACTGTCATAGCAACT 480
554 ATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACTGTCATAGCAACT 613
481 GGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540
614 GGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673
541 AGTGAAGACGAATACTTGGAAATTCAGGCGATCAACCCGGAGCAGTCAAGGGACTACGAG 600
674 AGTGAAGACGAATACTTGGAAATTCAGGCGATCAACCCGGAGCAGTCAAGGGACTACGAG 733
601 TGCAGTGCCTCCAAATGACGTTGGCCGGCCGTGGTACGGAGGTAAAGGTCAACCGTGAAC 660
734 TGCAGTGCCTCCAAATGACGTTGGCCGGCCGTGGTACGGAGGTAAAGGTCAACCGTGAAC 793
661 TATCCACCATACATTTACAGACCAAGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720

PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 XX (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-408281/43.
 DR P-PSDB; AAU12359.
 DR
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 3; Fig 375; 813pp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful to detect other PRO
 CC polypeptides, to link bioactive molecules to cells expressing PRO
 CC polypeptides, to modulate biological activities of cells expressing PRO
 CC polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumors by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample. Some
 CC of the 275 sequences are also useful to stimulate the release of tumour
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
 CC differentiation of chondrocytes, the proliferation or gene expression in
 CC pericyte cells, the release of proteoglycans from cartilage, the
 CC proliferation of inner ear utricular supporting cells or of T-
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules
 CC involved in binding interactions. The polynucleotides encoding PRO
 CC polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1035; DB 4; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAACCAATCCAGCAAAATGCAATTTCTATCTCTTGGCAATCTTCAGGGGCTG 60
 DB 134 ATGAAACCAATCCAGCAAAATGCAATTTCTATCTCTTGGCAATCTTCAGGGGCTG 193
 QY 61 GCTGCTCTGTGCTCTTCCAGAGGTGCGCGTGCAGCGAGATGCCACCTTCCCAAA 120
 DB 194 GCTGCTCTGTGCTCTTCCAGAGGTGCGCGTGCAGCGAGATGCCACCTTCCCAAA 253
 QY 121 GCTATGGACACGTGACCGTCCGCGAGGGGAGAGCGCCACCTCAGTGTGACTATTGAC 180
 DB 254 GCTATGGACACGTGACCGTCCGCGAGGGGAGAGCGCCACCTCAGTGTGACTATTGAC 313

QY 181 AACCGGTCAACCGGTGGCTGGCTAAACCGAGAGCAACATCTCTTATGTGGGAATGAC 240
 DB 314 AACCGGTCAACCGGTGGCTGGCTAAACCGAGCAACCATCTCTTATGTGGGAATGAC 373
 QY 241 AAGTGTGCTGGATCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGATC 300
 DB 374 AAGTGTGCTGGATCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGATC 433
 QY 301 GAGATCCAGAACGTGGATGTATGAGAGGGGCCCTTTACACCTGTCTGGTGCAGACAGAC 360
 DB 434 GAGATCCAGAACGTGGATGTATGAGAGGGGCCCTTTACACCTGTCTGGTGCAGACAGAC 493
 QY 361 AACCAACCAAGACCTCTAGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTTAGAG 420
 DB 494 AACCAACCAAGACCTCTAGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTTAGAG 553
 QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGCAACAATATTAGCCCTCACCTGCATAGCAACT 480
 DB 554 ATTCTTTCAGATATCTCCATTAATGAAGGCAACAATATTAGCCCTCACCTGCATAGCAACT 613
 QY 481 GGTAGACGAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTGTGGCTTTGTG 540
 DB 614 GGTAGACGAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTGTGGCTTTGTG 673
 QY 541 AGTGAAGACGATACCTTGAATTCAGGGGCATCACCCGGGAGCAGTCAGGGGACTAGAG 600
 DB 674 AGTGAAGACGATACCTTGAATTCAGGGGCATCACCCGGGAGCAGTCAGGGGACTAGAG 733
 QY 601 TGCAGTGCCTCCAATGACGTGGCGCGCGTGTGACGAGAGTAAAGGTTCACCGTGAAC 660
 DB 734 TGCAGTGCCTCCAATGACGTGGCGCGCGTGTGACGAGAGTAAAGGTTCACCGTGAAC 793
 QY 661 TATCCACCATACATTTTCAGAACCAAGGTAAGGTGTCCCGTGGGACAAAGGGGACA 720
 DB 794 TATCCACCATACATTTTCAGAACCAAGGTAAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCACGTGGTACAGGATGACAA 780
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCACGTGGTACAGGATGACAA 913
 QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAATC 840
 DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAATC 973
 QY 841 ATCTTCTTCAATGTCTCTGAACATCACTATGGAATGATGATGATGATGATGATGATG 900
 DB 974 ATCTTCTTCAATGTCTCTGAACATCACTATGGAATGATGATGATGATGATGATGATG 1033
 QY 901 CTGGGCCACCAATGCGAGCATCATGTATTTGGTCCAGGCGCGTCCAGGAGGTGAGC 960
 DB 1034 CTGGGCCACCAATGCGAGCATCATGTATTTGGTCCAGGCGCGTCCAGGAGGTGAGC 1093
 QY 961 AACGCGACGTGAGAGGGGAGGTGCGTCTGGGTGCTGCTCTTCTTGTGCTTGCACCTG 1020
 DB 1094 AACGCGACGTGAGAGGGGAGGTGCGTCTGGGTGCTGCTCTTCTTGTGCTTGCACCTG 1153
 QY 1021 CTCTCAAAATTTTGA 1035
 DB 1154 CTCTCAAAATTTTGA 1168

RESULT 5
 ABK33598
 ID ABK33598 standard; cDNA; 1679 BP.
 XX
 AC ABK33598;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE cDNA encoding human PRO protein, Seq ID No 125.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 breast cancer; prostate tumour; rectal tumour; liver tumour;

KW pericyte cell proliferation; chondrocyte cell proliferation;
 XX tumour necrosis factor-alpha; gene; ss.

OS Homo sapiens.

PN WO200208288-A2.

XX 31-JAN-2002.

PF 29-JUN-2001; 2001WO-US021066.

XX 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220585P.

PR 25-JUL-2000; 2000US-0220605P.

PR 25-JUL-2000; 2000US-0220607P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220638P.

PR 25-JUL-2000; 2000US-0220664P.

PR 25-JUL-2000; 2000US-0220666P.

PR 26-JUL-2000; 2000US-0220893P.

PR 28-JUL-2000; 2000WO-US020710.

PR 01-AUG-2000; 2000US-0222425P.

PR 22-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 10-NOV-2000; 2000WO-US030873.

PR 28-NOV-2000; 2000US-0253646P.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 28-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 22-MAR-2001; 2001US-00816744.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 25-MAY-2001; 2001WO-US017092.

PA (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX P-PSDB; AAU83654.

XX WPI; 2002-172001/22.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,

XX useful for treating a PRO related disorder and for diagnosing tumors such

XX as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor

XX or liver tumor.

XX Claim 2; Fig 125; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids

XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides

XX encode human secreted proteins. The PRO nucleic acids, polypeptides,

XX agonists and antagonists are useful for treating a PRO related disorder.

XX The PRO polypeptides are useful for diagnosing tumours, especially lung

XX cancer, colon cancer, breast tumor, prostate tumor, rectal tumour or

XX liver tumour. The PRO polypeptides are useful for stimulating the

XX proliferation of, or gene expression, in pericyte cells, for stimulating

XX the proliferation or differentiation of chondrocyte cells, for

XX stimulating the release of tumour necrosis factor-alpha from human blood,

XX for stimulating or inhibiting the proliferation of normal human dermal

XX fibroblast cells. The PRO polypeptide may also be used as molecular

XX weight markers and for tissue typing. The PRO nucleic acids have

XX applications in molecular biology, including use as hybridisation probes,

XX and in chromosome and gene mapping. ABK33536-ABK33657 represent human PRO

XX protein coding sequences of the invention

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 1035; DB 6; Length 1679;

XX Best Local Similarity 100.0%; Pred. No. 3.1e-07;

		Matches 1035;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAACCATCCAGCCAAATAATGCAAAATTTCTATCTTTGGGCAATCTTACGGGGCTG	60			
DB	134	ATGAAACCATCCAGCCAAATAATGCAAAATTTCTATCTTTGGGCAATCTTACGGGGCTG	193			
QY	61	GCTGCTGTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAA	120			
DB	194	GCTGCTGTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAA	253			
QY	121	GCTATGGACAAAGTACGGTCCGGCAGGGGAGAGCGCCCTCAGTGCACTATTGAC	180			
DB	254	GCTATGGACAAAGTACGGTCCGGCAGGGGAGAGCGCCCTCAGTGCACTATTGAC	313			
QY	181	AACCGGCTCACCGGGTGGCTTAAACCGCAGCACTCTCTATGCTGGGAATGAC	240			
DB	314	AACCGGCTCACCGGGTGGCTTAAACCGCAGCACTCTCTATGCTGGGAATGAC	373			
QY	241	AAGTGTGCTGGATCTCTCGGTGGTCTTCTGAGCAACACCCAAACGCAATC	300			
DB	374	AAGTGTGCTGGATCTCTCGGTGGTCTTCTGAGCAACACCCAAACGCAATC	433			
QY	301	GAGATCCAGAAAGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC	360			
DB	434	GAGATCCAGAAAGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC	493			
QY	361	AACCAACCAAGACCTTAGGGTCCACTTATGAGGGAACAATATTAGCTTCACTGATGAACT	480			
DB	494	AACCAACCAAGACCTTAGGGTCCACTTATGAGGGAACAATATTAGCTTCACTGATGAACT	613			
QY	481	GGTAGACCAAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTGTG	540			
DB	614	GGTAGACCAAGCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTGTG	673			
QY	541	AGTGAAGACGAATCTTTGGAATTCAGGGCATCACCGGGAGCAGTCCAGGGGACTAGAG	600			
DB	674	AGTGAAGACGAATCTTTGGAATTCAGGGCATCACCGGGAGCAGTCCAGGGGACTAGAG	733			
QY	601	TGCAAGTCCCTCCAAATGACGTCGGCGCCCGTGTAGGAGAGTAAGGTACCGGTGAAC	660			
DB	734	TGCAAGTCCCTCCAAATGACGTCGGCGCCCGTGTAGGAGAGTAAGGTACCGGTGAAC	793			
QY	661	TATCCACCATACATTTTCAAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA	720			
DB	794	TATCCACCATACATTTTCAAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA	853			
QY	721	CTGCAAGTGAAGCTCAGAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATGACAAA	780			
DB	854	CTGCAAGTGAAGCTCAGAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATGACAAA	913			
QY	781	AGACTGATTGAAGGAAGAAAGGGTGAAGTGAAGGAACAGACCTTCTCTCAAAATC	840			
DB	914	AGACTGATTGAAGGAAGAAAGGGTGAAGTGAAGGAACAGACCTTCTCTCAAAATC	973			
QY	841	ATCTTCTCAATGTCTCTGAAACATGACTATGGAACTACACTTGGTGGCTCCCAACAG	900			
DB	974	ATCTTCTCAATGTCTCTGAAACATGACTATGGAACTACACTTGGTGGCTCCCAACAG	1033			
QY	901	CTGGGCGCACCAATGCGCAGCATCATGTTTGGTCCAGGCGCGCTCAGCGAGGTGAGC	960			
DB	1034	CTGGGCGCACCAATGCGCAGCATCATGTTTGGTCCAGGCGCGCTCAGCGAGGTGAGC	1093			
QY	961	AACGCGCAGTCCAGAGGCGAGGCTGGCTGCTGGCTGCTCTTCTGTTGCACTG	1020			
DB	1094	AACGCGCAGTCCAGAGGCGAGGCTGGCTGCTGGCTGCTCTTCTGTTGCACTG	1153			
QY	1021	CTTCTCAAAATTTGA	1035			
DB	1154	CTTCTCAAAATTTGA	1168			

RESULT 6
 ABL88099
 ID ABL88099 standard; cDNA; 1679 BP.
 XX
 AC ABL88099;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO337 cDNA sequence SEQ ID NO:55.
 XX
 DE Human;
 KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW vutnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US019692.
 XX
 PR 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709323.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00804280.
 PR 22-MAR-2001; 2001US-00808689.
 PR 05-APR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 30-MAY-2001; 2001US-00866034.
 PR 30-MAY-2001; 2001US-00870574.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR P-ESDB; ABB84844.
 DR

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 XX Claim 2; Fig 55; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, lymphangitis, tumour
 CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1035; DB 6; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAACCATCCAGCCAAATGCAATTCATCTCTTGGGCAATCTTACGGGGCTG 60
 DB 134 ATGAAACCATCCAGCCAAATGCAATTCATCTCTTGGGCAATCTTACGGGGCTG 193
 QY 61 GCTGCTCTGTGCTCTTCCAGAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAA 120
 DB 194 GCTGCTCTGTGCTCTTCCAGAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAA 253
 QY 121 GCTATGGACAAAGTCAAGGTTCGGCAGGGGAGAGCGCCCTCAGTGCACTATTGAC 180
 DB 254 GCTATGGACAAAGTCAAGGTTCGGCAGGGGAGAGCGCCCTCAGTGCACTATTGAC 313
 QY 181 AACCGGGTCACCGGGTGGCTGCTAAACCGCAGCACCCTCTCTAGTGGGAAATGAC 240
 DB 314 AACCGGGTCACCGGGTGGCTGCTAAACCGCAGCACCCTCTCTAGTGGGAAATGAC 373
 QY 241 AAGTGGTGCCTGATCTCTGCGGTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
 DB 374 AAGTGGTGCCTGATCTCTGCGGTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
 QY 301 GAGATCCAGAACGTGGATGCTATGACGAGGGCCCTTACACCTGCTGCTGACAGAC 360
 DB 434 GAGATCCAGAACGTGGATGCTATGACGAGGGCCCTTACACCTGCTGCTGACAGAC 493
 QY 361 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGCAAGTATCTCCCAAATGTAGAG 420
 DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGCAAGTATCTCCCAAATGTAGAG 553
 QY 421 ATTTCTTCAGATATCTCATTAATGAAGGAAACAATATTAGCCTCCTGATAGCAACT 480
 DB 554 ATTTCTTCAGATATCTCATTAATGAAGGAAACAATATTAGCCTCCTGATAGCAACT 613
 QY 481 GGTAGACGAGCCTACGGTTACTTTGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 540
 DB 614 GGTAGACGAGCCTACGGTTACTTTGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
 QY 541 AGTGAAGACGAATATCTTGAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 600
 DB 674 AGTGAAGACGAATATCTTGAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 733
 QY 501 TGCAGTGCCTCCCAATGACGTGGCGGCCCGCTGGTACGGAGAGTAAGGTTCACCGTGAAC 660
 DB 734 TGCAGTGCCTCCCAATGACGTGGCGGCCCGCTGGTACGGAGAGTAAGGTTCACCGTGAAC 793
 QY 561 TATCCACCATACATTTTCAAGACCAAGGGTACAGGTGTCTCCCGTGGGACAAAGGGGACA 720

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Db      794  TATCCACCAATACATTTTCAGAACCAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY      721  CTGCACTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 780
Db      854  CTGCACTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
QY      781  AGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 840
Db      914  AGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 973
QY      841  ATCTTCTTCAATGTCTCTGAACATGACTATGGAACATACACTTGGTGGCTTCCCAACAG 900
Db      974  ATCTTCTTCAATGTCTCTGAACATGACTATGGAACATACACTTGGTGGCTTCCCAACAG 1033
QY      901  CTGGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGCTCAGCGAGGTGAGC 960
Db      1034  CTGGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGCTCAGCGAGGTGAGC 1093
QY      961  AACGSCAGCTCGAGGAGGCGAGGCTGCGTCTGGTGGCTTCTCTGCTTCTGACCTG 1020
Db      1094  AACGSCAGCTCGAGGAGGCGAGGCTGCGTCTGGTGGCTTCTCTGCTTCTGACCTG 1153
QY      1021  CTTCTCAATTTTGA 1035
Db      1154  CTTCTCAATTTTGA 1168

RESULT 7
ID      ABL95588
AC      ABL95588;
XX
XX
DT      19-JUL-2002 (first entry)
DE
DE
KW      Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
KW      Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW      atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW      cardiant; cytosatic; antiangiogenic; hypotensive; vulnerary;
KW      antiarteriosclerotic; gene; ss.
XX
OS      Homo sapiens.
XX
XX
PN      WO200208284-A2.
XX
PD      31-JAN-2002.
XX
PF
PF
XX      09-JUL-2001; 2001WO-US021735.
XX
PR      20-JUL-2000; 2000US-0219556P.
PR      25-JUL-2000; 2000US-0220624P.
PR      25-JUL-2000; 2000US-0220664P.
PR      28-JUL-2000; 2000WO-US020710.
PR      02-AUG-2000; 2000US-0222695P.
PR      17-AUG-2000; 2000US-00643657.
PR      23-AUG-2000; 2000WO-US023522.
PR      24-AUG-2000; 2000WO-US023522.
PR      07-SEP-2000; 2000US-0230978P.
PR      18-SEP-2000; 2000US-00664610.
PR      18-SEP-2000; 2000US-00665350.
PR      24-OCT-2000; 2000US-0242922P.
PR      08-NOV-2000; 2000US-00709238.
PR      08-NOV-2000; 2000WO-US030952.
PR      10-NOV-2000; 2000WO-US030873.
PR      01-DEC-2000; 2000WO-US032678.
PR      20-DEC-2000; 2000US-00747259.
PR      20-DEC-2000; 2000WO-US034956.
PR      22-JAN-2001; 2001US-00767609.
PR      28-FEB-2001; 2001US-00796498.
PR      28-FEB-2001; 2001WO-US006520.
PR      01-MAR-2001; 2001WO-US006666.

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PR      09-MAR-2001; 2001US-00802706.
PR      14-MAR-2001; 2001US-00808689.
PR      22-MAR-2001; 2001US-00816744.
PR      05-APR-2001; 2001US-00828366.
PR      10-MAY-2001; 2001US-00854208.
PR      10-MAY-2001; 2001US-00854280.
PR      25-MAY-2001; 2001US-00866028.
PR      25-MAY-2001; 2001US-00866034.
PR      25-MAY-2001; 2001WO-US017092.
PR      30-MAY-2001; 2001US-00870574.
PR      30-MAY-2001; 2001WO-US017443.
PR      01-JUN-2001; 2001WO-US017800.
PR      20-JUN-2001; 2001WO-US019692.
XX      (GETH ) GENENTECH INC.
PA      (BAKE/) BAKER K P.
PA      (FERK/) FERRARA N.
PA      (GERE/) GERBER H.
PA      (GERR/) GERRITSEN M E.
PA      (GODL/) GODDARD A.
PA      (GODC/) GODOWSKI P J.
PA      (GURN/) GURNEY A L.
PA      (HILL/) HILLAN K J.
PA      (MARS/) MARSTERS S A.
PA      (PANJ/) PAN J.
PA      (PAON/) PAONI N F.
PA      (STEP/) STEPHAN J F.
PA      (WATA/) WATANABE C K.
PA      (WILL/) WILLIAMS P M.
PA      (WOOD/) WOOD W I.
XX
XX      Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
XX      Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX      WPI; 2002-171999/22.
XX      P-PSDB; ABB95450.
XX
XX      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX      useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX      infarction), endothelial or angiogenic disorders in a mammal.
XX
XX      Claim 1; Fig 55; 567pp; English.
XX
XX      The present invention provides the protein and coding sequences of human
XX      PRO proteins. These are useful for treating or diagnosing a
XX      cardiovascular, endothelial or angiogenic disorder, including cardiac
XX      hypertrophy, trauma, cancer, age-related macular degeneration,
XX      atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX      angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX      angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX      healing. The present sequence is a coding sequence of the invention
XX
SQ      Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match      100.0%; Score 1035; DB 6; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGAAACCATCCAGCCAAATGCAATTTCTCTTGGGCAATCTTACCTTTCACGGGCTG 60
Db      134  ATGAAACCATCCAGCCAAATGCAATTTCTCTTGGGCAATCTTACCTTTCACGGGCTG 193
QY      61  GCTGCTCTGTCTCTTCCAGAGAGTCCCGTGGCAGCGAGATGCCACCTTCCCAAA 120
Db      194  GCTGCTCTGTCTCTTCCAGAGAGTCCCGTGGCAGCGAGATGCCACCTTCCCAAA 253
QY      121  GCTATGGACAACGTGACCGTCCGCGAGGGGAGAGCGCACCTCAGTGCACTATTGAC 180
Db      254  GCTATGGACAACGTGACCGTCCGCGAGGGGAGAGCGCACCTCAGTGCACTATTGAC 313
QY      181  AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTTATGCTGGGATGAC 240

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17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 11-AUG-2000; 2000WO-US022031.
 23-AUG-2000; 2000WO-US023522.
 24-AUG-2000; 2000WO-US023328.
 08-NOV-2000; 2000WO-US030952.
 01-DEC-2000; 2000WO-US030873.
 20-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001US-00796498.
 01-MAR-2001; 2001US-0006520.
 09-MAR-2001; 2001US-00802706.
 14-MAR-2001; 2001US-00808689.
 22-MAR-2001; 2001US-00816744.
 05-APR-2001; 2001US-00828366.
 10-MAY-2001; 2001US-00854280.
 10-MAY-2001; 2001US-00854280.
 18-MAY-2001; 2001US-00860216.
 25-MAY-2001; 2001US-00866028.
 25-MAY-2001; 2001US-00866034.
 01-JUN-2001; 2001US-00871092.
 01-JUN-2001; 2001US-00872035.
 01-JUN-2001; 2001US-00871780.
 05-JUN-2001; 2001US-00874503.
 14-JUN-2001; 2001US-00882636.
 19-JUN-2001; 2001US-00886342.
 20-JUN-2001; 2001US-00891692.
 21-JUN-2001; 2001US-00887879.
 22-JUN-2001; 2001US-00887879.
 29-JUN-2001; 2001US-00891066.
 09-JUL-2001; 2001US-00891735.
 18-JUL-2001; 2001US-00908827.
 08-AUG-2001; 2001US-00924419.
 09-AUG-2001; 2001US-00927796.
 16-AUG-2001; 2001US-00931836.
 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-341980/32.
 P-PSDB; ABO17803.

New secreted and transmembrane PRO nucleic acids, for treating
 inflammation, organ failure, atherosclerosis, cardiac injury,
 infertility, birth defects, premature aging, acquired immunodeficiency
 syndrome (AIDS), or cancer.

Claim 2; Fig 375; 660pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which
 has 80 % sequence identity to, or the full-length coding sequence of, one
 of 275 nucleotide sequences and which encodes a corresponding
 polypeptide selected from 275 amino acid sequences, where all sequences
 are given in the specification. The polypeptide encoded by (I) is used to
 detect PRO polypeptides. The polypeptide molecule to a cell expressing a
 PRO polypeptide, modulate a biological activity of a cell, stimulate the
 release of tumour necrosis factor (TNF)-alpha from human blood, modulate
 the uptake of glucose or free fatty acid by cells, stimulate or inhibit
 the proliferation or differentiation of cells or gene expression,
 stimulate the release of proteoglycans, stimulate the release of cytokine
 from peripheral blood mononuclear cells, inhibit the binding of A-peptide
 to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
 acid and polypeptide encoded by it, are useful for treating inflammatory
 diseases, organ failure, atherosclerosis, cardiac injury, infertility,

CC birth defects, premature aging, acquired immunodeficiency syndrome
 CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
 CC hybridisation probes, in chromosome and gene mapping, and in generating
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
 CC This sequence encodes a novel human secreted and transmembrane PRO
 CC polypeptide

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAACCATCCAGCCAAAATGCAAAATCTCTCTTGGGCAATCTTCCAGGGGCTG 60
 DB 134 ATGAAAACCATCCAGCCAAAATGCAAAATCTCTCTTGGGCAATCTTCCAGGGGCTG 193
 QY 61 GCTGCTCTGTGTCTCTTCCAGGAGTGCCTGCGGAGCGGAGATGCCACTTCCCCAAA 120
 DB 194 GCTGCTCTGTGTCTCTTCCAGGAGTGCCTGCGGAGCGGAGATGCCACTTCCCCAAA 253
 QY 121 GCTATGACAAAGTACGCTCCGCGAGGAGCGCCACCTCAGGTGCACCTATTGAC 180
 DB 254 GCTATGACAAAGTACGCTCCGCGAGGAGCGCCACCTCAGGTGCACCTATTGAC 313
 QY 181 AACCGGCTACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 240
 DB 314 AACCGGCTACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 373
 QY 241 AAGTGGTGCCTGGATCCTCGCTGGTCTCTTCCAGGAGCGGAGATGCCACTTCCCCAAA 300
 DB 374 AAGTGGTGCCTGGATCCTCGCTGGTCTCTTCCAGGAGCGGAGATGCCACTTCCCCAAA 433
 QY 301 GAGATCCAGAACTGATGATGACAGGGGCCCTTTACACCTGCTCGGTGCAGACAGAC 360
 DB 434 GAGATCCAGAACTGATGATGACAGGGGCCCTTTACACCTGCTCGGTGCAGACAGAC 493
 QY 361 AACACCCAAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAAATGTAGAG 420
 DB 494 AACACCCAAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAAATGTAGAG 553
 QY 421 ATTCTTTCAGATATCTCCATTATGAGGGAACAATATTAGCCTCAGCTGCATAGCAACT 480
 DB 554 ATTCTTTCAGATATCTCCATTATGAGGGAACAATATTAGCCTCAGCTGCATAGCAACT 613
 QY 481 GGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
 DB 614 GGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
 QY 541 AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGAGAGCAGTCAGGGGACTACGAG 600
 DB 674 AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCGGAGAGCAGTCAGGGGACTACGAG 733
 QY 601 TGCAGTGCCTCCAAATGACGTGCGCGCCGCGGTGTTACGGAGAGTAAGAGTCAACCGTGAAC 660
 DB 734 TGCAGTGCCTCCAAATGACGTGCGCGCCGCGGTGTTACGGAGAGTAAGAGTCAACCGTGAAC 793
 QY 661 TATCCACCATACATTTTCAAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
 DB 794 TATCCACCATACATTTTCAAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 721 CTGCGAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGAGATGACAAA 780
 DB 854 CTGCGAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGAGATGACAAA 913
 QY 781 AGACTGATTGAAGAGGAAGAGGGGTGAAGCTGGAAGAGAGACACCTTCTCTCAAAATCTC 840
 DB 914 AGACTGATTGAAGAGGAAGAGGGGTGAAGCTGGAAGAGAGAGACACCTTCTCTCAAAATCTC 973
 QY 841 APTCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCTGGCTCCCAACAG 900
 DB 974 APTCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCTGGCTCCCAACAG 1033


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RESULT 10
ACD42387
ID ACD42387 standard; cDNA; 1679 BP.
AC
AC ACD42387;
DT
DT 05-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antidiabetic;
KW ophthalmological; cytostatic; immunostimulant; gene therapy;
KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
KW protein secretion disorder; pancreas disorder; diabetes;
KW vascular permeability; retinal neuron cell survival; retinal disorder;
KW immune response; inflammation; mononuclear cell infiltration;
KW eosinophil infiltration; apoptosis; neoplastic growth; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003040014-A1.
XX
PD 27-FEB-2003.
XX
PF 01-FEB-2002; 2002US-00066269.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059111P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0098601P.
PR 10-SEP-1998; 98US-0098803P.
PR 10-SEP-1998; 98US-0098811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 24-SEP-1998; 98WO-US019437.
PR 27-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169435P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 30-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
XX (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gershtein ME, Goddard A;
PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy WA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
XX WPI; 2003-503396/47.
DR P-Psdb; ABC25175.
XX
PT New secreted and transmembrane PRO polypeptides, useful for treating
PT diabetes, retinal disorders and stimulating an immune response.
XX
PS Claim 2; Fig 51; 254pp; English.
XX
CC The invention describes an isolated polypeptide (I) having at least 80 %
CC amino acid sequence identity to 30 secreted and transmembrane
CC polypeptides. PRO polypeptides are also useful for stimulating
CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
CC factor stimulated proliferation of endothelial cells, stimulating
CC proliferation of stimulated T-lymphocytes and for inducing proliferation
CC of PDB12 pancreatic ductal cells and are thus useful in the treatment of
CC disorders which involve protein secretion by the pancreas, including
CC diabetes. PRO polypeptides are useful for inducing vascular permeability
CC and in enhancing survival of retinal neurons cells and are thus useful
CC for the treatment of retinal disorders. PRO polypeptides are also useful
CC for stimulating an immune response and inducing inflammation by inducing
CC mononuclear cell and eosinophil infiltration at the site of infection of
CC an animal. The PRO polypeptides are further useful for inducing apoptosis
CC in endothelial cells for inhibiting neoplastic growth. This sequence
CC encodes a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAACCATCCAGCCAAATTCACAAATCTATCTCTGGCAATCTTACCGGGCTG 60
DB 134 ATGAACCATCCAGCCAAATTCACAAATCTATCTCTGGCAATCTTACCGGGCTG 193
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QY	61	GCTGCTCTGTGTTCTCTTCCAAAGAGTGCCCGCTGCGACGCGAGATGCCACTTCCCCAAA	120
Db	194	GCTGCTCTGTGTTCTCTTCCAAAGAGTGCCCGCTGCGACGCGAGATGCCACTTCCCCAAA	253
QY	121	GCTATGGACAACGTGACGGTCCGGCCAGGGGGAGAGCGCCACCCCTCAGGTGCATATTGAC	180
Db	254	GCTATGGACAACGTGACGGTCCGGCCAGGGGGAGAGCGCCACCCCTCAGGTGCATATTGAC	313
QY	181	AACGGGTACACCGGGTGGCTGGCTAAACCGCAGACACATCTCTATGCTGGGAATGAC	240
Db	314	AACGGGTACACCGGGTGGCTGGCTAAACCGCAGACACATCTCTATGCTGGGAATGAC	373
QY	241	AAAGTGTGCTCGATCCTCGCGTGGTCTTCTGAGCAACCCAAAACGCAAGTACAGCATC	300
Db	374	AAAGTGTGCTCGATCCTCGCGTGGTCTTCTGAGCAACCCAAAACGCAAGTACAGCATC	433
QY	301	GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCGACAGAC	360
Db	434	GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCGACAGAC	493
QY	361	AACACACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATGTTAGAG	420
Db	494	AACACACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATGTTAGAG	553
QY	421	ATTTCCTTCAGATATCTCCATTAATGAAGGNAACATATTAGCTCTCACCTGCATAGCAACT	480
Db	554	ATTTCCTTCAGATATCTCCATTAATGAAGGNAACATATTAGCTCTCACCTGCATAGCAACT	613
QY	481	GGTAGACGAGCCCTACGGTTACTTTGAGAGACATCTCTCCCAAGCGGTTGGCTTTGTG	540
Db	614	GGTAGACGAGCCCTACGGTTACTTTGAGAGACATCTCTCCCAAGCGGTTGGCTTTGTG	673
QY	541	AGTGAACAGCAATCTTGGAAATTCAGGGCATACCCGGGAGCAGTCCAGGGGACATACGAG	600
Db	674	AGTGAACAGCAATCTTGGAAATTCAGGGCATACCCGGGAGCAGTCCAGGGGACATACGAG	733
QY	601	TGCAGTGCCTCCCAATGACGTGGCCGCGCGCTGGTACGAGAGTAAAGGTCACCGTCAAC	660
Db	734	TGCAGTGCCTCCCAATGACGTGGCCGCGCGCTGGTACGAGAGTAAAGGTCACCGTCAAC	793
QY	661	TATCCACATACATTTCAGAAGCCAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACA	720
Db	794	TATCCACATACATTTCAGAAGCCAAGGTTACAGGTGTCCCGTGGGACAAAAGGGGACA	853
QY	721	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACCAAGGATGACAAA	780
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACCAAGGATGACAAA	913
QY	781	AGACTGATTGAAGAAAGAAAGGGGTGAAGTGAAGAAACAGACTTTCTCTCTCAAAATCTC	840
Db	914	AGACTGATTGAAGAAAGAAAGGGGTGAAGTGAAGAAACAGACTTTCTCTCTCAAAATCTC	973
QY	841	ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATCTACACTTCGGTGGCTCCCAACAG	900
Db	974	ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATCTACACTTCGGTGGCTCCCAACAG	1033
QY	901	CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGCGCCGTCCAGCGAGGTGAGC	960
Db	1034	CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGCGCCGTCCAGCGAGGTGAGC	1093
QY	961	AACGGCACGTCCAGAGGGCAGGTCTGGCTCTGGCTCTCTCTCTCTCTCTCTCTCTCTCT	1020
Db	1094	AACGGCACGTCCAGAGGGCAGGTCTGGCTCTGGCTCTCTCTCTCTCTCTCTCTCTCTCT	1153
QY	1021	CTTCTCAAAATTTGA	1035
Db	1154	CTTCTCAAAATTTGA	1168

RESULT 11
ACD42857
ID ACD4
XX

AC	ACD42857;	
XX		
XX	09-SEP-2003 (first entry)	
XX		
XX	Novel human secreted and transmembrane protein PRO337 cDNA.	
XX		
XX	Human; secreted and transmembrane protein; PRO; virucide; gene therapy;	
KW	cell death; growth induction cascade; blood coagulation cascade;	
KW	viral infection; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
XX	US2003050239-A1.	
PN		
XX	13-MAR-2003.	
PD		
XX		
XX	15-OCT-2001; 2001US-00978191.	
XX		
XX	17-OCT-1997; 97US-0062250P.	
PR	03-NOV-1997; 97US-0064249P.	
PR	13-NOV-1997; 97US-0065311P.	
PR	21-NOV-1997; 97US-0066364P.	
PR	10-MAR-1998; 98US-0077450P.	
PR	11-MAR-1998; 98US-0077632P.	
PR	11-MAR-1998; 98US-0077649P.	
PR	12-MAR-1998; 98US-0077791P.	
PR	13-MAR-1998; 98US-0078004P.	
PR	17-MAR-1998; 98US-00040220.	
PR	20-MAR-1998; 98US-0078886P.	
PR	20-MAR-1998; 98US-0078910P.	
PR	20-MAR-1998; 98US-0078936P.	
PR	20-MAR-1998; 98US-0078939P.	
PR	25-MAR-1998; 98US-0079294P.	
PR	26-MAR-1998; 98US-0079656P.	
PR	27-MAR-1998; 98US-0079663P.	
PR	27-MAR-1998; 98US-0079664P.	
PR	27-MAR-1998; 98US-0079689P.	
PR	27-MAR-1998; 98US-0079728P.	
PR	27-MAR-1998; 98US-0079786P.	
PR	30-MAR-1998; 98US-0079920P.	
PR	30-MAR-1998; 98US-0079923P.	
PR	31-MAR-1998; 98US-0080105P.	
PR	31-MAR-1998; 98US-0080107P.	
PR	31-MAR-1998; 98US-0080165P.	
PR	31-MAR-1998; 98US-0080194P.	
PR	01-APR-1998; 98US-0080327P.	
PR	01-APR-1998; 98US-0080328P.	
PR	01-APR-1998; 98US-0080333P.	
PR	01-APR-1998; 98US-0080334P.	
PR	08-APR-1998; 98US-0081049P.	
PR	08-APR-1998; 98US-0081070P.	
PR	08-APR-1998; 98US-0081071P.	
PR	09-APR-1998; 98US-0081195P.	
PR	09-APR-1998; 98US-0081203P.	
PR	09-APR-1998; 98US-0081229P.	
PR	15-APR-1998; 98US-0081817P.	
PR	15-APR-1998; 98US-0081819P.	
PR	15-APR-1998; 98US-0081838P.	
PR	15-APR-1998; 98US-0081952P.	
PR	15-APR-1998; 98US-0081955P.	
PR	21-APR-1998; 98US-0082568P.	
PR	21-APR-1998; 98US-0082569P.	
PR	22-APR-1998; 98US-0082700P.	
PR	22-APR-1998; 98US-0082704P.	
PR	22-APR-1998; 98US-0082797P.	
PR	22-APR-1998; 98US-0082804P.	
PR	23-APR-1998; 98US-0082796P.	
PR	27-APR-1998; 98US-0083336P.	
PR	28-APR-1998; 98US-0083322P.	
PR	29-APR-1998; 98US-0083392P.	
PR	29-APR-1998; 98US-0083495P.	
PR	29-APR-1998; 98US-0083496P.	

241 AAGTGGTGGCTGGATCCTCGCTGGTCTCTTCTGAGCAACACCCAAACGACGATCAGCATC 300
Db |||||
374 AAGTGGTGGCTGGATCCTCGCTGGTCTCTTCTGAGCAACACCCAAACGACGATCAGCATC 433
Qy |||||
301 GAGATCCAGAACGTTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGACAGAC 360
Db |||||
434 GAGATCCAGAACGTTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGACAGAC 493
Qy |||||
361 AACCAACCAAGACCTCTAGGTGCTCACTTATGTCAGTATCTCCAAAATTTAGAG 420
Db |||||
494 AACCAACCAAGACCTCTAGGTGCTCACTTATGTCAGTATCTCCAAAATTTAGAG 553
Qy |||||
421 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATAGCTCTACCTCATAGCAACT 480
Db |||||
554 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATAGCTCTACCTCATAGCAACT 613
Qy |||||
481 GGTAGACGAGCTTACGTTTCTTGGAGACATCTCTCCAAAAGCGTTGGCTTTGTG 540
Db |||||
614 GGTAGACGAGCTTACGTTTCTTGGAGACATCTCTCCAAAAGCGTTGGCTTTGTG 673
Qy |||||
541 AGTGAAGACGAATCTTGGAAATTCAGGSCATCACCGGAGCAGTCAAGGACTAGGAG 600
Db |||||
674 AGTGAAGACGAATCTTGGAAATTCAGGSCATCACCGGAGCAGTCAAGGACTAGGAG 733
Qy |||||
601 TGCAGTGCCTCCAAATGACGTGGCGCGCGCTGTGACGAGAGTAAGGTCAACCGTGAAC 660
Db |||||
734 TGCAGTGCCTCCAAATGACGTGGCGCGCGCTGTGACGAGAGTAAGGTCAACCGTGAAC 793
Qy |||||
661 TATCCACCATACATTTTCAGNAGCAAGGGTACAGGTGTCCCTGGGACAAAAGGGGACA 720
Db |||||
794 TATCCACCATACATTTTCAGNAGCAAGGGTACAGGTGTCCCTGGGACAAAAGGGGACA 853
Qy |||||
721 CTGAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAATTCAGTGGTACAGGATGACAAA 780
Db |||||
854 CTGAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAATTCAGTGGTACAGGATGACAAA 913
Qy |||||
781 AGACTGATTAAGAAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 840
Db |||||
914 AGACTGATTAAGAAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 973
Qy |||||
841 ATCTTCTTCAATCTCTGACATGATGCTATTTGGTCCAGGGCCCTCAGCAGGTGAGC 900
Db |||||
974 ATCTTCTTCAATCTCTGACATGATGCTATTTGGTCCAGGGCCCTCAGCAGGTGAGC 1033
Qy |||||
901 CTGGGCCACCAATGCCAGCATCTGCTATTTGGTCCAGGGCCCTCAGCAGGTGAGC 960
Db |||||
1034 CTGGGCCACCAATGCCAGCATCTGCTATTTGGTCCAGGGCCCTCAGCAGGTGAGC 1093
Qy |||||
961 AACGGCAGCTCGAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db |||||
1094 AACGGCAGCTCGAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
Qy |||||
1021 CTCTCAAAATTTGA 1035
Db |||||
1154 CTCTCAAAATTTGA 1168

RESULT 12

ACD68655
ID ACD68655 standard; cDNA; 1679 BP.

XX AC ACD68655;

XX AC ACD68655;

DT 17-SEP-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO337 cDNA.

XX Human; secreted and transmembrane protein; PRO; cytostatic;

XX antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;

XX chondrocyte stimulator; pericyte stimulator; fibroblast modulator;

XX pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;

XX colon tumour; breast tumour; prostate tumour; rectal tumour;

XX liver tumour; bone disorder; cartilage disorder; sports injury;

arthrititis; wound; gene; ss.

XX Homo sapiens.

XX US2003045687-A1.

XX 06-MAR-2003.

XX 12-AUG-2002; 2002US-00218631.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-512315/48.

XX P-PSDB; AB033767.

XX New genes, and its encoded secreted and transmembrane polypeptides,

XX useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or

XX pericyte proliferation, especially for treating lung tumors, arthritis or

XX wounds in a mammal.

XX Claim 2; Fig 125; 314pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a

XX sequence with at least 80% identity to: (a) a nucleotide encoding any of

XX 122 PRO (secreted and transmembrane) polypeptides whose sequences are

XX fully defined in the specification; or (b) any of 122 nucleotide

XX sequences having e.g. 4834, 2504 or 1759 bp fully defined in the

XX specification; or the full length coding sequence of any of these 122

XX nucleotide sequences. The PRO polypeptides or polynucleotides are useful

XX as pharmaceuticals, diagnostics, biosensors or bioreactors. These are

XX particularly useful for detecting tumours (e.g. lung tumour, colon

XX tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)

XX in a mammal, for stimulating the release of TNF-alpha from human blood,

XX for stimulating the proliferation or differentiation of chondrocyte

XX cells, for stimulating proliferation of pericyte cells, or for modulating

XX normal human dermal fibroblast proliferation. The PRO nucleic acid or

XX polypeptide is also useful for treating tumours or various bone and/or

XX cartilage disorders (e.g. sports injuries or arthritis), or wounds. The

XX PRO polypeptides are useful in drug screening, particularly as targets

XX for therapeutic intervention in these diseases, and in the diagnostic

XX determination of the presence of these diseases. The PRO polypeptides are

XX also useful as molecular weight markers, or for chromosome

XX identification. The PRO genes are useful as hybridisation probes, or for

XX screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may

XX also be used in gene therapy, particularly for replacing a defective

XX gene. This sequence encodes a novel human secreted and transmembrane PRO

XX polypeptide

XX SQ

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 1035; DB 7; Length 1679;

XX Best Local Similarity 100.0%; Pred. No. 3.1e-07;

XX Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 ATGAAACCATCCAGCCCAAAATGCAAAATCTATCTCTGGCAATCTTCACGGGGCTG 60

XX 134 ATGAAACCATCCAGCCCAAAATGCAAAATCTATCTCTGGCAATCTTCACGGGGCTG 193

XX 61 GCTGCTCTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 120

XX 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 253

XX 121 GCTATGGAACAGTGCAGTCCCGCAGCGGGGAGCGCCACCTTCAGTGCACCTATTGAC 180

XX 254 GCTATGGAACAGTGCAGTCCCGCAGCGGGGAGCGCCACCTTCAGTGCACCTATTGAC 313

QY 181 AACCGGCTCACCGGCTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
Db |
QY 314 AACCGGCTCACCGGCTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
Db |
QY 241 AAGTGGTCTGGATCTCGCGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 300
Db |
QY 374 AAGTGGTCTGGATCTCGCGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 433
QY 301 GAGATCCAGAGCGTGGATGGTATGACGAGGCGCTTACACCTGCTCGGTGAGCAGAC 360
Db |
QY 434 GAGATCCAGAGCGTGGATGGTATGACGAGGCGCTTACACCTGCTCGGTGAGCAGAC 493
QY 361 AACACCCCAAGACCTCTAGGCTCCACCTCATTTGCAAGTATCTCCCAAAATTTAGAG 420
Db |
QY 494 AACACCCCAAGACCTCTAGGCTCCACCTCATTTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTCAGATATCTCAATTAATGAAGGAAACAATATTAGCTCACTGCAATAGCACT 480
Db |
QY 554 ATTCTTCAGATATCTCAATTAATGAAGGAAACAATATTAGCTCACTGCAATAGCACT 613
QY 481 GGTAGACAGACCTTACGCTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTG 540
Db |
QY 614 GGTAGACAGACCTTACGCTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTG 673
QY 541 AGTGAAGACGAATCTTGAATTCAGGCAATCACCCGGGAGCAGTCAAGGAGCTACGAG 600
Db |
QY 674 AGTGAAGACGAATCTTGAATTCAGGCAATCACCCGGGAGCAGTCAAGGAGCTACGAG 733
QY 601 TGCAGTGGCTCAATGAGTGGCGCGCGCTGGTACGAGAGTAAAGGTCAACGTGAAC 660
Db |
QY 734 TGCAGTGGCTCAATGAGTGGCGCGCGCTGGTACGAGAGTAAAGGTCAACGTGAAC 793
QY 661 TATCCACCATACATTTCAAGCCAAAGGTCAGAGTGTCCCGTGGGACAAAGGGGACA 720
Db |
QY 794 TATCCACCATACATTTCAAGCCAAAGGTCAGAGTGTCCCGTGGGACAAAGGGGACA 853
QY 721 CTGAGTGTGAAGCTCAGAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAA 780
Db |
QY 854 CTGAGTGTGAAGCTCAGAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGATGACAAA 913
QY 781 AGACTGATTGAAGGAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAACTC 840
Db |
QY 914 AGACTGATTGAAGGAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAACTC 973
QY 841 ATCTCTTCAATGTCTCGAATCATGACTATGGAACTACACTTGGTGGCTCCCAACAG 900
Db |
QY 974 ATCTCTTCAATGTCTCGAATCATGACTATGGAACTACACTTGGTGGCTCCCAACAG 1033
QY 901 CTGGCCACACCAATGCCAGCATATGCTATTTGGTCCAGGCGCGTCAAGGAGTGAGC 960
Db |
QY 1034 CTGGCCACACCAATGCCAGCATATGCTATTTGGTCCAGGCGCGTCAAGGAGTGAGC 1093
QY 961 AACGGCAGCTCAGAGAGGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1020
Db |
QY 1094 AACGGCAGCTCAGAGAGGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153
QY 1021 CTTCTCAAAATTTGA 1035
Db |
QY 1154 CTTCTCAAAATTTGA 1168

RESULT 13

ACA67181
ID ACA67181 standard; cDNA; 1679 BP.

XX ACA67181;

AC ACA67181;

XX 23-JUN-2003 (first entry)

DE cDNA encoding human PRO polypeptide #188.

XX Human; PRO polypeptide; secreted and transmembrane protein;

XX anti-PRO antibody; diagnostic assay; gene expression; diabetes;

bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
hearing loss; coagulation disorder; stroke; heart attack; cardiac;
antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;
antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.

Homo sapiens.

XX US2003004311-A1.

XX 02-JAN-2003.

XX 19-DEC-2001; 2001US-00028072.

XX 18-JUN-1997; 97US-0049911P.

XX 26-AUG-1997; 97US-0056974P.

XX 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059115P.

XX 17-SEP-1997; 97US-0059117P.

XX 17-SEP-1997; 97US-0059122P.

XX 17-SEP-1997; 97US-0059184P.

XX 18-SEP-1997; 97US-0059263P.

XX 19-SEP-1997; 97US-0059352P.

XX 19-SEP-1997; 97US-0059588P.

XX 24-SEP-1997; 97US-0059836P.

XX 17-OCT-1997; 97US-0062250P.

XX 17-OCT-1997; 97US-0062285P.

XX 17-OCT-1997; 97US-0062287P.

XX 17-OCT-1997; 97US-0063755P.

XX 24-OCT-1997; 97US-0062814P.

XX 24-OCT-1997; 97US-0062816P.

XX 24-OCT-1997; 97US-0063045P.

XX 24-OCT-1997; 97US-0063082P.

XX 27-OCT-1997; 97US-0063127P.

XX 27-OCT-1997; 97US-0063327P.

XX 28-OCT-1997; 97US-0063329P.

XX 28-OCT-1997; 97US-0063350P.

XX 28-OCT-1997; 97US-0063561P.

XX 29-OCT-1997; 97US-0063704P.

XX 29-OCT-1997; 97US-0063733P.

XX 29-OCT-1997; 97US-0063735P.

XX 29-OCT-1997; 97US-0063738P.

XX 03-NOV-1997; 97US-0064248P.

XX 07-NOV-1997; 97US-0064809P.

XX 12-NOV-1997; 97US-0065186P.

XX 17-NOV-1997; 97US-0065846P.

XX 21-NOV-1997; 97US-0066364P.

XX 24-NOV-1997; 97US-0066511P.

XX 24-NOV-1997; 97US-0066770P.

XX 11-DEC-1997; 97US-0069212P.

XX 11-DEC-1997; 97US-0069278P.

XX 11-DEC-1997; 97US-0069344P.

XX 16-DEC-1997; 97US-0069694P.

XX 23-JAN-1998; 98US-0072320P.

XX 04-FEB-1998; 98US-0073612P.

XX 09-FEB-1998; 98US-0074086P.

XX 09-FEB-1998; 98US-0074082P.

XX 12-MAR-1998; 98US-0077791P.

XX 20-MAR-1998; 98US-0078910P.

XX 25-MAR-1998; 98US-0079294P.

XX 27-MAR-1998; 98US-0079663P.

XX 31-MAR-1998; 98US-0080165P.

XX 12-JUN-1998; 98WO-US012456.

XX 28-AUG-1998; 98WO-US014552.

XX 10-SEP-1998; 98WO-US017888.

XX 14-SEP-1998; 98WO-US018924.

XX 14-SEP-1998; 98WO-US019093.

XX 14-SEP-1998; 98WO-US019094.

XX 16-SEP-1998; 98WO-US019177.

XX 17-SEP-1998; 98WO-US019330.

XX 17-SEP-1998; 98WO-US019437.

QY 1021 CTTCTCAAAATTTGA 1035
 Db 1154 CTTCTCAAAATTTGA 1168

RESULT 14
 ID ACA63892
 AC ACA63892; standard; cDNA; 1679 BP.
 DT 16-JUN-2003 (first entry)
 DE Novel human secreted and transmembrane protein PR0337 cDNA.
 XX
 KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
 KW antidiabetic; gene therapy; inflammatory disease; organ failure;
 KW atherosclerosis; cardiac injury; infertility; birth defect;
 KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;
 KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;
 KW tissue typing; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002192706-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 24-OCT-2001; 2001US-00999832.
 XX
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 30-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 31-MAR-1998; 98US-0079923P.
 PR 31-MAR-1998; 98US-0080105P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080165P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080328P.
 PR 01-APR-1998; 98US-0080333P.
 PR 01-APR-1998; 98US-0080334P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 08-APR-1998; 98US-0081071P.
 PR 09-APR-1998; 98US-0081195P.
 PR 09-APR-1998; 98US-0081203P.
 PR 09-APR-1998; 98US-0081229P.
 PR 15-APR-1998; 98US-0081817P.
 PR 15-APR-1998; 98US-0081819P.
 PR 15-APR-1998; 98US-0081838P.
 PR 15-APR-1998; 98US-0081952P.

15-APR-1998; 98US-0081955P.
 21-APR-1998; 98US-0082568P.
 21-APR-1998; 98US-0082569P.
 22-APR-1998; 98US-0082700P.
 22-APR-1998; 98US-0082704P.
 22-APR-1998; 98US-0082797P.
 22-APR-1998; 98US-0082804P.
 23-APR-1998; 98US-0082796P.
 07-OCT-1998; 98WO-US021141.
 20-NOV-1998; 98WO-US024855.
 05-JAN-1999; 99WO-US000106.
 08-MAR-1999; 99WO-US005028.
 10-MAR-1999; 99WO-US005190.
 14-MAY-1999; 99WO-US010733.
 02-JUN-1999; 99WO-US012252.
 30-NOV-1999; 99WO-US028313.
 02-DEC-1999; 99WO-US028551.
 02-DEC-1999; 99WO-US028565.
 16-DEC-1999; 99WO-US030095.
 30-DEC-1999; 99WO-US031243.
 30-DEC-1999; 99WO-US031274.
 05-JAN-2000; 2000WO-US000219.
 06-JAN-2000; 2000WO-US000277.
 06-JAN-2000; 2000WO-US00376.
 11-FEB-2000; 2000WO-US003565.
 18-FEB-2000; 2000WO-US004341.
 24-FEB-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005841.
 10-MAR-2000; 2000WO-US006319.
 21-MAR-2000; 2000WO-US007532.
 30-MAR-2000; 2000WO-US008439.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032578.
 20-DEC-2000; 2000WO-US034556.
 28-FEB-2001; 2001WO-US006520.
 22-MAR-2001; 2001WO-US009552.
 25-MAY-2001; 2001WO-US017092.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019892.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 Stewart TA, Tumas D, Williams PM, Wood WI;
 MPI; 2003-328860/31.
 P-FSDB; ABU72281.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

Claim 2; Fig 221; 453pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which is at least 80 % sequence identity to, or the full-length coding sequence of, any of 118 300-2100 nucleotide sequences, which encodes its corresponding PRO polypeptide selected from 118 100-700 amino acid sequences, all given in the specification. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic

CC acids are useful as hybridisation probes, in chromosome and gene mapping,
CC and in generating antisense RNA or DNA. The polypeptides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful
CC in tissue typing. This sequence encodes a novel human secreted and
CC transmembrane PRO polypeptide

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAAACCATCCAGCCAAAATGCAAAATCTATCTCTTGGGCAATCTTACCGGGCTG	60
Db	134	ATGAAACCATCCAGCCAAAATGCAAAATCTATCTCTTGGGCAATCTTACCGGGCTG	193
QY	61	GCTGCTCTGTGTCCTCTTCCAGGAGTGCCTCGCGCAGCGGAGATGCCACTTCCCCAAA	120
Db	194	GCTGCTCTGTGTCCTCTTCCAGGAGTGCCTCGCGCAGCGGAGATGCCACTTCCCCAAA	253
QY	121	GCTATGACAACGTGACGGTCCGCGAGGGGAGAGCGCACCTCAGGTGCACTATTGAC	180
Db	254	GCTATGACAACGTGACGGTCCGCGAGGGGAGAGCGCACCTCAGGTGCACTATTGAC	313
QY	181	AACCGGGTCACCCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC	240
Db	314	AACCGGGTCACCCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC	373
QY	241	AAGTGTGCTGTGATCTCTCGGTTGGTCTTCTGTAGCAACACCCAAACGCAGTACAGCATC	300
Db	374	AAGTGTGCTGTGATCTCTCGGTTGGTCTTCTGTAGCAACACCCAAACGCAGTACAGCATC	433
QY	301	GAGATCCAGAACGTGGATGTGATGACGAGGGCCCTTACACCTGCTCGGTGCACAGAC	360
Db	434	GAGATCCAGAACGTGGATGTGATGACGAGGGCCCTTACACCTGCTCGGTGCACAGAC	493
QY	361	AACCAACCAAGACCTCTAGSGTCCACTCATTTGCAAGTATCTCCAAAATTGTAGAG	420
Db	494	AACCAACCAAGACCTCTAGSGTCCACTCATTTGCAAGTATCTCCAAAATTGTAGAG	553
QY	421	ATTTCCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCTCACTGCATAGCAACT	480
Db	554	ATTTCCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCTCACTGCATAGCAACT	613
QY	481	GGTAGACACAGACCTACGGTTACTTGGAGACACACTCTCTCCAAAGCGGTTGGCTTTGTG	540
Db	614	GGTAGACACAGACCTACGGTTACTTGGAGACACACTCTCTCCAAAGCGGTTGGCTTTGTG	673
QY	541	AGTGAAGACGATATCTTGGAAATTCAGGGCATACCCGGGAGCAGTCAAGGGGACTACGAG	600
Db	674	AGTGAAGACGATATCTTGGAAATTCAGGGCATACCCGGGAGCAGTCAAGGGGACTACGAG	733
QY	601	TGCAGTGCCTTCCAAATGACGTGGCCGCGCCGTGTGACGAGAGTAAAGGTCACCGTGAAC	660
Db	734	TGCAGTGCCTTCCAAATGACGTGGCCGCGCCGTGTGACGAGAGTAAAGGTCACCGTGAAC	793
QY	661	TATCCACATACATTTCAGAAAGCAAGGTTACAGGTGTCCCGGTGGGACAAAAGGGGACA	720
Db	794	TATCCACATACATTTCAGAAAGCAAGGTTACAGGTGTCCCGGTGGGACAAAAGGGGACA	853
QY	721	CTGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGCGTACAAGGATGACAAA	780
Db	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGCGTACAAGGATGACAAA	913
QY	781	AGACTGATTTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTCTCTCAAAAATC	840
Db	914	AGACTGATTTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTCTCTCAAAAATC	973
QY	841	ATCTTCTTCATGTCTCTGACATGACTATTGGGAACCTACACTTCGGTGGCTCCAAACAG	900
Db	974	ATCTTCTTCATGTCTCTGACATGACTATTGGGAACCTACACTTCGGTGGCTCCAAACAG	1033
QY	901	CTGGGCCACACCAAATGCCAGCATCATGTATTTGGTCCAGCGCCGCTCAGCGAGTGCAGC	960

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PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-0086028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
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PR 09-JUL-2001; 2001WO-US021735.
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PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-332040/31.
DR P-PSDB; ABU66757.
DR
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
```

PT typing, and in chromosome identification.

XX Claim 2; Fig 375; 660pp; English.

XX The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The PRO polypeptides are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipspIDEntry.html

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAACCATCCAGCCAAATAATGCAATTCATCTCTTTGGGCAATCTTCACGGGGCTG 60
Db 134 ATGAAACCATCCAGCCAAATAATGCAATTCATCTCTTTGGGCAATCTTCACGGGGCTG 193
Qy 61 GCTGCTCTGTCTCTTCCAGGAGTCCCGTGGCGAGCGGAGTCCACCTTCCCAAA 120
Db 194 GCTGCTCTGTCTCTTCCAGGAGTCCCGTGGCGAGCGGAGTCCACCTTCCCAAA 253
Qy 121 GCTATGACAACTGACGGTCCGCGAGGAGCGCCACCTTCAGTGCATTTATGAC 180
Db 254 GCTATGACAACTGACGGTCCGCGAGGAGCGCCACCTTCAGTGCATTTATGAC 313
Qy 181 AACCGGGTCAACCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 240
Db 314 AACCGGGTCAACCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 373
Qy 241 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACCCCAACCGCAGTACAGCATC 300
Db 374 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACCCCAACCGCAGTACAGCATC 433
Qy 301 GAGATCCAGAACCTGGATGTATGACGAGGGCCCTTTACACCTGCTCGGTGCAGACAGAC 360
Db 434 GAGATCCAGAACCTGGATGTATGACGAGGGCCCTTTACACCTGCTCGGTGCAGACAGAC 493
Qy 361 AACCAACCAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCAAAATTTGTAGAG 420
Db 494 AACCAACCAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCAAAATTTGTAGAG 553
Qy 421 ATTTCTTCAGATATCTCCATTTAATGAAGGAAACAATATTAGCTTCACCTGCATAGCAACT 480
Db 554 ATTTCTTCAGATATCTCCATTTAATGAAGGAAACAATATTAGCTTCACCTGCATAGCAACT 613
Qy 481 GGTAGACCAAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGTTGGCTTTGTG 540
Db 614 GGTAGACCAAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAGCGTTGGCTTTGTG 673
Qy 541 AGTGAAGACGAATCTTGAAATTCAGGGCATACCCGGGAGCAGTACAGGGACTACAGAG 600
Db 674 AGTGAAGACGAATCTTGAAATTCAGGGCATACCCGGGAGCAGTACAGGGACTACAGAG 733
Qy 601 TGCAGTGCCTCCCAATGACGTGGCGCCCGTGTGTACGGAGTAAAGGTACCGTGAAC 660
Db 734 TGCAGTGCCTCCCAATGACGTGGCGCCCGTGTGTGTACGGAGTAAAGGTACCGTGAAC 793

PS Claim 2; Fig 51; 255pp; English.

XX The invention describes an isolated, secreted and transmembrane

CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting

CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,

CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth

CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for

CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a

CC cell expressing the polypeptide. The bioactive molecule causes cell

CC death. (II) is useful as hybridisation probes, in chromosome and gene

CC mapping, in generation of antisense RNA and DNA, in the preparation of

CC PRO polypeptide, for generating transgenic animals or knockout animals

CC which in turn are useful in the development and screening of

CC therapeutically useful reagents, and for the genetic analysis of

CC individuals with genetic disorders, in gene therapy, and for chromosome

CC identification. (I) or Ab is useful for the preparation of medicament for

CC treating conditions which are responsive to the PRO polypeptide or anti-

CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes

CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for

CC inhibiting tumour growth, enhances vascular permeability and immune

CC response, for inducing regeneration of auditory hair cells and for

CC treating hearing loss in mammals, and for treating bone and/or cartilage

CC disorders such as sports injuries and arthritis. This sequence encodes a

CC novel human secreted and transmembrane polypeptide associated

CC oligonucleotide

XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCAAAATGACAAATCTATCTCTTGGCAATCTTCACGGGGCTG 60

DB 134 ATGAAACCATCCAGCAAAATGACAAATCTATCTCTTGGCAATCTTCACGGGGCTG 193

QY 61 GCTGCTCTGTGCTCTCTTCCAAAGAGTGGCCGTCGCGAGCGAGATGCCACCTTCCCAAA 120

DB 194 GCTGCTCTGTGCTCTCTTCCAAAGAGTGGCCGTCGCGAGCGAGATGCCACCTTCCCAAA 253

QY 121 GCTATGGCAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCACTATTGAC 180

DB 254 GCTATGGCAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGTGCACTATTGAC 313

QY 181 AACCGGGTCACCGGGTGGCTGGCTTAACCGCAGCACCACCTCTATGCTGGGATGAC 240

DB 314 AACCGGGTCACCGGGTGGCTGGCTTAACCGCAGCACCACCTCTATGCTGGGATGAC 373

QY 241 AAGTGGTGGCTGGATCTCTCGGTGCTCTTGTGAGCAACACCAACGAGTACGATC 300

DB 374 AAGTGGTGGCTGGATCTCTCGGTGCTCTTGTGAGCAACACCAACGAGTACGATC 433

QY 301 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 360

DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493

QY 361 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG 420

DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG 553

QY 421 ATTCTCTCAGATATCTCCATTAATGAGGGAACAATATTAGCCTCACTGCAATAGCACT 480

DB 554 ATTCTCTCAGATATCTCCATTAATGAGGGAACAATATTAGCCTCACTGCAATAGCACT 613

QY 481 GGTAGACCAAGCGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540

DB 614 GGTAGACCAAGCGCTACGGTTACTTGGAGACACATCTCTCTCCAAAGCGGTGGCTTTGTG 673

QY 541 AGTGAAGACGAATATCTTGAATTTACGGGCATCACCGGGAGCAGTTCAGGGGACTACGAG 600

DB 674 AGTGAAGACGAATATCTTGAATTTACGGGCATCACCGGGAGCAGTTCAGGGGACTACGAG 733

QY 601 TGCAGTGCCTCCAATGACGTGGCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGGTGAC 660

DB 734 TGCAGTGCCTCCAATGACGTGGCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGGTGAC 793

QY 661 TATCCACCATACATTTCAAGAACCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 720

DB 794 TATCCACCATACATTTCAAGAACCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853

QY 721 CTGCAAGTGTGAAGCTCAGCAGTCCCTCCAGCAGAGATTCAGTGTGTACAGGATGACAAA 780

DB 854 CTGCAAGTGTGAAGCTCAGCAGTCCCTCCAGCAGAGATTCAGTGTGTACAGGATGACAAA 913

QY 781 AGACTGATTGAAGGAAAGAAAGAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAATCTC 840

DB 914 AGACTGATTGAAGGAAAGAAAGAGGGGTGAAGTGGAAAAACAGACCTTCTCTCAAAATCTC 973

QY 841 ATCTTCTTCAATGTCTCTGAACATGACATATATGGGAACATACCTTGGTGGCTCCCAACAG 900

DB 974 ATCTTCTTCAATGTCTCTGAACATGACATATATGGGAACATACCTTGGTGGCTCCCAACAG 1033

QY 901 CTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGGCTCAGCGAGGTGAGC 960

DB 1034 CTGGGCGACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGGCTCAGCGAGGTGAGC 1093

QY 961 AACGCGACGTCGAGGAGGCGAGGCTGCTGCTGGTGTGCTCTTCTGGTCTTGACCTG 1020

DB 1094 AACGCGACGTCGAGGAGGCGAGGCTGCTGCTGGTGTGCTCTTCTGGTCTTGACCTG 1153

QY 1021 CTCTCAAAATTTGA 1035

DB 1154 CTCTCAAAATTTGA 1168

RESULT 17

ACA72056

ID ACA72056 standard; cDNA; 1679 BP.

XX AC ACA72056;

XX AC ACA72056;

DT 11-AUG-2003 (first entry)

XX

DE Human secreted and transmembrane PRO polypeptide #37 cDNA.

XX Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine;

KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;

KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;

KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;

KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;

KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;

KW glomerulonephritis; lung disease; pulmonary hypertension; preeclampsia;

KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;

KW inflammatory bowel disease; reproductive disorder; premature labour.

XX

OS Homo sapiens.

XX

PN US2002177553-A1.

XX

XX 28-NOV-2002.

PD

PF 15-OCT-2001; 2001US-00978192.

XX

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PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066364P.

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PR 11-MAR-1998; 98US-0077649P.

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PR 17-MAR-1998; 98US-00040220.

PR 20-MAR-1998; 98US-0078866P.

PR 20-MAR-1998; 98US-0078910P.

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PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079234P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
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PR 30-MAR-1998; 98US-0079923P.
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PR 07-OCT-1998; 98WO-US021141.
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PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
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PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
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PR 14-MAY-1999; 99WO-US010733.
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PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
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PR 16-DEC-1999; 99WO-US030095.
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PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00702338.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-328499/31.
DR P-PSDB; ABUS4961.
XX
XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
XX
XX Claim 2; SEQ ID NO 522; 55pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC Parkinson's disease; cardiovascular disease e.g. hypertension and
CC myocardial ischaemia; kidney disease e.g. renal failure and
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC bowel disease; reproductive disorders e.g. premature labour and
CC pre-eclampsia; carcinogenesis. The present sequence represents a cDNA
CC encoding a PRO polypeptide of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20020177553
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAACCATCCAGCCAAAATGCAATTTCTATCTCTGGGCAATCTTCACGGGGCTG 60
DB 134 ATGAAAACCATCCAGCCAAAATGCAATTTCTATCTCTGGGCAATCTTCACGGGGCTG 193
QY 61 GCTGCTCTGTGTCTTTCGAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGTGTCTTTCGAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGACAACTGACGCTGCGCAGCGGAGGAGCGCACCTCAGGTGCATTATGAC 180
DB 254 GCTATGACAACTGACGCTGCGCAGCGGAGGAGCGCACCTCAGGTGCATTATGAC 313
QY 181 AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCAGCACCCTCTATGCTGGGATGAC 240
DB 314 AACCGGGTCACCGGGTGGCTGGCTTAAACCGCAGCAGCACCCTCTATGCTGGGATGAC 373
QY 241 AAGTGTGCTTGGATCCTGCGTGTGTCCTTCTGAGCAACACCCAAACGAGTACAGATC 300
DB 374 AAGTGTGCTTGGATCCTGCGTGTGTCCTTCTGAGCAACACCCAAACGAGTACAGATC 433
QY 301 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACCTGCTCGGTGCGAGAGAC 360
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACCTGCTCGGTGCGAGAGAC 493
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QY 361 AACACCCACAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAG 420
Db 494 AACACCCACAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAG 553
QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGAGCAATATTAGCCTCACCTGCATGACCACT 480
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGAGCAATATTAGCCTCACCTGCATGACCACT 613
QY 481 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
Db 614 GGTAGACAGAGCCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
QY 541 AGTGAAGACGAATCTTGAAATTCAGGCGCATCACCCGGGAGCAGCTCAGGGGACTTACGAG 600
Db 674 AGTGAAGACGAATCTTGAAATTCAGGCGCATCACCCGGGAGCAGCTCAGGGGACTTACGAG 733
QY 601 TGCAGTGCCTCCAAATGACGTGGCCCGCCCGTGGTACGGAGAGTAAAGTCAACCTGTAAC 660
Db 734 TGCAGTGCCTCCAAATGACGTGGCCCGCCCGTGGTACGGAGAGTAAAGTCAACCTGTAAC 793
QY 661 TATCCACCATACATTTCAAGCCCAAGGCTACAGGTGTCCCGTGGGACAAAGGGGACA 720
Db 794 TATCCACCATACATTTCAAGCCCAAGGCTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTTCCAGTGGTACAAGGATGACAAA 780
Db 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTTCCAGTGGTACAAGGATGACAAA 913
QY 781 AGACTGATGAAGGAGAAAGGGGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Db 914 AGACTGATGAAGGAGAAAGGGGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 973
QY 841 ATCTTCTTCAATGTCTCTGACATGATGGAATGGAATGGAATGGAATGGAATGGAATG 900
Db 974 ATCTTCTTCAATGTCTCTGACATGATGGAATGGAATGGAATGGAATGGAATGGAATG 1033
QY 901 CTGGGCCACACCAATGCCAGCATCATGTATTGTTGTCAGGCGCCGTGAGCGAGGTGAGC 960
Db 1034 CTGGGCCACACCAATGCCAGCATCATGTATTGTTGTCAGGCGCCGTGAGCGAGGTGAGC 1093
QY 961 AACGCGACGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
Db 1094 AACGCGACGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1153
QY 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

RESULT 18
ID ABX89328
XX ABX89328 standard; cDNA; 1679 BP.
AC ABX89328;
XX
XX
DT 13-MAY-2003 (first entry)
XX
DE DNA encoding novel secreted and transmembrane protein PRO337.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
OS Homo sapiens.
XX

PN XX
PD XX
XX
PF XX
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 22-DEC-1999; 98WO-US030720.
PR 30-DEC-1999; 98WO-US031243.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US003376.
PR 18-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00909827.
PR 08-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Deenoysers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-148238/14.
DR P-PSDB; ABUS9838.
XX
PT Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
PS Claim 2; Fig 375; 659pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumors. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or Crohn's
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's

CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC encodes a novel human PRO protein
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATCCAGCCCAAAATGCAAAATCTATCTCTTGGGCAATCTTACGGGGCTG 60
DB 134 ATGAAACCATCCAGCCCAAAATGCAAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193
QY 61 GCTGCTCTGTGCTCTTCCAGGAGTGCCGTCGCGAGGAGATGCCACCTTCCCCAAA 120
DB 194 GCTGCTCTGTGCTCTTCCAGGAGTGCCGTCGCGAGGAGATGCCACCTTCCCCAAA 253
QY 121 GCTATGGACAACCTGACCGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
DB 254 GCTATGGACAACCTGACCGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTCACCCGGGTGGCTGCTAAACCCGAGACCACTCTCTATGCTGGGAATGAC 240
DB 314 AACCGGGTCACCCGGGTGGCTGCTAAACCCGAGGAGCGCCACCTCAGGTGCACTATTGAC 373
QY 241 AAGTGGTGCTGGATCCTCGCTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
DB 374 AAGTGGTGCTGGATCCTCGCTGCTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 301 GAGATCCAGAACGCTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 360
DB 434 GAGATCCAGAACGCTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493
QY 361 AACCCACCAAGACCTCTAGGGTCAACCTCATTTGTGGCAAGTATCTCCCAAAATTTAGAG 420
DB 494 AACCCACCAAGACCTCTAGGGTCAACCTCATTTGTGGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCCTGCATAGCAACT 480
DB 554 ATTCTTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCCTGCATAGCAACT 613
QY 481 GGTAGACACAGAGCTACCGGTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 540
DB 614 GGTAGACACAGAGCTACCGGTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 541 AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
DB 674 AGTGAAGACGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
QY 601 TGCAGTGCCTCCCAATGACCTGGCGCGCCGCTGGTACGGAGAGTAAAGTCAACCGTGAAC 660
DB 734 TGCAGTGCCTCCCAATGACCTGGCGCGCCGCTGGTACGGAGAGTAAAGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTTTCAAGACCAAGGTCAGGTGTCCTCCGTGGGACAAAGGGGACA 720
DB 794 TATCCACCATACATTTTCAAGACCAAGGTCAGGTGTCCTCCGTGGGACAAAGGGGACA 853
QY 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTACAGGATGACAA 780
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGTACAGGATGACAA 913
QY 781 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 840
DB 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 973
QY 841 ATCTTCTTCAATGCTCTGAAACATGACTATGGGAATACACTTGTGGCTCCCAACAG 900
DB 974 ATCTTCTTCAATGCTCTGAAACATGACTATGGGAATACACTTGTGGCTCCCAACAG 1033
QY 901 CTGGGCAACCAATGCCAGCATCTGCTATTGTTGTCAGGGCCCTCAGCGAGGTGAGC 960

09-AUG-2001; 2001US-009277796.
16-AUG-2001; 2001US-00931836.
19-DEC-2001; 2001US-00028072.
(GETH) GENENTECH INC.
Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
WPI; 2003-466355/44.
P-PSDB; ABO25028.
New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PRO4978, useful in molecular biology, chromosome and gene mapping, in
generating antisense RNA and DNA, and in gene therapy.
Claim 2; Fig 375; 659pp; English.
The invention relates to an isolated nucleic acid comprising at least 80%
sequence identity to a PRO (secreted and transmembrane protein) cDNA
comprising a nucleic acid (a) encoding a PRO polypeptide, or its
extracellular domain (with or without its associated signal peptide),
which comprises any of the 275 120-850 residue amino acid sequences,
given in the specification; (b) comprising any of the 275 300-3500
nucleotide sequences, given in the specification; or (c) comprising the
full-length coding sequence of the nucleotide sequences given in the
specification, or of the DNA deposited under any of the American Type
Culture Collection (ATCC) Accession Numbers listed in the specification.
Also included are a vector comprising the novel nucleic acid, a host cell
comprising the vector, producing a PRO polypeptide, the isolated PRO
polypeptides detailed above, a chimeric molecule comprising the PRO
polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
antibody, detecting a PRO polypeptide in a sample suspected of containing
the PRO polypeptide, linking a bioactive molecule to a cell expressing a
PRO polypeptide, modulating at least one biological activity of a cell
expressing a PRO polypeptide, stimulating the release of tumour necrosis
factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
modulating the uptake of glucose or PFA by skeletal muscle cells or
adipocyte cells, stimulating the proliferation or differentiation of
adipocyte cells (or proliferation of or gene expression in pericyte
cells), stimulating the proliferation of inner ear utricular supporting
cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
binding of A-peptide to factor VIIA, or differentiation of adipocyte
cells, detecting the presence of a tumour in a mammal and an
oligonucleotide probe derived from any of the nucleotide sequences given
in the specification. The polynucleotide is useful in molecular biology,
including uses as hybridisation probes, in chromosome and gene mapping,
in generating antisense RNA and DNA, and in gene therapy. The
polynucleotide may also be used in preparing PRO polypeptides by
recombinant techniques, and in generating either transgenic animals or
knock-out animals which, in turn, are useful in the development and
screening of therapeutically useful reagents. The PRO polypeptide or the
antibody is used in preparing a medicament for treating a condition
responsive to the polypeptide or antibody, such as tumours, and in
various diagnostic assays. The present sequence encodes a PRO polypeptide
Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 ATGAAACCATCCAGCCAAATGCAATCTTCTTGGGCAATCTTCACGGGGCTG 60
DB 134 ATGAAACCATCCAGCCAAATGCAATCTTCTTGGGCAATCTTCACGGGGCTG 193
QY 61 GCTGCTCTGTGTCTCTTCCAAAGGAGTGCCGTCGCGAGCGAGATGCCACCTTCCCCAAA 120
DB 194 GCTGCTCTGTGTCTCTTCCAAAGGAGTGCCGTCGCGAGCGAGATGCCACCTTCCCCAAA 253
QY 121 GCTATGGACAACGTGACGGTTCGCGAGGGGGAGAGCGCCACCTCAGGTGCTATTGAC 180

Db 254 GCTATGACACACGCTGACGGTCCGCGAGGGGAGAGCCACCCCTCAGGTGCATATTGAC 313
QY 181 AACCGGGTACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGATGAC 240
Db 314 AACCGGGTACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGATGAC 373
QY 241 AAGTGTGCTGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGACGATACAGCATC 300
Db 374 AAGTGTGCTGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGACGATACAGCATC 433
QY 301 GAGATCCAGAACGTGGATGATGAGAGGGCCCTTACACTGCTCGGTGAGACAGAC 360
Db 434 GAGATCCAGAACGTGGATGATGAGAGGGCCCTTACACTGCTCGGTGAGACAGAC 493
QY 361 AACACCCAAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 420
Db 494 AACACCCAAAGACCTCTAGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGCTAGCAACT 480
Db 554 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGCTAGCAACT 613
QY 481 GGTAGACAGAGCTTACGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTGTG 540
Db 614 GGTAGACAGAGCTTACGTTACTTGGAGACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 541 AGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAGTACAGGAGTACGAG 600
Db 674 AGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAGTACAGGAGTACGAG 733
QY 601 TGCAGTGCCTTCAATGACGTGGCGCGCGCGTGGTACGAGAGTAAAGTCAACCGTGAAC 660
Db 734 TGCAGTGCCTTCAATGACGTGGCGCGCGCGTGGTACGAGAGTAAAGTCAACCGTGAAC 793
QY 661 TATCCACCATACATTCAGAGCCAGGGGTACAGGTGTCCTCGTGGACAAAGGGGACA 720
Db 794 TATCCACCATACATTCAGAGCCAGGGGTACAGGTGTCCTCGTGGACAAAGGGGACA 853
QY 721 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAA 780
Db 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAA 913
QY 781 AGACTGATTGAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTTCCTCAAAACTC 840
Db 914 AGACTGATTGAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTTCCTCAAAACTC 973
QY 841 ATCTTCTTCAATGTCTGAAACATGACTATGGGAACATACACTTGGCGGCTCCAAACAG 900
Db 974 ATCTTCTTCAATGTCTGAAACATGACTATGGGAACATACACTTGGCGGCTCCAAACAG 1033
QY 901 CTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGCGCGCGTACGCGAGGTGAGC 960
Db 1034 CTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGCGCGCGTACGCGAGGTGAGC 1093
QY 961 AACGGCAGTCCGAGGGCAGGCTGGTCTGGTGTGCTGCTCTTCTGGTCTTGCACCTG 1020
Db 1094 AACGGCAGTCCGAGGGCAGGCTGGTCTGGTGTGCTGCTCTTCTGGTCTTGCACCTG 1153
QY 1021 CTCTCAAAATTTGA 1035
Db 1154 CTCTCAAAATTTGA 1168

RESULT 21

ACA60526

ID ACA60526 standard; cDNA; 1679 BP.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX Human; secreted and transmembrane polypeptide; PRO;
KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
KW FGFR-2; PRO004; PRO4350; PRO2630; PRO265; PRO951; bioactive molecule;
KW toxin; radiolabel; antibody; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tissue typing; gene; ss.

OS Homo sapiens.

XX US2002177165-A1.

XX PD 28-NOV-2002.

XX 01-FEB-2002; 2002US-00066500.

XX 26-AUG-1997; 97US-0056974P.

PR 17-SEP-1997; 97US-0059115P.

PR 18-SEP-1997; 97US-0059263P.

PR 19-SEP-1997; 97US-0059588P.

PR 17-OCT-1997; 97US-0062285P.

PR 24-OCT-1997; 97US-0062818P.

PR 27-OCT-1997; 97US-0063082P.

PR 29-OCT-1997; 97US-0063329P.

PR 21-NOV-1997; 97US-0063733P.

PR 25-NOV-1997; 97US-0066840P.

PR 16-DEC-1997; 97US-0069694P.

PR 09-FEB-1998; 98US-0074086P.

PR 09-FEB-1998; 98US-0074092P.

PR 25-MAR-1998; 98US-0079294P.

PR 08-APR-1998; 98US-0081049P.

PR 14-JUL-1998; 98WO-US014552.

PR 10-AUG-1998; 98US-0095998P.

PR 18-AUG-1998; 98US-0097000P.

PR 09-SEP-1998; 98US-0099601P.

PR 10-SEP-1998; 98US-0099803P.

PR 10-SEP-1998; 98US-0099811P.

PR 10-SEP-1998; 98US-0099812P.

PR 14-SEP-1998; 98WO-US018824.

PR 16-SEP-1998; 98WO-US019093.

PR 17-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98US-0100858P.

PR 17-SEP-1998; 98WO-US019437.

PR 24-SEP-1998; 98US-0101922P.

PR 28-OCT-1998; 98US-0106032P.

PR 20-NOV-1998; 98US-0109304P.

PR 20-NOV-1998; 98WO-US024855.

PR 25-NOV-1998; 98WO-US025190.

PR 01-DEC-1998; 98WO-US025108.

PR 08-MAR-1999; 99WO-US005028.

PR 23-MAR-1999; 99US-0125778P.

PR 02-JUN-1999; 99WO-US012252.

PR 15-JUN-1999; 99US-0139695P.

PR 20-JUL-1999; 99US-0145070P.

PR 26-JUL-1999; 99US-0145698P.

PR 17-AUG-1999; 99US-0149396P.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 30-NOV-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 02-DEC-1999; 99WO-US028565.

PR 07-DEC-1999; 99US-0169495P.

PR 20-DEC-1999; 99WO-US030999.

PR 05-JAN-2000; 2000WO-US000219.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004342.

PR 01-MAR-2000; 2000WO-US004414.

PR 02-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams EM;
 PI Wood WL, Zhang Z;
 XX
 DR WPI; 2003-328482/31.
 DR P-PSDB; ABU72061.
 XX
 PT Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, for identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX
 PS Claim 2; Fig 51; 254pp; English.
 XX
 CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
 CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411,
 CC PRO10036, PRO346, PRO6307, PRO6003, fibroblast growth factor receptor
 CC (FGFR)-3, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or
 CC PRO951 polypeptide, and for linking a bioactive molecule to a cell
 CC expressing the above polypeptides. The bioactive molecule, a toxin,
 CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
 CC identify other proteins or molecules involved in binding interaction. The
 CC polynucleotide (II) encoding (I) is useful in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, for generating
 CC transgenic animals or knockout animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, to
 CC construct hybridisation probes for mapping the gene which encodes the PRO
 CC and for the genetic analysis of individuals with genetic disorders, in
 CC gene therapy, for chromosome identification and as a chromosome marker.
 CC (I) and (II) are useful for tissue typing. This sequence encodes a novel
 CC human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1035; DB 7; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.le-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAACACCATCCAGCAAAATGCAATTTCTATCTTTGGCAATCTTACGGGGGTG 60
 DB 134 ATGAAACACCATCCAGCAAAATGCAATTTCTATCTTTGGCAATCTTACGGGGGTG 193
 QY 61 GTGTCTGTGTCTTCTTCCAGAGGTGCGGTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
 DB 194 GTGTCTGTGTCTTCTTCCAGAGGTGCGGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253
 QY 121 GCTATGGACAAGTACGCTCCGGCAGGGGAGAGGCCACCTCAGGTGCACTATTGAC 180
 DB 254 GCTATGGACAAGTACGCTCCGGCAGGGGAGAGGCCACCTCAGGTGCACTATTGAC 313

QY 181 AACCGGTGTCACCGGTGGCTGCTGCTAAACCGCAGACCATCTCTCTATGCTGGGAATGAC 240
 DB 314 AACCGGTGTCACCGGTGGCTGCTGCTAAACCGCAGACCATCTCTCTATGCTGGGAATGAC 373
 QY 241 AAGTGGTGCCTGGATCCTCGGTGGTCTCTCTGAGCAACACCCAAACGACGTACAGCATC 300
 DB 374 AAGTGGTGCCTGGATCCTCGGTGGTCTCTCTGAGCAACACCCAAACGACGTACAGCATC 433
 QY 301 GAGATCCAGAAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 360
 DB 434 GAGATCCAGAAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493
 QY 361 AACCAACCCAAAGACCTCTAGGGTCCACCTCACTGTCGCAAGTATCTCCCAAAATGTAGAC 420
 DB 494 AACCAACCCAAAGACCTCTAGGGTCCACCTCACTGTCGCAAGTATCTCCCAAAATGTAGAC 553
 QY 421 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACTGCTATGCAACT 480
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACTGCTATGCAACT 613
 QY 481 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
 DB 614 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
 QY 541 AGTGAAGACGAATATTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTACCGAG 600
 DB 674 AGTGAAGACGAATATTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTACCGAG 733
 QY 601 TGCAGTGCCTCCAATGACGTGGCCGCGCCCTGTGTGACGAGAGTAAAGGTCAACGTGAAC 660
 DB 734 TGCAGTGCCTCCAATGACGTGGCCGCGCCCTGTGTGACGAGAGTAAAGGTCAACGTGAAC 793
 QY 661 TATCCACCATACATTCAGAGGCCAAGGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 720
 DB 794 TATCCACCATACATTCAGAGGCCAAGGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
 QY 721 CTGCACTGTGAAGCCTCAGCAGTGCCTCTCAGCAGAAATTCAGTGGTACAAGGATGACAAA 780
 DB 854 CTGCACTGTGAAGCCTCAGCAGTGCCTCTCAGCAGAAATTCAGTGGTACAAGGATGACAAA 913
 QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAATC 840
 DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAATC 973
 QY 841 ATCTTCTTCAATGTCTCTGACATGACTATGGAACATGACTATGGAACATGACTATGGAAC 900
 DB 974 ATCTTCTTCAATGTCTCTGGAACATGACTATGGAACATGACTATGGAACATGACTATGGAAC 1033
 QY 901 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGGTGAGCGAGGTGAGC 960
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGGTGAGCGAGGTGAGC 1093
 QY 961 AACGGCAGTGCAGAGGCGAGGCTGGTCTGGCTGCTGCTGCTCTTCTGCTTGGTCACTG 1020
 DB 1094 AACGGCAGTGCAGAGGCGAGGCTGGTCTGGCTGCTGCTGCTCTTCTGCTTGGTCACTG 1153
 QY 1021 CTCTCTCAAAATTTGA 1035
 DB 1154 CTCTCTCAAAATTTGA 1168
 RESULT 22
 ID ACA04516 standard; cDNA; 1679 BP.
 XX
 AC ACA04516;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO337 DNA.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;

Qy	121	GCTATGGACAA	CGTGACGGTCCGGCAGGGGGAGCGCCACCCTCAGGTGCACTATTGAC	180
Db	254	GCTATGGACAA	CGTGACGGTCCGGCAGGGGGAGCGCCACCCTCAGGTGCACTATTGAC	313
Qy	181	AACCGGCTAC	CCCGGGTGGCTCGCTAAACCGGAGACCACTCCTCTATGCTGGGAATGAC	240
Db	314	AACCGGCTAC	CCCGGGTGGCTCGCTAAACCGGAGACCACTCCTCTATGCTGGGAATGAC	373
Qy	241	AAGTGGTGCC	TGGATCCTCGCGTGGTCCCTTCTTGAGCAACCCAAACGCACTACAGCATC	300
Db	374	AAGTGGTGCC	TGGATCCTCGCGTGGTCCCTTCTTGAGCAACCCAAACGCACTACAGCATC	433
Qy	301	GAGATCAGAA	CGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC	360
Db	434	GAGATCAGAA	CGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC	493
Qy	361	AACCAACCA	AGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCAAAAATTGAGAG	420
Db	494	AACCAACCA	AGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCAAAAATTGAGAG	553
Qy	421	ATTTCTTCAG	ATATCTCAATTAATGAAGGAAACAATATTAGCTCTCAGCTGCATAGCAACT	480
Db	554	ATTTCTTCAG	ATATCTCAATTAATGAAGGAAACAATATTAGCTCTCAGCTGCATAGCAACT	613
Qy	481	GGTAGACGAG	CCCTACGGTTACTTTGAGACACACTCTCCCAAAGCGGTTGGCTTTGTG	540
Db	614	GGTAGACGAG	CCCTACGGTTACTTTGAGACACACTCTCCCAAAGCGGTTGGCTTTGTG	673
Qy	541	AGTGAAGAC	GGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG	600
Db	674	AGTGAAGAC	GGAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG	733
Qy	601	TGCAGTGCCT	CAATGACGTGGCCGCGCCGTGGTACGGAGATTAAGGTCAACCGTGAAC	660
Db	734	TGCAGTGCCT	CAATGACGTGGCCGCGCCGTGGTACGGAGATTAAGGTCAACCGTGAAC	793
Qy	661	TATCCACCAT	ACATTTTCAGAAAGCAAGGTTACAGTGTCCCGGTGGGACAAAAGGGGACA	720
Db	794	TATCCACCAT	ACATTTTCAGAAAGCAAGGTTACAGTGTCCCGGTGGGACAAAAGGGGACA	853
Qy	721	CTGCAGTGTG	AAGCTCTCAGCAGTCCCTCTACAGAAATTCAGTGGTATCAAGGATGACAAA	780
Db	854	CTGCAGTGTG	AAGCTCTCAGCAGTCCCTCTACAGAAATTCAGTGGTATCAAGGATGACAAA	913
Qy	781	AGACTGATTG	AAGGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC	840
Db	914	AGACTGATTG	AAGGAAGAAAGAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC	973
Qy	841	ATCTTCTTT	CAATGTCTCTGAACATGACTATGGAACTACACTTCGTGGCTCCAAACAG	900
Db	974	ATCTTCTTT	CAATGTCTCTGAACATGACTATGGAACTACACTTCGTGGCTCCAAACAG	1033
Qy	901	CTGGGCGCAC	CAACATGCCAGCATCATGTATTTGGTCCAGCGCCGCTCAGCGAGTGAGC	960
Db	1034	CTGGGCGCAC	CAACATGCCAGCATCATGTATTTGGTCCAGCGCCGCTCAGCGAGTGAGC	1093
Qy	961	AACGGCAGCT	CCAGGAGGGCAGGCTCGCTCTGGCTCTGCTGCTCTTCTGGTCTTGACACTG	1020
Db	1094	AACGGCAGCT	CCAGGAGGGCAGGCTCGCTCTGGCTCTGCTGCTCTTCTGGTCTTGACACTG	1153
Qy	1021	CTTCTCAAAT	TTTGA 1035	
Db	1154	CTTCTCAAAT	TTTGA 1168	

RESULT 23

ACA66437

XX
ID ACA66437 standard; cDNA; 1679 BP.

AC ACA66437;

XX
DT 24-JUN-2003 (first entry)

XX Human cdna encoding secreted/transmembrane protein PRO337.
DE
XX
XX Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW malignancy; cancer; ovarian cancer; colorectal cancer; sarcoma;
KW leukaemia; lymphoma; inflammatory disease; necrosis; atherosclerosis;
KW infertility; premature aging; psoriasis; inflammatory disease;
KW renal disease; arthritis; immune-mediated alopecia; stroke; encephalitis;
KW hepatitis; multiple sclerosis; gene therapy.

18-FEB-2000; 2000WO-US004341.
 24-FEB-2000; 2000WO-US005004.
 01-MAR-2000; 2000WO-US005601.
 02-MAR-2000; 2000WO-US005841.
 10-MAR-2000; 2000WO-US006319.
 21-MAR-2000; 2000WO-US007532.
 30-MAR-2000; 2000WO-US008439.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 24-AUG-2000; 2000WO-US023328.
 08-NOV-2000; 2000US-00703238.
 10-NOV-2000; 2000WO-US030873.
 27-NOV-2000; 2000US-00723749.
 01-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000US-00747259.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001WO-US008520.
 22-MAR-2001; 2001US-00816744.
 22-MAR-2001; 2001US-00816920.
 22-MAR-2001; 2001WO-US009552.
 10-MAY-2001; 2001US-00854208.
 10-MAY-2001; 2001US-00854280.
 23-MAY-2001; 2001WO-US017092.
 01-JUN-2001; 2001US-00872035.
 01-JUN-2001; 2001WO-US017800.
 05-JUN-2001; 2001US-00874503.
 14-JUN-2001; 2001US-00882636.
 19-JUN-2001; 2001US-00886342.
 20-JUN-2001; 2001WO-US019692.
 28-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 30-JUL-2001; 2001US-00918585.
 (GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 Kijavirij, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 Stewart TA, Tumas D, Williams PM, Wood WI;
 WPI: 2003-341189/32.
 P-PSDB; ABU80428.

New genes and secreted and transmembrane polypeptides (e.g. PRO337 or PRO1559), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple sclerosis in mammals.

Claim 2; Fig 221; 460pp; English.

The invention relates to a new isolated nucleic acid molecule comprises a sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 PRO polypeptides whose sequences are fully defined in the specification; or (b) any of 94 nucleotide sequences fully defined in the specification; or the full length coding sequence of any these 94 nucleotide sequences. Also included are an isolated PRO polypeptide scoring at least 80% positives when compared to any of the PRO polypeptide sequences cited above (or an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) an amino acid sequence encoded by the nucleotide deposited with ATCC numbers listed in the specification; (b) the PRO polypeptide, lacking its associated signal peptide; or (c) an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide), a vector comprising the nucleic acid molecule, a host cell comprising the vector (and producing a PRO polypeptide), a chimeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence and an anti-PRO antibody. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,

CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease, CC necrosis, atherosclerosis, infertility, premature aging, psoriasis, CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia, CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The CC PRO polypeptides are useful in drug screening, particularly as targets CC for therapeutic intervention in these diseases, and in the diagnostic CC determination of the presence of these diseases. The PRO polypeptides are CC also useful as molecular weight markers, or for chromosome CC identification. The PRO genes are useful as hybridisation probes, or for CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may CC also be used in gene therapy, particularly for replacing a defective CC gene. The present sequence encodes a PRO polypeptide

XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;

Best Local Similarity 100.0%; Pred. No. 3.1e-07; Indels 0; Gaps 0;
 Matches 1035; Conservative 0; Mismatches 0;

QY	1	ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTTGGGCAATTTTCACGGGGCTG	60
Db	134	ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTTGGGCAATTTTCACGGGGCTG	193
QY	61	GCTGCTCTGTGCTCTTCCAGGAGTGCCGTGGCGAGCGGAGATGCCACTTCCCAAA	120
Db	194	GCTGCTCTGTGCTCTTCCAGGAGTGCCGTGGCGAGCGGAGATGCCACTTCCCAAA	253
QY	121	GCTATGGACAAGTGACGGTCCGGAGGGGAGAGGCCACCTCAGTGCACTATTGAC	180
Db	254	GCTATGGACAAGTGACGGTCCGGAGGGGAGAGGCCACCTCAGTGCACTATTGAC	313
QY	181	AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCACCTCTCTATCTGGGAATGAC	240
Db	314	AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCACCTCTCTATCTGGGAATGAC	373
QY	241	AAGTGTGCTGATCTCTCGGTGGTCTCTTGTAGCAACCAACCAACGAGTACAGCATC	300
Db	374	AAGTGTGCTGATCTCTCGGTGGTCTCTTGTAGCAACCAACCAACGAGTACAGCATC	433
QY	301	GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC	360
Db	434	GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC	493
QY	361	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG	420
Db	494	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG	553
QY	421	ATTTCTTCAGATATCTCCATTATGAGGGACCAATATTAGCTCCTCACCTGATCAACT	480
Db	554	ATTTCTTCAGATATCTCCATTATGAGGGACCAATATTAGCTCCTCACCTGATCAACT	613
QY	481	GGTAGACCAAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG	540
Db	614	GGTAGACCAAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG	673
QY	541	AGTGAAGACCAATCTTGGAAATTCAGGGCATCCCGGGAGCAGTCAGGGGACTAGAG	600
Db	674	AGTGAAGACCAATCTTGGAAATTCAGGGCATCCCGGGAGCAGTCAGGGGACTAGAG	733
QY	601	TGCAGTGCCTCCCAATGACGTGGCGCGCGCTGTAGGGAGGTAAAGGTCCACCGTGAAC	660
Db	734	TGCAGTGCCTCCCAATGACGTGGCGCGCGCTGTAGGGAGGTAAAGGTCCACCGTGAAC	793
QY	661	TATCCACCATACATTTTCAGAAAGCCAAAGGTGTACAGGTGTCTCCCGTGGACAAAAGGGGACA	720
Db	794	TATCCACCATACATTTTCAGAAAGCCAAAGGTGTACAGGTGTCTCCCGTGGACAAAAGGGGACA	853
QY	721	CTCAGTGTGAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA	780
Db	854	CTCAGTGTGAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA	913
QY	781	AGACTGATTGAGAAAGAAAGGGGTCAAGTGTGAAACAGACCTTCTCTCAAAACTC	840

PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
PS Claim 2; Fig 375; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
CC comprises the full-length coding sequence of the DNA deposited under
CC American Type Culture Collection (ATCC) accession number in a list given
CC in the specification. Also included are vectors and host cells for
CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
CC extracellular domains and mature sequences, methods of detecting PRO
CC proteins, methods for stimulating the release of TNF-alpha (tumour
CC necrosis factor alpha) from human blood, (and the proliferation of
CC differentiation of chondrocyte cells, the proliferation of, or gene
CC expression in pericyte cells, the release of proteoglycans from
CC cartilage, proliferation of inner ear utricular supporting cells, the
CC proliferation of T-lymphocyte cells, the release of a cytokine from
CC peripheral blood mononuclear cells (PBMC), or the proliferation of
CC endothelial cells), a method for modulating the uptake of glucose or free
CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
CC cells, a method for detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences cited
CC above. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, AIDS (acquired
CC immunodeficiency syndrome), cancer, or diabetic complications. The
CC nucleic acids are useful as hybridisation probes, in chromosome and gene
CC mapping, and in generating antisense RNA or DNA. The polypeptides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
CC are useful in tissue typing. The present sequence encodes a PRO protein
CC of the invention
XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 7; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCAGCCAAATGCAATCTATCTCTGGCAATCTTCAGGGGCTG 60
DB 134 ATGAAACCATCAGCCAAATGCAATCTATCTCTGGCAATCTTCAGGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAAAGAGTGGCCGTCGCGAGGGAGATGCCACCTTCCCAAA 120
DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGGCCGTCGCGAGGGAGATGCCACCTTCCCAAA 253
QY 121 GCTATGCAACAGTGCAGTCCGCGAGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
DB 254 GCTATGCAACAGTGCAGTCCGCGAGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313
QY 181 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
DB 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 241 AAGTGGTGGCTGGATCCTCGCTGGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
DB 374 AAGTGGTGGCTGGATCCTCGCTGGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 301 GAGATCCAGAACGTTGATGTATGACGAGGGCCCTTACCTGCTCGGTGCGACAGAC 360
DB 434 GAGATCCAGAACGTTGATGTATGACGAGGGCCCTTACCTGCTCGGTGCGACAGAC 493
QY 361 AACCAACCAAGACCTTAGGGTCCAGTCAATGTCAGATNTCTCCCAAAATGTAGAG 420
DB 494 AACCAACCAAGACCTTAGGGTCCAGTCAATGTCAGATNTCTCCCAAAATGTAGAG 553
QY 421 ATTCTCTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCAGCTGATAGCAACT 480

DB 554 ATTCTCTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCAGCTGATAGCAACT 613
QY 481 GGTAGACCAAGAGCTTACGGTTACTTTGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 540
DB 614 GGTAGACCAAGAGCTTACGGTTACTTTGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 541 AGTGAACAGCAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCCAGGGGACTACGAG 600
DB 674 AGTGAACAGCAATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCCAGGGGACTACGAG 733
QY 601 TGCAGTGCCTCCAAATGACGTGGCCGCCCGTGGTACGAGAGTAAAGGTACCGTGAAC 660
DB 734 TGCAGTGCCTCCAAATGACGTGGCCGCCCGTGGTACGAGAGTAAAGGTACCGTGAAC 793
QY 661 TATCCACATACATTTCCAGAGCCCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
DB 794 TATCCACATACATTTCCAGAGCCCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGAGTGGTACAAAGGATGACAAA 780
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGAGTGGTACAAAGGATGACAAA 913
QY 781 AGACTGATGAAGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAACTC 840
DB 914 AGACTGATGAAGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAACTC 973
QY 841 ATCTTCTCAATGTCTCTGAACATGACTATGCGGAACCTACACTTGGTGGGCTCCAAACAAG 900
DB 974 ATCTTCTCAATGTCTCTGAACATGACTATGCGGAACCTACACTTGGTGGGCTCCAAACAAG 1033
QY 901 CTGGGCCACACCAATGCGCAGCATCATGCTATTTGGTCCAGCGCGGCTCAGGAGGTGAGC 960
DB 1034 CTGGGCCACACCAATGCGCAGCATCATGCTATTTGGTCCAGCGCGGCTCAGGAGGTGAGC 1093
QY 961 AACGCGACGTGAGAGGGGAGGCTGGCTGGGCTGGGCTGGCTTCTGCTTGGCTTGCACCTG 1020
DB 1094 AACGCGACGTGAGAGGGGAGGCTGGCTGGGCTGGGCTGGCTTCTGCTTGGCTTGCACCTG 1153
QY 1021 CTCTCTCAAAATTTGA 1035
DB 1154 CTCTCTCAAAATTTGA 1168
RESULT 26
ACR65657
ID ACR65657 standard; cDNA; 1679 BP.
XX
AC ACR65657;
XX AC
XX DT 19-JUN-2003 (first entry)
XX DE Human cDNA encoding secreted/transmembrane protein PRO337.
XX
XX Human; ss; gene; secreted protein; transmembrane protein; PRO;
XX KW genetic disorder; gene therapy.
XX OS Homo sapiens.
XX
XX US2003032057-A1.
PN
XX
XX 13-FEB-2003.
PD
XX
XX 15-NOV-2001; 2001US-00002796.
PF
XX
XX 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.

XX WPI; 2003-341960/32.
 DR P-PS2B; ABU79804.
 XX Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX Claim 2; Fig 51; 255pp; English.
 PS
 XX The invention relates to an isolated, secreted/transmembrane polypeptide,
 CC termed PRO polypeptide, having at least 80% sequence identity to a
 CC sequence selected from any one of the 37 sequences appearing as ABU79779
 CC -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
 CC under any one of the ATCC numbers given in the specification. Also
 CC included are an isolated nucleic acid molecule having at least 80%
 CC sequence identity to a sequence selected from any one of the 37 cDNA
 CC sequences defined in the specification (or encoding the mature PRO
 CC protein or a PRO protein extracellular domain), a PRO expression vector,
 CC a host cell comprising the vector, PRO fusion proteins, anti-PRO
 CC antibodies and a method for linking a bioactive molecule to a cell
 CC expressing the above PRO polypeptides, the bioactive molecule is a toxin,
 CC radiolabel or an antibody and causes the death of the cell. PRO or the
 CC antibody is useful for modulating at least one biological activity of
 CC cell expressing the above polypeptides. PRO is useful for identifying
 CC agonists or antagonists of PRO, for preparing a variant of PRO, as
 CC molecular weight markers for protein electrophoresis purpose and PRO is
 CC nucleic acid is useful for recombinantly expressing those markers. PRO is
 CC also useful as therapeutic agent. PRO is useful in assays to identify
 CC other proteins or molecules involved in binding interaction. PRO nucleic
 CC acid is useful as hybridisation probes, in chromosome and gene mapping,
 CC in generation of antisense RNA and DNA, in the preparation of PRO
 CC polypeptide, in gene therapy, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and
 CC screening of therapeutically useful reagents, to construct hybridisation
 CC probes for mapping the gene which encodes the PRO and for the genetic
 CC analysis of individuals with genetic disorders, for chromosome
 CC identification, as a chromosome marker, and for generating probes for
 CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
 CC Western analysis. The antibody is useful in diagnostic assays for PRO,
 CC e.g. detecting its expression in specific cells, tissues or serum, for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. PRO or Ab is useful for the preparation of medicament for
 CC treating conditions which is responsive to the PRO polypeptide or anti-
 CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
 CC present sequence encodes a PRO polypeptide
 XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 1035; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 1 ATGAAAACCATCCAGCCAAATAATGCAATTTCTATCTCTGGGCAATCTTCAGGGGCTG 60
 Db 134 ATGAAAACCATCCAGCCAAATAATGCAATTTCTATCTCTGGGCAATCTTCAGGGGCTG 193
 QY 61 GCTGCTCTGTGTCCTTCCCAAGGAGTGCCGTCGAGCGGAGATGCCACCTTCCCCAAA 120
 Db 194 GCTGCTCTGTGTCCTTCCCAAGGAGTGCCGTCGAGCGGAGATGCCACCTTCCCCAAA 253
 QY 121 GCTATGGACAAACGTCAGCGTCCGGCAGGGGAGAGGCCACCTCAGGTGCATATTGAC 180
 Db 254 GCTATGGACAAACGTCAGCGTCCGGCAGGGGAGAGGCCACCTCAGGTGCATATTGAC 313
 QY 181 AACCGGTCACCCGGGTGGCTGTCTTAAACCGCAGCACCATCTCTATCTCTGGGATGAC 240
 Db 314 AACCGGTCACCCGGGTGGCTGTCTTAAACCGCAGCACCATCTCTATCTCTGGGATGAC 373
 QY 241 AAGTGGTGCTTGGATCCTCGCGTGGTCTTCTTCAGCAAAACACCCAAACGAGTACAGCATC 300
 Db 374 AAGTGGTGCTTGGATCCTCGCGTGGTCTTCTTCAGCAAAACACCCAAACGAGTACAGCATC 433

RESULT 27	
ADA45894	
ID	ADA45894 standard; cDNA; 1679 BP.
XX	
AC	ADA45894;
XX	
XX	20-NOV-2003 (first entry)
DT	
XX	
DE	Novel human secreted and transmembrane protein PRO337 cDNA.
XX	
KW	Human; secreted and transmembrane protein; PRO; Gene; ss;
KW	tumour necrosis factor alpha release; TNF-alpha release;
KW	glucose uptake modulator; PFA uptake modulator;
KW	cell proliferation stimulator; cell differentiation stimulator;
KW	cell differentiation inhibitor; cytokine release stimulator; tumour;
KW	lung tumour; colon tumour; breast tumour; prostate tumour; rectal
KW	tumour;
KW	cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW	gene therapy; chromosome identification; chromosome marker.
XX	
OS	Homo sapiens.

PR	18-FEB-2000;	2000WO-US004342
PR	18-FEB-2000;	2000WO-US004342
PR	22-FEB-2000;	2000WO-US004414
PR	24-FEB-2000;	2000WO-US004914
PR	24-FEB-2000;	2000WO-US005004
PR	24-FEB-2000;	2000WO-US005004
PR	01-MAR-2000;	2000WO-US005601
PR	02-MAR-2000;	2000WO-US005746
PR	02-MAR-2000;	2000WO-US005841
PR	10-MAR-2000;	2000WO-US006319
PR	15-MAR-2000;	2000WO-US006884
PR	20-MAR-2000;	2000WO-US007377
PR	21-MAR-2000;	2000WO-US007532
PR	30-MAR-2000;	2000WO-US008439
PR	17-MAY-2000;	2000WO-US013705
PR	22-MAY-2000;	2000WO-US014042
PR	30-MAY-2000;	2000WO-US014941
PR	02-JUN-2000;	2000WO-US015264
PR	28-JUL-2000;	2000WO-US020710
PR	11-AUG-2000;	2000WO-US022031
PR	23-AUG-2000;	2000WO-US023522
PR	24-AUG-2000;	2000WO-US023328

Tue Jun 1 09:37:50 2004

CC detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources (I) and (II) are useful for tissue typing. This sequence encodes
 CC a novel human secreted and transmembrane PRO polypeptide.

XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1035; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAACCATCCAGCCAAAATGCAATTTCTATCTCTTGGCAATCTTCAGGGGCTG 60
 DB 134 ATGAAACCATCCAGCCAAAATGCAATTTCTATCTCTTGGCAATCTTCAGGGGCTG 193
 QY 61 GCTGCTCTGCTCTTCCAAAGAGTGCCGTCGCGAGCGAGATGCCACCTTCCCAAA 120
 DB 194 GCTGCTCTGCTCTTCCAAAGAGTGCCGTCGCGAGCGAGATGCCACCTTCCCAAA 253
 QY 121 GCTATGGACAAAGTGAACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGACTATTGAC 180
 DB 254 GCTATGGACAAAGTGAACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGACTATTGAC 313
 QY 181 AACCGGTACCCGGTGGCTGGCTAAACCGCAGCAGCATCTCTATCTGCGGAATGAC 240
 DB 314 AACCGGTACCCGGTGGCTGGCTAAACCGCAGCAGCATCTCTATCTGCGGAATGAC 373
 QY 241 AAGTGTGCTCGATCCTCGCGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
 DB 374 AAGTGTGCTCGATCCTCGCGTGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
 QY 301 GAGATCCAGAACTGGATGTATGAGCAGGGGCGCTTACCTGCTCGGTGAGACAGAC 360
 DB 434 GAGATCCAGAACTGGATGTATGAGCAGGGGCGCTTACCTGCTCGGTGAGACAGAC 493
 QY 361 AACACCCCAAGACCTCAGGTGCTCAAGTGTCTCCCAAAATTTAGAG 420
 DB 494 AACACCCCAAGACCTCAGGTGCTCAAGTGTCTCCCAAAATTTAGAG 553
 QY 421 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCCTCCTCATAGCAACT 480
 DB 554 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCCTCCTCATAGCAACT 613
 QY 481 GGTAAGCAGAGCTCAGGTATCTTGAGACACATCTCTCCAAAGGGTGGCTTTGTG 540
 DB 614 GGTAAGCAGAGCTCAGGTATCTTGAGACACATCTCTCCAAAGGGTGGCTTTGTG 673
 QY 541 AGTGAAGCAGAACTACTTTGAAATTTCCAGGCAATCACCAGGAGCAGTCAAGGAGTACGAG 600
 DB 674 AGTGAAGCAGAACTACTTTGAAATTTCCAGGCAATCACCAGGAGCAGTCAAGGAGTACGAG 733
 QY 601 TGCAGTGCCTCCAAATGAGTGGCGCGCCCGTGTGTAAGGAGTAAAGGTCAAGTCAAC 660
 DB 734 TGCAGTGCCTCCAAATGAGTGGCGCGCCCGTGTGTAAGGAGTAAAGGTCAAGTCAAC 793
 QY 661 TATCCACATACATTTGAGACCAAGGTACAGGTGTCCTCCGTCGAGCAAAAGGGGACA 720
 DB 794 TATCCACATACATTTGAGACCAAGGTACAGGTGTCCTCCGTCGAGCAAAAGGGGACA 853
 QY 721 CTGCAAGTGAAGCTCAGCAGTGTCCCTCAGCAGAAATTCAGTGTGTAAGGAGTACAAA 780
 DB 854 CTGCAAGTGAAGCTCAGCAGTGTCCCTCAGCAGAAATTCAGTGTGTAAGGAGTACAAA 913
 QY 781 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAACTC 840
 DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAACTC 973
 QY 841 ATCTTCTTCAATGTCTGTAACATGACTATGGGAACTACCTTGGTGGCTCCCAACAG 900
 DB 974 ATCTTCTTCAATGTCTGTAACATGACTATGGGAACTACCTTGGTGGCTCCCAACAG 1033
 QY 901 CTGGGCCACCAATATGCCAGCATCATGTTATTTGGTCCAGGCGCGCTCAGGAGGTGAGC 960

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 WPI; 2003-584997/55.
 P-PSDB; ADA45895.

Novel secreted and transmembrane polypeptide for modulating biological
 activity of cell expressing the polypeptide, identifying agonists or
 antagonists of polypeptide, and as molecular weight markers.

Claim 2; Fig 375; 659pp; English.

The invention describes 305 nucleic acids encoding PRO (secreted and
 transmembrane) polypeptides (I). (I) is useful for stimulating the
 release of TNF- α from human blood, for modulating the uptake of
 glucose or FFA by skeletal muscle cells or adipocyte cells, for
 stimulating the proliferation or differentiation of chondrocyte cells,
 for stimulating the proliferation of or gene expression in pericyte
 cells, for stimulating the release of proteoglycans from cartilage, for
 stimulating the proliferation of inner ear utricular supporting cells,
 for stimulating the proliferation of T-lymphocyte cells, for stimulating
 the release of a cytokine from PBMC cells, for inhibiting the binding of
 A-peptide to factor VIIa, for inhibiting the differentiation of adipocyte
 cells, for stimulating proliferation of endothelial cells, for detecting
 the presence of tumour in a mammal. The tumour is lung, colon, breast,
 prostate, rectal, cervical or liver tumour. The oligonucleotide probes
 are useful for isolating genomic and cDNA nucleotide sequences or
 antisense probes. (I) is also useful as therapeutic agent. PRO is useful
 in assays to identify other proteins or molecules involved in binding
 interaction. A polynucleotide (II) encoding (I) is useful in chromosome
 and gene mapping, in generation of antisense RNA and DNA, in the
 preparation of PRO polypeptide, for generating transgenic animals or
 knockout animals which in turn are useful in the development and
 screening of therapeutically useful reagents, in gene therapy, for
 chromosome identification, as chromosome marker, and for generating
 probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.

PR 02-DEC-1999; 99WO-US028551

Baker KP, Beresini M, DeForge L, Denoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tunas D, Watanabe CK, Wood WI, Zhang Z;

361 AACACCCAAAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCCAAATTTAGAG 420
 494 AACACCCAAAGACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCCAAATTTAGAG 553
 421 ATTTCTTCAGATATCTCATTAATGAAGGAAACATATAGCTTACCTGATACCAACT 480
 554 ATTTCTTCAGATATCTCATTAATGAAGGAAACATATAGCTTACCTGATACCAACT 613
 481 GTTAGACAGAGCCCTACGCTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 540
 614 GTTAGACAGAGCCCTACGCTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673
 541 AGTGAAGACCAATATCTTGGAAATTCAGGGGCAATCCCGGAGCAGTCAAGGAGTACGAG 600
 674 AGTGAAGACCAATATCTTGGAAATTCAGGGGCAATCCCGGAGCAGTCAAGGAGTACGAG 733
 601 TGCAGTGCCTCAATGAATGCTGCGCCGCGCTGCTACGGAGAGTAAGGTCAACCTGGAAC 660
 734 TGCAGTGCCTCAATGAATGCTGCGCCGCGCTGCTACGGAGAGTAAGGTCAACCTGGAAC 793
 661 TATCCACCATATATTTTCAAGAGCCCAAGGTCAGGTCCTCCCGTGGGACAAAGGGGACA 720
 794 TATCCACCATATATTTTCAAGAGCCCAAGGTCAGGTCCTCCCGTGGGACAAAGGGGACA 853
 721 CTGCACTGTGAAGCCTTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGGATGACAAA 780
 854 CTGCACTGTGAAGCCTTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTAAGGATGACAAA 913
 781 AGACTGATTTGAAGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 840
 914 AGACTGATTTGAAGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 973
 841 ATCTTCTTCAATGCTCTGCAATGACTATGGAATTCAGTGTGTCCTCCAAAG 900
 974 ATCTTCTTCAATGCTCTGCAATGACTATGGAATTCAGTGTGTCCTCCAAAG 1033
 901 CTGGGCGCACCAATGCCAGCATCTGCTATTTGGTTCAGGCGCCCTCAGCAGGTTGAGC 960
 1034 CTGGGCGCACCAATGCCAGCATCTGCTATTTGGTTCAGGCGCCCTCAGCAGGTTGAGC 1093
 961 AAGGCGACGTCGAGGAGGAGGAGGCTGGCTGCTGCTGCTCTCTTGGTCTTTCACCTG 1020
 1094 AAGGCGACGTCGAGGAGGAGGAGGCTGGCTGCTGCTGCTCTCTTGGTCTTTCACCTG 1153
 1021 CTCTCTCAAAATTTGA 1035
 1154 CTCTCTCAAAATTTGA 1168
 RESULT 29
 ABT44288
 ID ABT44288 standard; cDNA; 1679 BP.
 XX
 AC ABT44288;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO337 cDNA.
 XX
 KW PRO: proliferation; pericyte cell; TNF-alpha; blood; chondrocyte; ss;
 KW differentiation; dermal fibroblast; tumour; gene therapy; gene;
 KW cycostatic.
 XX
 OS Homo sapiens.
 XX
 FN US2003050448-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 28-AUG-2002; 2002US-00230414.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.

DR WPI; 2003-687639/65.
 DR P-PSDB; ADA76326.
 XX
 PT New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
 PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 2; Fig 375; 659pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating differentiation of adipocyte cells, for stimulating
 CC proliferation of or gene expression in pericyte cells, for stimulating
 CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
 CC cells, for inducing endothelial cell tube formation and for treating
 CC various bone and/or cartilage disorders such as sports injuries and
 CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
 CC from cartilage are useful for treating sports-related joint problems,
 CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
 CC polypeptides are also useful for treating various mammalian haemoglobin-
 CC associated disorders such as various thalassaemias and conditions which
 CC may benefit from enhanced local immune system cell infiltration. This
 CC sequence represents a human PRO polynucleotide of the invention. Note:
 CC The sequence data for this patent is also available in electronic format
 CC from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1035; DB 8; Length 1679;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ATGAAACCATCCAGCCAAATGACAAATTTCTATCTTGGCAATCTTCCAGGGGCTG 60
 134 ATGAAACCATCCAGCCAAATGACAAATTTCTATCTTGGCAATCTTCCAGGGGCTG 193
 61 GCTGCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGAGATGCACTTCCCAAA 120
 194 GCTGCTGTGTCTCTTCCAGGAGTGCCTGCGCAGCGAGATGCACTTCCCAAA 253
 121 GCTATGGACAGTGAACGCTCGGCGAGGGGAGAGGCCACCTCAGGTGCACTATTGAC 180
 254 GCTATGGACAGTGAACGCTCGGCGAGGGGAGAGGCCACCTCAGGTGCACTATTGAC 313
 181 AACCAGGCTCACCAGGCTGCTGCTTCCAGGAGTGCCTGCGCAGCGAGATGCACTTCCCAAA 240
 314 AACCAGGCTCACCAGGCTGCTGCTTCCAGGAGTGCCTGCGCAGCGAGATGCACTTCCCAAA 373
 241 AAGTGGTGTGCTGGATCTCTCGCTGTGCTCTTGTGAGCAACCCAAACGAGTACGATC 300
 374 AAGTGGTGTGCTGGATCTCTCGCTGTGCTCTTGTGAGCAACCCAAACGAGTACGATC 433
 301 GAGATCCAGAAAGTGGATGTGTGATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC 360
 434 GAGATCCAGAAAGTGGATGTGTGATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC 493

	09-APR-2002; 2002US-00119480.	
	(GETH) GENENTECH INC.	
Baker KP, Desnoyers L,	Gerritsen ME, Goddard A, Godowski PJ;	
Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;		
P-PSDB; ABJ72290.		
WPI; 2003-521818/49.		
New nucleic acid encoding for a PRO protein, useful for the manufacture		
of a medicament for diagnosing or treating tumors or for measuring or		
detecting expression of an associated gene.		
Claim 2; Fig 125; 315pp; English.		
The invention relates to a novel isolated nucleic acid encoding a fully		
defined PRO polypeptide. The molecules of the invention may be useful for		
stimulating proliferation or gene expression in pericyte cells or the		
release of TNF-alpha from human blood. Other possible uses include the		
stimulation or inhibition of chondrocyte proliferation or		
differentiation, the stimulation of human dermal fibroblast cell		
proliferation and the detection of the presence of a tumour within a		
mammal. Furthermore, the nucleic acid may be useful for the manufacture		
of a medicament for diagnosing or treating a tumour within a mammal or		
for measuring or detecting the expression of an associated gene, as well		
as during gene therapy. The current sequence is that of the human PRO		
cDNA of the invention		
Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;		
Query Match	100.0%; Score 1035; DB 8; Length 1679;	
Best Local Similarity	100.0%; Pred. No. 3.1e-07;	
Matches 1035; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGAAACCATCAGCCAAAATGCACAATCTATCTTGGGCAATCTTCACGGGGCTG	60
Db	134 ATGAAACCATCAGCCAAAATGCACAATCTATCTTGGGCAATCTTCACGGGGCTG	193
QY	61 GCTGCTGTGTCTCTTCCAAGGAGTGCGCGGAGCGGAGATGCCACTTTCCCCTCAA	120
Db	194 GCTGCTGTGTCTCTTCCAAGGAGTGCGCGGAGCGGAGATGCCACTTTCCCCTCAA	253
QY	121 GCTATGGACAACGTGACGGTCCGGAGGGGAGAGCGCACCTTCAGTGCACATTATGAC	180
Db	254 GCTATGGACAACGTGACGGTCCGGAGGGGAGAGCGCACCTTCAGTGCACATTATGAC	313
QY	181 AACCGSGTCACC CGGTCCTTGAACCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG	240
Db	314 AACCGSGTCACC CGGTCCTTGAACCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG	373
QY	241 AAGTGTGTGCTGTGATCTCTCGGTGTCCTTTCGAGCAACACCCAAACCGAGTACAGATC	300
Db	374 AAGTGTGTGCTGTGATCTCTCGGTGTCCTTTCGAGCAACACCCAAACCGAGTACAGATC	433
QY	301 GAGATCCAGAACGTGATGTATGACGAGGCGGCTTACCTGCTCGGTGAGCAGACGAC	360
Db	434 GAGATCCAGAACGTGATGTATGACGAGGCGGCTTACCTGCTCGGTGAGCAGACGAC	493
QY	361 AACACCCAAAGACCTCTTAGGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG	420
Db	494 AACACCCAAAGACCTCTTAGGGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG	553
QY	421 ATTTCCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGGCTCACTGATGAGCAACT	480
Db	554 ATTTCCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGGCTCACTGATGAGCAACT	613
QY	481 GGATAGACGAGCGCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG	540
Db	614 GGATAGACGAGCGCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG	673
QY	541 AGTGAACGCAATACTTTGAAATTTACGGGCGATCCACCGGGAGCAGTCAGGGGCACTACGAG	600

20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US000502.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023528.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US034998.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-0080689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-521854/49.
DR P-PSDB; ADA18976.
XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumors.
XX Claim 2; Fig 375; 660pp; English.
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, cervical and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for modulating the uptake of glucose or FFA by adipocyte
CC cells, for stimulating the proliferation of or gene expression in
CC pericyte cells, for stimulating the release of proteoglycans from
CC cartilage, for stimulating the proliferation of inner ear utricular
CC supporting cells, for stimulating the release of cytokines from PBMC
CC cells, for inhibiting the binding of A-peptide to factor VIIA, for
CC inhibiting the differentiation of adipocyte cells and for stimulating the
CC proliferation of endothelial cells. This sequence represents a human PRO
CC polynucleotide of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1035; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAACCATTCAGCCAAATGCAATTTCTCTCTGCGCAATCTTTCACGGGGCTG 60
134 ATGAAACCATTCAGCCAAATGCAATTTCTCTCTGCGCAATCTTTCACGGGGCTG 193
QY 61 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCGAGGAGATGCCACCTTCCCAA 120
194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCGAGGAGATGCCACCTTCCCAA 253
QY 121 GCTATGGACAACTGACCGTCCGGCAGGGGAGAGCGCCACCTCAGTGTCATTTCAC 180
254 GCTATGGACAACTGACCGTCCGGCAGGGGAGAGCGCCACCTCAGTGTCATTTCAC 313

Tue Jun 1 09:37:50 2004

QY 181 AACGGGTCAACCGGTGGCTGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 240
 Db |
 QY 314 AACGGGTCAACCGGTGGCTGCTAAACCGCAGCACCATCTCTATGTGGGAATGAC 373
 Db |
 QY 241 AAGTGGTCCCTGGATCCCTGGGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 300
 Db |
 QY 374 AAGTGGTCCCTGGATCCCTGGGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
 Db |
 QY 301 GAGATCCAGAACGCTGGATGTGTATACGAGGCGCCCTTACACCTGCTCGGTGCAGACAGAC 360
 Db |
 QY 434 GAGATCCAGAACGCTGGATGTGTATACGAGGCGCCCTTACACCTGCTCGGTGCAGACAGAC 493
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 QY 361 AACCAACCAAGACCTCTAGGGTCCACCTCAATGTGCAAGTATCTCCCAAAATTGTAGAG 420
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 Job time : 463.39 secs

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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 15:29:05 ; Search time 89.2373 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 1.0 , Gapext 0.1

Searched: 682709 seqs, 277475446 residues
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1032	99.7	1032	4	US-09-700-397-1
3	939	90.7	939	4	US-09-700-397-5
4	489.9	47.3	1238	2	US-08-414-657D-3
5	489.9	47.3	1238	4	US-09-135-080-3
6	482.5	46.6	1014	2	US-08-414-657D-5
7	482.5	46.6	1014	4	US-09-135-080-7
8	477	46.1	1195	4	US-09-976-594-403
9	463.9	44.8	977	2	US-08-414-657D-1
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11	453.7	43.8	945	2	US-08-414-657D-8
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Sequence 1011, Ap					
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ALIGNMENTS

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RESULT 1
US-09-700-397-2
; Sequence 2, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1693
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone OC001 derived from human brain
; NAME/KEY: CDS
; LOCATION: (130)..(1161)
; NAME/KEY: sig_peptide
; LOCATION: (130)..(213)
; NAME/KEY: mat_peptide
; LOCATION: (214)..( )
US-09-700-397-2
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Query Match	100.0%	Score 1035;	DB 4;	Length 1693;
Best Local Similarity	100.0%;	Pred. No. 9,8e-11;		
Matches 1035;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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DB	130	ATGAAACCATCCAGCCAAAATGCACAATTCATCTCTTGGGCAATCTTCACGGGCTG	189	
QY	61	GCTGCTCTGTCTCTTCCAAAGGAGTGCCTGGCGCAGCGAGATGCCACCTTCCCCAAA	120	
DB	190	GCTGCTCTGTCTCTTCCAAAGGAGTGCCTGGCGCAGCGAGATGCCACCTTCCCCAAA	249	
QY	121	GCTATGGCAACGTGACGGTCCGGCAGGGGAGAGCGCCACGCTCAGGTGCACATTATGAC	180	
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QY	181	AACCGGGTCACCGGGTGCCCTGGCTTAAACCGCAGCAGCATCTCTATGCTGGGAATGAC	240	
DB	310	AACCGGGTCACCGGGTGCCCTGGCTTAAACCGCAGCAGCATCTCTATGCTGGGAATGAC	369	
QY	241	AAGTGGTGCTGGATCTCTCGCTGTCTCTTCTGAGCAACACCCAAACCGAGTACAGCATC	300	
DB	370	AAGTGGTGCTGGATCTCTCGCTGTCTCTTCTGAGCAACACCCAAACCGAGTACAGCATC	429	
QY	301	GAGATCCAGAACGTTGGATGTGTATGAGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	360	
DB	430	GAGATCCAGAACGTTGGATGTGTATGAGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	489	
QY	361	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG	420	
DB	490	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG	549	
QY	421	ATTTCCTTCAGATATCTCCCAATTAATGAAGGGAAACAATATTAGCGCTCACCTGCGATGCAACT	480	
DB	550	ATTTCCTTCAGATATCTCCCAATTAATGAAGGGAAACAATATTAGCGCTCACCTGCGATGCAACT	609	
QY	481	GGTAGACCAAGAGCCTACGGTTACTGTGGAGACACATCTCTCCCAAGCGGCTGTGTGTG	540	

Db	610	GGTAGACGAGCCTACGGTTACTTTGGAGACACATCTCCCAAAGCGGTTGGCTTTGTG	669
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Db	670	AGTGAAGACGAATACATTGTGAATAATCAGGCGCATCACCCGGGAGCAGTCAGGGGACTACGAG	729
QY	601	TGCAGTGCCTCCAAATGACGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCAACCGTGAAC	660
Db	730	TGCAGTGCCTCCAAATGACGTGGCGCGCCCGTGGTACGAGAGTAAAGGTCAACCGTGAAC	789
QY	661	TATCCACCATACATTTTCAGAGCCAAAGGTACAGGTGTCCCGTGGGCAAAAAGGGGACA	720
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QY	781	AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAAAAGACACTTTCTCTCAAACTTC	840
Db	910	AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAAAAGACACTTTCTCTCAAACTTC	969
QY	841	ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCGCTGCCAACAG	900
Db	970	ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCGCTGCCAACAG	1029
QY	901	CTGGGCCACACCAATGCGCAGCATCATGCTATTTTGGTCCAGCGCCGCTCAGCGAGGTGAGC	960
Db	1030	CTGGGCCACACCAATGCGCAGCATCATGCTATTTTGGTCCAGCGCCGCTCAGCGAGGTGAGC	1089
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QY	1021	CTTCTCAAAATTTGA	1035
Db	1150	CTTCTCAAAATTTGA	1164

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RESULT 2
US-09-700-397-1
; Sequence 1, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: 061459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-1

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Query Match	99.7%	Score 1032;	DB 4;	Length 1032;
Best Local Similarity	100.0%;	Pred. No. 4.6e-11;		
Matches 1032;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAAACCATCGACGCAAAATGCAAAATCTATCTCTTGGGCAATCTTCACGGGGCTG	60	
Db	1	ATGAAACCATCGACGCAAAATGCAAAATCTATCTCTTGGGCAATCTTCACGGGGCTG	60	
QY	61	GCTGCTGTGTCTCTTCCAGAGAGTGCCCGTGGCGAGAGATGCCACCTTCCCCAAA	120	
Db	61	GCTGCTGTGTCTCTTCCAGAGAGTGCCCGTGGCGAGAGATGCCACCTTCCCCAAA	120	

Db 781 AACTACACTTGGCTCCCAACAGCTGGGCCACACCAATGCCAGCATCATGCTATT 840
QY 934 GGTCCAGGCGCGTCAAGCGAGTGAGCAACGACGTCGAGGAGGCGAGCTGCGTCTGG 993
Db 841 GGTCCAGGCGCGTCAAGCGAGTGAGCAACGACGTCGAGGAGGCGAGCTGCGTCTGG 900
QY 994 CTGCTCCCTCTTCTGCTCTTTCACCTGCTCTTCAAAATTT 1032
Db 901 CTGCTCCCTCTTCTGCTCTTTCACCTGCTCTTCAAAATTT 939

RESULT 4
US-08-414-657D-3
Sequence 3, Application US/08414657D
Patent No. 5861283
GENERAL INFORMATION:
APPLICANT: Levitt, Pat
APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1238 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 56...1069
OTHER INFORMATION:
US-08-414-657D-3

Query Match 47.3%; Score 489.9; DB 2; Length 1238;
Best Local Similarity 61.6%; Pred. No. 2.9;
Matches 724; Conservative 0; Mismatches 178; Indels 273; Gaps 101;
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QY 487 CCAGAGCCTTACCGTT---ACTTGGAGACACATCTCTC-CCAAAGCGTTGG-----CTT 536
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QY 537 TG--TGAGTGAAGACGAATCTTGAATTCAGGCAATCACCCGGGAGCAGTCAGGGAC 594
Db 580 TGAAGGA--GAAGAAGATATCTGGAGATCTTAGGCATCACCAGGGAACAGTCAGGCA 637
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Db 638 TATGAGTGAAGGTGCCA---ACGAGGTCTCTCTCG-----CGATGTCAAAAGTCA 689
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Db 690 AGGTCACTGTGAATCTCCACCACCATCACAGAGTCAAGAGCAATGAAGCCACCACAG 749
QY 688 G-GTACAGGTGTCCTCGTGGGACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCC 746
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Tue Jun 1 09:37:50 2004

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US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56..1069
; OTHER INFORMATION:
;
US-09-135-080-3
Query Match 47.3%; Score 489.9; DB 4; Length 1238;
Best Local Similarity 61.6%; Pred. No. 2.9;
Matches 724; Conservative 0; Mismatches 178; Indels 273; Gaps 101;

Qy 2 TGAATAACA-T-CC-AGCCAAAATG-C---ACAAATTTCTCTTGGCAATC-T 49
Db 34 TG---ACCAACTCGCGAGGCCACATGGTCGGGAGAGTTCAACCTGATCGG-AAACAGT 89
Qy 50 T-CACGGG---GCTG-G-CTGCTCTGTCTCTTT-CCA-AGGAGTGCCTGCGCAGC 99
Db 90 TGCACACTGGTCTACTGAGACTGTCTGCTT-TCTTCCACAGGACTGCCCTTTCGCGC 148
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Qy 747 CTCAGCAGAAATCCAGTGTGTACAAAGGATGACAAAGAGACTGATTGAAGGAAAG---AAAG 803
Db 790 TGCACCTGACTTTGAGTGTGTACCGGATGACACCAG---GAT--AA--ACAGTGAACAG 842
Qy 804 G--GTAAAAGTGA--A--ACAGA---CCTTTCTCTCAAACTCA---T--CTTCTTCA 850
Db 843 GCCTTGAGATT--AAGAGCACTGAGGGCCAGTCTC-C---CTGACGGTGAC-----CA 890
Qy 851 ATGTCTCT---GAAATGACTATGGAACACTACACTTGGCTGGCTCCCAAGCTGGGCC 907
Db 891 ACGTCACTGAGGAAC---ACTACGGCAACTATACCTGTGTGGCTGCCAACAGCTGGCG 947
Qy 908 ACACCAATGCCAGCATCATGCTATTGTTGCTCAGGCGCC---GTGAGGAGGTGAG----- 959
Db 948 TCACCAATGCCAGCTAGTCTCT-TTT---CAGAC-CCGGTGC-----GGTGAAGAGAA 996
Qy 960 CAACGGCACTTCAGGAGGCGAGGTG--CGT-----C--TGGCTGCT---GCTCTTCT 1007
Db 997 CAACGG-A--TCCA-----TCAGTCTGGCGGTACCACTGTGGTGTGCTGGCAGCGTC-CCT 1047
Qy 1008 GGTCTTGCACCTGCTTCT---CAAAATTT-----GA 1035
Db 1048 GTTC-TGC-----CTTCTCAGCAATGTTAATAGA 1076

```

RESULT 6
 US-08-414-657D-5
 ; Sequence 5, Application US/08414657D
 ; Patent No. 5861283
 ; GENERAL INFORMATION:
 ; APPLICANT: Levitt, Pat
 ; APPLICANT: Pimenta, Aurea
 ; APPLICANT: Fischer, Itzhak
 ; APPLICANT: Zhukareva, Victoria

328 ACATGCTCAGTTCAGAC--AC-AGCATGAGCCC-AAGACCTCTCAA--GTTTACTTGATT 381

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,080
FILING DATE: 17-AUG-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/414,657
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214
TELEFAX: 609-620-3259
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1014 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1014
OTHER INFORMATION:
US-09-135-080-7

Query Match 46.6%; Score 482.5; DB 4; Length 1014;
Best Local Similarity 62.3%; Pred. No. 2.8;
Matches 711; Conservative 0; Mismatches 173; Indels 257; Gaps 100;
QY 22 ATG--C---ACAATCTATCTTGGGCAATC--TT--CAACGGG---GCTG-G-GTGT 66
DB 1 ATGGTCGGAGAGTTCACCTGATCGG-AAACAGTTGCCACTGGTCTTACTGAGACTGCT 59
QY 67 CTGTGCTCTT--CCA-AGAGTGCCCGTGGCGAGGGAGAGCGCCACCTCAGGTGCACTAT--T-----G 178
DB 60 CTGGCT-TCCTCCACAGAGCTGCCCGTTCGAGCGTGGAT-----TTTAAACGAGGC-A 112
QY 125 TGGACAACTGACGGTCCGGCGAGGGGAGAGCGCCACCTCAGGTGCACTAT--T-----G 178
DB 113 CGGACAAATCATCCGTGAGCGAGGGGAGAGCGCCACCTCAGGTG---TGTGGTAGAG 169
QY 179 ACACCGGTCAACCG--GGTGGCTGGCTTAACCGC---AGCACATCTCTATCTGCTGG 233
DB 170 ACAC---G-ACCTGAAAGTGGCTGGTTGAACCGCTCTGGCATCATCTTC---GCTGG 221
QY 234 GAATGACAACTGCTGGATCTCGCGTGGTCTTCTGAGC-----AACACCCAAAC 287
DB 222 ACAGCACTGCTCTGACCCCTCG---GGT-----TGAGCTGGAGAAACGCC---AT 270
QY 288 GC-----AGTACAGCAT-CCAGATCCAGAACGTGGATGTGTATGACAGGG--CCCTTAC 339
DB 271 GCTCTGGAATACAGCTCCGA-ATCCAGAGGTGGATGTCTATGATGAGGATCC--TAC 327
QY 340 ACTGCTCGGTGAGACAGACACCA---CCCAAGACCTCT--AGGGTCCACCTCAT 393
DB 328 ACATGCTCAGTTACAGC--AC-AGCATGAGGCC--AAGACCTTCAA--GTTTACTTGATT 381
QY 394 GTGCAAGTATCTCCCAA--AT-TGTAGAGATTTCTTCAGATATCTTCATTAATGAAGGGA 451
DB 382 GTACAGT-TCCACCAAGATCTCCA-ACATCTCTCGGATGTCACTGTGAATGAGGGCA 439
QY 452 ACAATATTAGCTCCTGACATGACAACTGGTACAGAGCCCTACCGTT---ACTTGA 508
DB 440 GCAATGTAACCTGCTGTGATGCGCAATGGCGCCCTGACCT---GTTATCATCCTGGA 496
QY 509 GACATCTCTC-CCAAAGCGGTTGG-----CTTTGTGA--GTGAAGACGAATACTGG 559

DB 497 GACAC--CTTACACCA---C--TTGAGAGAGATTT--TGAAGGAGAGAGATATCTGG 547
QY 560 AAATTGAGGATATCACCAGGAGCAGTACAGGAGTACAGTGCCTTCCAAATCAGC 619
DB 548 AGATCTTAGCATCACCAGGAAACAGTCAAGGCAATATGATGCAAGCTGCGCA---ACG 604
QY 520 TGGCGCGCCGTTGATACGA-G-----AGTAAAGGTCAACCGTGAACATAT---CCAC 667
DB 605 AGGTCTCTCTCG-----CGATGTCAACAAAGTCAAGTCACTGTGAATATCCACCCAC 659
QY 668 CAT-ACA---TTTCAGAAAGCAGGTTACAGGTGTCC--CCGTGGGCAAAAGGG--GACA 720
DB 660 CATCAGAGTCTAAG-AG-CAATG--A-AG-----CCACC-----ACA-----GGACGACA 701
QY 721 --CTGC-----AGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGGA 773
DB 702 AGCTTCCCTCAAAATGTGAAGCCTCAGCGGTGCTGACCTGACTTTGAGTGGTACCGGGA 761
QY 774 TGACAAAGACTGATTGAAGGAAAG---AAAGGG--GTGAAAGTGA--A--ACAGA---822
DB 762 TGACACAG---GAT--AA--ACAGTGCMAACGCTTGAGATT--AAGAGCACTGAGGG 812
QY 823 CCTTCTCTCAAAACTCA---T---CTTCTCAATGTCTCT---GAACATGACTATGGA 874
DB 813 CCAGTCTCTC---CTGACCGTGCAC-----CAACGTCACTGAGGAAC---ACTACGGCA 859
QY 875 ACTACACTTGGTGGCTCCAAACAGCTGGCCACCAACCAATGCCAGCATCATGCTATTG 934
DB 860 ACTATACCTGTGGCTGCCAAACAGCTCGCGCTCCACCAATGCCAGCTAGTCTCT-TTT- 917
QY 935 GTCCAGCGCC--GTCAGCGAGGTGAG-----CAACGGCACGTGAGAGGGGAGGCTG 986
DB 918 ---CAGAC--CCGGTCTC-----GGTGAGAGGAATCAACGG-A--TCCA-----TCAGTCTG 960
QY 987 --CGT-----C--TGCTCTCT---GCCTCTTCTGCTTGGCTGACCTGCTTCT---CAAAAT 1031
DB 961 GCCGTACCACTGTGGCTCTGCGCAGCGTC-CCTGTTCT-TGC-----CTTCTCAGCAATG 1013
QY 1032 T 1032
DB -014 T 1014

RESULT 8
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 403
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CB1
US-09-976-594-403

Query Match 46.1%; Score 477; DB 4; Length 1195;
Best Local Similarity 61.0%; Pred. No. 4.9;
Matches 706; Conservative 0; Mismatches 171; Indels 281; Gaps 100;
QY 22 ATG--C---ACAATCTATC---TCTTGGGCAATC---TT---CAGGG---GCTG-G-CT 63

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Db      953  --TCAGTCTGGCGTACCAGCTGTGGCTGTCTGGCAGCATC-TCTGTCTC-TGC-----CTTC 100
      1025  T---CAAAATTTT-----GA 1035
      1004  TCAGCAAAATCTTAATAGA 1021

RESULT 9
US-08-414-657D-1
; Sequence 1, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2...976
; OTHER INFORMATION:
US-08-414-657D-1

Query Match      44.8%; Score 463.9; DB 2; Length 977;
Best Local Similarity 61.9%; Pred. No. 6.1; Mismatches 0; Indels 248; Gaps 94
Matches 685; Conservative

QY      22  ATGC-----ACAATT-CTATCTCTTGGGCAATCTTCACGGGGTGGCTGTCTGTGTCTCT 76
Db      3  AT-CGGAAACAGTTGC-----CACT--GG---TCCT-ACTGAGAT---TGCTCTGCCT-TCT 48
QY      77  T-CCA-AGAGTGCCTGTGGCAGCGGAGATGCCACCTTCCCAAGCTATGCAACGT 134
Db      49  TCCCAAGAGACTGCCTGTTCGACGGGTGAT-----TTTAAACCGAGGC-ACGGACAACAT 102
QY      135  GACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGC--ACTA-TTGACAAACGGG---T 188
Db      103  CACCGTGGAGCGAGGGGACACAGCCATCTCTCAGGTGCGTCTTAGAAGACA-----GAAGT 158

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189 CACCCGGTGGCTGGCTAAACCG--CAGCACATCTCTATGCTGGATGACAACTGG 246
159 CA--AAGGTGGCTGGTGAACCGTCTG--GCATCATTTTGTGCTGACATGACAACTGG 214
247 TGCCTGGATCTCGCGTGGCTCTTCTGAGC-----AACAC--CCAAAC-----GCAGTACAGC 297
215 TCTCTGGACCCAGC--GGT-----TGAGCTGGAGAA--ACGCCATCTCTGGAATACAGC 265
298 AT--CGAGATCCAGAACGTTGGATGTGTATGACAGGG--CCCTTACACTGCTCGGTGAG 354
266 CTCGGA--ATCCAGAGGTGGATGCTATGATGAGGGTTCC--TACACTTGTCTCAGTTTCAG 322
355 ACAGACACACCA-----CCCAAGACCT--CTAGGTCCACCTCATTTGCAAGTATCTCCC 408
323 AC--AC--AGCATGAGCC--AAAGCCTCCAA--GTTTACTGTGATGATCAAG-----TCCC 372
409 A--AAATTGTAGAGATTTCTTCAAGATATCTCC-----AT-----T--AATGAAGGGAACA 454
373 ACCAA-----AGA--TCTCCA--ATATCTCTCGATGTCACTGTGAATGAGGCGACGA 422
455 ATATTAGCTC--ACCTGCATAGCAACTGGTAGACAGAGCTTACGGTT-----ACTTGAG 509
423 ACGT--GACTCTGGTCTGCAATGCGCAATGGCGCTCTGAACT--GTTATCACCTGGAG 477
510 ACACATCT--CTCCCA-----RAGCGTGGCTTTGTGA--GTGAAGACGAATCTTGAA 561
478 ACAC--CTTACACCACTGGAG-----GGAATT--TGAGGAGAGAGAAATATCTGGAG 529
562 ATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTTCCCAATGACGTG 621
530 ATCTTGGCATCACAGGGAGCAGTCAGGCAATATGATGCAAAAGCTGCCAACAGGTC 589
622 GCCGCGCCGCTGGT---ACGGAGATTAAGTCACTGAGTGAATCC--ACCA--TA--CAT 675
590 TCCCTGGCGGATGTCAAAC--A--AGTCAAGTCACTGTGAATATCTCTCCCACTATCA-- 644
676 TCAGAAGCCAAAGGTACA--GGTGTCCCGTGGGCAAAAGG--GACA--CTGC-----724
645 -CAGAAATCCAGAG--CAATGAAGCCACC-----ACA-----GGACGACAACTTCACTCA 692
725 AGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGAGGATGACA-----778
693 AATGTGAGCCCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGATGACACTAGGA 752
779 -AAGACTG--A-----TTGAGGA--AAGA--RAGGGTGAAGTGAAGAAACAGACT 825
753 TAAATAGTGCCAAATGGCCCTTGA--GATTAAGAGCAGCG-----AG--GG-----798
826 TTCTCTCTCAAAAC--TCATCTTCTCAATGTCTCTGAACATGACTATGGAACTACACTT 883
799 TTCC--CT--GACGGTGA-----C--CAAGCTCACTGAGGAGCACTACGCACTACACT 848
884 GCGTGGCTCCAAAGAGTGGGCCAACCAATGCCAGCATCATGCTATTGTTGTCAGGGC 943
849 GTGTGGCTGCAACAAAGTGGGGGTCAACCAATGCCAGCCTAGTCTCTTTTCAAGCTGG--906
944 CCGTACAGAGGTGAG-----CAACGGACGTGAGGAGGGGAGGCTG--CGT-----C- 990
907 --GTC-----GGTGAGAGGAATAAATGG--A--TCCA-----TCAGTCTGGCCGATCACT 951
991 -TGCGTGTCT---GCTCTTCTGGTCT 1012
952 GTGGCTGTGGCAGCATC--TCTGCTCT 977

RESULT 10

US-09-135-080-1

; Sequence 1, Application US/09135080
; Patent No. 6423627
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea

APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,080
FILING DATE: 17-AUG-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/414,657
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214
TELEFAX: 609-620-3259
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 2..976
OTHER INFORMATION:
US-09-135-080-1

Query Match 44.8%; Score 463.9; DB 4; Length 977;
Best Local Similarity 61.9%; Pred. No. 6.1;
Matches 685; Conservative 0; Mismatches 174; Indels 248; Gaps 94;
QY 22 ATGC-----ACAAATT-CTATCTCTTGGGCAATCTTACGGGGCTGGCTGTCTCTCT 76
Db 3 AT--CGGAAACAGTTGC---CACT--GG---TCCT--ACTGAGAT---TGCTCTGCCT-TCT 48
QY 77 T--CCA--AGGAGTCCGCTGCGCAGCGGAGATGCCACCTTCCCAAGCTATGCAACACT 134
Db 49 TCCACAGACTGCTCTGTTCGCGAGGTGGAT-----TTTAAACCGAGGC-ACGACAACT 102
QY 135 GACGGTCCGCGCAGGGGAGGAGCCACCTCAGGTGC--ACTA--TTGACAAACGGG--T 188
Db 103 CACCGTGAGCGAGGGGACACAGCCATCTCAGTGGGTCTTAGAAGACAA-----GAACT 158
QY 189 CACCGGGTGGCTGGCTAAACCG--CAGCACATCTCTATGCTGGGATGACAACTGG 246
Db 159 CA--AAGGTGGCTGGTGAACCGTCTG--GCATCATTTTGTGAGGATGACAACTGG 214
QY 247 TGCCTGGATCTCGGTGGTCTCTTGAGC-----AACAC--CCAAAC-----GCAGTACAGC 297
Db 215 TCTCTGGACCCAGC--GGT-----TGAGCTGGAGAA--ACGCCATCTCTGGAATACAGC 265
QY 298 AT--CGAGATCCAGAACGTTGGATGTGTATGACAGGG--CCCTTACACTGCTGGTGGAG 354
Db 266 CTCGGA--ATCCAGAGGTGGATGCTATGATGAGGGTTCC--TACACTTGTCTCAGTTTCAG 322
QY 355 ACAGACAAACA-----CCCAAGACCT--CTAGGTCCACCTCATTTGTCAGATATCTCCC 408

Db	323	AC--AC-AGCATGAGCCC-AAGACCTCCCAA--GTTTACTTGATCGTACAAG-----TCCC	372
QY	409	A--AAATTGTAGAGATTCTTCAGATATCTCC-----AT-----T-AATGAAGGGAACA	454
Db	373	ACCAA-----AGA--TCTCCA-ATATCTCCTCGGATGTCACTGTGATGAGGGGACGA	422
QY	455	ATATTAGCCTC--ACCTGCATAGCAACTGTGTAGACAGAGCCTACGGTT---ACTTGAG	509
Db	423	ACGT--GACTCTGGTCTGCATGGCCATGGCCGCTCTGAACCT---GTTATCACTGGAG	477
QY	510	ACACATCT--CTCCCA-----AAGCGGTTGGCTTTGTGA--CTGAAGACGAATACTGTGAA	561
Db	478	ACAC--CTTACACCAACTGGAAG-----GGAATT--TGAAGAGAGAGAATAATCTGGAG	529
QY	562	ATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAAATGACGTG	621
Db	530	ATCCTTGGCATCACAGGGAGCAGTCAGGCAAAATATGATGCAAACTGCCAACAGGTC	589
QY	622	GCCGGCCCGTGGT---ACGGAGAGTAAAGTCAACCGTGAACATATCC--ACCA-TA-CATT	675
Db	590	TCCTCGGGGATGTCAAAAC--A-AGTCAAGGTCACTGTGAACATATCTCTCCCACTATCA--	644
QY	676	TCAGAAGCCAAAGGTFACA--GGTGTCCCGTGGGACAAAAGGG--GACA--CTGC-----	724
Db	645	-CAGNAATCCAAG--CAATGNAGCCACC-----ACA---GGACGACAGCTTCACTCA	692
QY	725	AGTGTGAAGCCTCAGCAGTCGCCCTCAGCAGAAATCCAGTGGTACAGGATGACA-----	778
Db	693	AATGTGAGGCCCTCGGCAGTCGCCCTGCACCTGACTTTGAGTGTACCCGGATGACACTAGA	752
QY	779	-AAGACTG--A-----TTGAAGN--AAGA--AAGGGGTGAAGTGGAAAACAGACCT	825
Db	753	TAAATAGTGCCAAATGGCCCTTGA--GATTAAAGACGG-----AG-GG---CCAGTC--	798
QY	826	TTTCCCTCTCAAAAC--TCATCTTTCAATGTCTCTGAACATCACTATGGGAATACACTTT	883
Db	799	TTCC-CT---GACGGTGA---C--CAACGTCACTGAGGAGCACTACGCCAACTACACCT	848
QY	884	GGTGGCCTCCAACAAGCTGGGGCCACCAATGCCAGCATCATGCTATTTTGGTCCAGGGG	943
Db	849	GTGTGGCTGCCAACAGCTGGGGGTACCAATGCCACCGCTAGTCTCTTTTCAGACCTGG--	906
QY	944	CCGTCAAGCAGGTGTGAG-----CAACGGCACTCGAGGAGGGCAGGCTG--CGT-----	990
Db	907	--GTC-----GGTGAGAGGAATAAATGG-A--TCCA-----TCAGTCTGGCCGTACCACT	951
QY	991	-TGGCTGTCT----GCCTCTTCTGGTCT	1012
Db	952	GTGGCTGTCTGGCAGCATC-TCTGCTCT	977

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RESULT 11
US-08-414-657D-8
; Sequence 8, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...945
OTHER INFORMATION:
US-08-414-657D-8

Query Match	43.8%;	Score 453.7;	DB 2;	Length 945;
Best Local Similarity	62.8%;	Pred. No. 9.2;		
Matches	664;	Conservative	0;	Mismatches 166; Indels 227; Gaps 89;
QY	22	ATG--C---ACAATCTATCTCTGGCAATC--TT--CACGGG---GCTG-G-CTGCT	66	
DB	1	ATGTCGGGAGATTCAACCTGATCGG-AAACAGTTGCCACTGGTCTCTACTGAGACTGCT	59	
QY	67	CTGTGTCTCTTT-CCA-AGGAGTGGCCGTCGACGGAGATGCCACCTTCCCAAAAGCTA	124	
DB	60	CTGCCT-TCITCCACAGGACTGCCCGTTGCGAGCGTGGAT-----TTTAAACCGAGGC-A	112	
QY	125	TGGACAACGTCGACGGTCCGCGAGGGGAGAGGGCCACCTCAGTGGCACTAT--T---G	178	
DB	113	CGGACAAATCAACCGTCGAGGAGGGGGACACGGCCATCCTCAGGTG---TGTGGTAGAAG	169	
QY	179	ACAACGGGTCAACCG--GGTGGCTGTGCTAAACCGC--AGCACCATCTCTATGCTGG	233	
DB	170	ACAA-----G-AACTCGAAGTGGCCTGTTGAACCGCTCTGSCATCATCTTC--GCTGG	221	
QY	234	GAATGACAAGTGGTCCCTGGATCCTCGCGTGGTCTCTTGAC-----ACACCCAAAC	287	
DB	222	ACACGACAAGTGGTCTCTGAGCCCTCG--GGT-----TGAGCTGGAGAAACGCC--AT	270	
QY	288	GC-----AGTACAGCAT--CGAGATCCAGAACGTGGATGTATGACGAGG--CCCTTAC	339	
DB	271	GCTCTGGATACAGCCTCCGA-ATCCAGAGGTGGATGCTATGATGAAGGATCC--TAC	327	
QY	340	ACCTGCTCGTGGACAGACAAACCA-----CCCAAAGACCTCT--AGGTCACCTCAT	393	
DB	328	ACATGCTCAGTTTCAGAC--AC-AGCATGAGCCC-AAGACCTCTCAA--GTTTACTTGATT	381	
QY	394	GTGCAAGTATCCCAA-AT--TGTAGAGATTCTTCAGATATCTCCATTAATGAAGGA	451	
DB	382	GTACAGT--TCCACAAAGATCTCCA-ACATCTCTCGGATGTCATGTGAATGAGGCA	439	
QY	452	ACAATATTAGCCTCACCTGCATAGCAACTGGTAGACGAGCCTACGGTT----ACTTGA	508	
DB	440	GCAATGTAACCTGGTCTGCATGGCCAAATGGGCGCCCTGAACT---GTTATCACCTGGA	496	
QY	509	GACATCTCTC-CCAAAGCGGTTGG-----CTTTGTGA--GTGAAGACGAATACTTGG	559	
DB	497	GACAC--CTTACACCA--C--TTGAAGAGAAAT--TGAAGAGAGAAATATCTGG	547	

QY 159 -C-ACCCTC-----AGG---TG---CTAT---TGACAAACGGG-----187
Db 2608 ACAACCTCTGTACCTGGAGGATCATGTGAGCATGCGCATGCAATGCAATGACAACTTGACCTT 2667
QY 188 -T-CA-CCC-GG-----GTG---GC-----CTGGC-----TAAACC--G-C-213
Db 2668 CTCATCCCTGGCAGCTGTGACAGCTTGTCTGGCTCTCTGTCTGATATGTAACACAGGTAC 2727
QY 214 AGCA--CC---ATC-----CTCTATGCTG--GGA-AT---GACA---AG-TGGTGC--249
Db 2728 AACAGGCGGTA-CTGTGAGCTCTGTCTGATGATATTTTGGAGATGCACTGATGCGGA 2786
QY 250 -----CTG-GATCC--TCGC-----GTGG--TCCT--TCGGA-----GCAACACC 283
Db 2787 AGAACTGTGACCCCTGTCTGTGTAATGCGCGTGGCTCTCTCTGAGGTTTGGCCACAGTC 2846
QY 284 AAAC--G-CAGT---ACAGCATCGAGATCCAGAACGT-----G-GATGTG---TAT 324
Db 2847 AAACCTGGACGTGTGAGTGCA--GAG--CC--AACGTTTCAGGGTCAGAGATGTGACAAAT 2900
QY 325 GACGA--GGGCCCT-----TACA-----CCTGC-----345
Db 2901 G-CAAGCTGGAGCTTTGGCTTACATTCAGCAAGGGGCTGTGTTCCCTGCAACTGCAAT 2959
QY 346 -----TCG---GTGCAGACA--GACAA-----CCACCC-----368
Db 2960 TCTTTTGGGCTAAAGTCATTCGACTGTGAAGAGATGACAAATGTTGGTGCCAACTTGA 3019
QY 369 -----AAA--GACCTTAGGGTCCAC--CTCATTTGCAAGTATCTCCCAA--410
Db 3020 GTCACAGGGAAGAAATGTGACGGCT-GTGCCACGGCT-ATT-T-CAA---CTTCCAAG 3071
QY 411 AA-----TTGTAGAGAT-TTCT--TCAG-----ATA--TCT--CAATTAAT 444
Db 3072 AAGGAGGCTGCACAGCTTGT-GA-ATGTTCTCATCTGGGTAAATATTGTGACCCA--AA-3126
QY 445 GA-AGGGAACAT--ATTAGCTCACTGC-ATAGCACTGTGAGACCAGA--G-CCT-495
Db 3127 GACTGGG--CGATGCAATTTGCC-CACC--CAATA--CCATTGG-AG--AGAAATGTTCTA 3176
QY 496 ACGGT-----TACTTGGAGACATCTCTCCCAAGC--GGTT-----GGCTTTGTGAG 542
Db 3177 AATGTGACCCCAATCTTGGGCGCCACAGATTACCA--CTGTTTGAAGGCTTGTAAAC 3232
QY 543 TGAAG-AC---GAATACTTGG-----AAATTCAGG-----GCA---T 572
Db 3233 TGCAGCACAGTGGGATCCTTGGATTTCCAATGCAATGTAAATACAGGGCCAATGCAACTGT 3292
QY 573 CACCC-----GG-----GA--GCAGTC-AGG-----GG-ACTA---596
Db 3293 CATCAAAATCTCTGGTCAAAATGTACAGAGTGCAGTGCAGGTGCTGGAACCTACCTT 3352
QY 597 CGAGTGCA-----GTG-----CCTC-----CA-ATG-----AC--GTG-----621
Db 3353 CG-CTGCAATCTCTGTGACTGCTCTCTCCCTGGGACAGATGCCAACCTGTGATTGCA 3411
QY 622 GGC-----GGGCCCGTGGT-----AC--GG-AGAGTA-----AAGGTACCGT-GA 658
Db 3412 GACTAAAAAATGCTCTGTAGTGATCAAACTGGGCGAGTGCACTTGTGAAGGTGAATGTGGA 3471
QY 659 A--CTATCCAC-----CA-----T-----ACATT-----TCAGAAGCCAAAG-----687
Db 3472 AGGC-ATCCACTGTGACAGATGCGGCGCTGGCAAAATTCGACTC-GATGCCAAGATCCA 3529
QY 688 -----GG-TACAG-----G-----TG--TC-----CCC-GTG-----GGA-CAAAAGG-715
Db 3530 CTTGGCTGCAGCAGCTGCTATTCTCTGGGCACTACTACCCAGTGTCTGTGAAGCAAAAGGA 3589
QY 716 -----GGACATGCAAGT-----TGAAGCTCAGAG-----T-CCCT-----748
Db 3590 CTGATCGGAC-GTG-GGTGACTCTGAAGGCTGAGCAGACCAATTCACCCCTGGTAGATG 3647

QY 749 -----CAGCA--GA-----AT-----TCCAG-----TGGT-----766
Db 3648 AGCTCTGACGACACGACCCACCAAGGCAATGTTTTTCAACATCCAGAGATGTTGCC 3707
QY 767 ACAAG-----GATGACAAAAG-----ACT-----GA--787
Db 3708 ACATGACCTGTATGAGAGAAGATCTCCATTTGGAACCTTTTATTGGAACTTCCAGAAC 3767
QY 788 -----TTGAAGGAAGAA--A--GGGG-----TG-AA-----809
Db 3768 AATTTGAAGGAAGAAAGTTGATGCCCTATGGGGGCAAACTCAAGTATGCAATCTATTTCG 3827
QY 310 AG--T--GGA--AAACAG-----ACCT-T--TCCTC-----TCA-----A 835
Db 3928 AGCTCGGAGAGAAACAGGTTTCTTACATATATCTCAAGTATGATTCGAGGTGGGA 3887
QY 936 A--ACTCAT-CT-----TCTTCA-----ATG-----TC-TCTGA-----A 861
Db 3888 CACCTACTCATGTAGAAATTTATGTCAGGCATATGGCTCTCTGATTTGGCCAAATGA 3947
QY 862 C-----ATGAC-----TATGG-----872
Db 3948 CAAGGCATGAATGAATGACAGAGAAAGATGGAATATTATGGGATGATCCTCGAG 4007
QY 873 -----GAACT--AC-----ACTTGGGTG-----888
Db 4008 TCCATAGAACTGTGACCCGAGAGACTT-CTTGGATATACTATATGATATTCATTACAT 4066
QY 889 -----GG-CT-----C-CAA-----CA--898
Db 4067 CTTATCAAGCTACTTTATGGAATTTTCATGCAACAAAGCAGGATTTCTGAAATCTCAATG 4126
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Db 4127 GAGTAGCTGAACAGGACGTGGGAACACATGACTCTCCAGCTGACTTGAATGAAAAA 4186
QY 922 -----AT-----CAT--GCTATT-TGG-----TCC-----AGGC-----GCCG-----T 947
Db 4187 TGTGATTTCCCTGGGCTATTCTGGCTGTCTGTGAGGCATGCTTGGCCGGATTTAT 4246
QY 948 C-A--GG-----AGGT-----GACCAAC-----GGCAC-----968
Db 4247 CGACTGGCTTCTCAACCAAGGTGGCCGACCCCTGCAACCCCTGGGCACTGTGTGCCA 4306
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QY 993 -----GCTG-----CTG-----C-----CTCTT-----CT--G-----GTC 1011
Db 4367 CAACATCACACTGTGTGCTGACTTCTGTGAAGCATGTGCTCTTGGATCTATGGAATTGC 4426
QY 1012 -----TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030
Db 4427 AAGGATTCGCAATGACTGTGCAAGATGTGCTGCCCTCTGATTTCTTCAGTAACAT 4486
QY 1031 TT 1032
Db 4487 TT 4488

RESULT 14

US-08-125-077-3

; Sequence 3, Application US/08125077

; Patent No. 5872231

; Patent No. 5872231 5840863

; GENERAL INFORMATION:

; APPLICANT: Engvall, Eva

; APPLICANT: Leivo, Ilmo

; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

; TITLE OF INVENTION: Fragments and Uses Thereof

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/125,077
 FILING DATE: 22-SEP-1993
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US PCT/US 94/10730
 FILING DATE: 21-SEP-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/472,319
 FILING DATE: 30-JAN-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/919,951
 FILING DATE: 27-JUL-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9721

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6942 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-125-077-3

Query Match 43.08; Score 445.5; DB 2; Length 6942;
 Best Local Similarity 38.18; Pred. No. 4.9e+02;
 Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;

QY 1 ATGAAAACCAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36
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 QY 37 TCTTGGGAATCTT-----CAC-GG-----GGC-----TGGC-- 62
 DB 2249 TCTTGTG-AAATCTTGTGGCCTAGGCACAGCGAGTTAAACGGCACTATTTTGGTGGCAT 2307
 QY 63 -----TGCT-----CTGT-----GTCTCT-- 77
 DB 2308 CTGTGAGCCATGTCTAGTCTTTGGTCAATGGGAGTCTGTGTATGACGCTCACTGGGAATG 2367
 QY 78 CC-----AAGGA-----GT-GCCC-----GTG-----C-- 94
 DB 2368 CTTGAATGTAAAGATACACAGGTGGCCCATATTGTGATAAATGCTTCTCTGGTTTCTA 2427
 QY 95 --GC-AGC-----GG-----AGA-TGCCA-----CCT-----T 113
 DB 2428 TGGCAGGCTTAAAGAAACCTCTGAAGACTGTCAACCCCTGTGCTCTCCACTCAATAT 2487
 QY 114 CC-----CCAA-----AGC-----TA-----TGGA--CAAC-GTGA 136
 DB 2488 CCATCCAAATACTTTAGCCCAACGTGCCATTTAGACCGGAGTCTTGGATGATCTGTGA 2547
 QY 137 -----CGGTCCGG-----CAGG-----GGAGA-----GC----- 158
 DB 2548 TGGATGCCCTGTGCGGTGACACAGGACCAACGCTGTGAGAGGTGTGAGAAGGCTATTTGG 2607
 QY 159 -C-ACCCTC-----AGG-----TG-----CA--CTAT-----TGACAACCGGG----- 187

DB 2608 ACAACCTCTGTACCTGGAGGATCATGTACGCCATGCAATGCAATGCAACACCTTGACTT 2667
 QY 188 -T-CA-CCC-GG-----GTG--GC-----CTGGC-----TAAACC--G--C 213
 DB 2668 CTCCATCTCTGGCAGCTGTGACAGCTTGTCTGGCTCTGTCTGATATGTAACACAGGTAC 2727
 QY 214 AGCA--CC--ATC-----CTCTATGCTG--GGA-AT-----GACA-----AG-TGGTGC-- 249
 DB 2728 AACAGGCCGGA-CTGTGAGCTCTGTCTGATGATATTTTGGAGATCAGTTGATCGGA 2786
 QY 250 -----CTG-GATCC-----TGGC-----GTGG--TCCT--TCTGA-----GCAACACCC 283
 DB 2787 AGAATCTGACGCCCTGTGCTGTAAATGCGGTGGCTCTTCTCTGAGGTTTGGCAGCTC 2846
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 DB 2901 G-CAAGGCTGGGACCTTTGGCCTACAATCAGCAAGGGGCTGTGTTCCCTGCAACTGCAAT 2959
 QY 346 -----TCG--GTGCAGACA--GACAA-----CCACCC-- 368
 DB 2960 TCTTTTGGGTCTAAGTCACTGCTGTGAAGAGTGGAACAATGTTGGTCCCACTGGA 3019
 QY 369 -----AAA--GACCTCTAGGTCCAC--CTCATTTGCAAGTATCTCCCAA-- 410
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 QY 411 AA-----TTGTAGAGAT-TTCT--TCAG-----ATA--TCT--CCATTAT 444
 DB 3072 AAGGAGGCTGCACAGCTTGT-GA-ATGTTCTCATCTGGTAAATAATTTGACCCA--AA- 3126
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 DB 3177 AATGTGCACCAATACCTGGGCAAGATTAACCA--CTGTTGTAAGGC-TTGTAAAC 3232
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 DB 3233 TGACGACAGTGGGATCTTGGATTTCCAAATGCAATGTAATAACAGCCAACTGCACTGT 3292
 QY 573 CACCC-----GG-----GA--GCAGTC-AGG-----GG-ACTA----- 596
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 DB 3353 CG-CTGCAATCTCTGTGACTGTCTCTCCCTGGGACAGATGCCACACCTGTGATTGGA 3411
 QY 622 GCC-----GGCCCGTGTG--AC--GG-AGAGTA-----AAGGTCACTGTG-CA 658
 DB 3412 GACTAAATAATGCTCTGTAGTATCAAACTGGGAGTGCACCTGTGAAGTGAATGGA 3471
 QY 659 A--CTATCCAC-----CA-----T--ACATF-----TCAGAAGCCAG-- 687
 DB 3472 AGGC-ATCCACTGTGACAGATGCGGCTGCGCAAAATTCGGACTC-GATGCCAAGATCCA 3529
 QY 688 --GG-TACAG--G--TG--TC-----CCC-GTG-----GGA-CAAAAGG-- 715
 DB 3530 CTTGGCTGCACAGCTCTATTGCTTCGGCACTACTACCCAGTGTCTGAAGCAAAAGGA 3589
 QY 716 -----GGACACTGCACTG--TGAAGCTCAGCAG-----T-CCCC-- 748
 DB 3590 CTGATCCGAC-GTG--GGTGACTCTGAAGGCTGAGCAGACCAATCTACCCCTGTAGATG 3647
 QY 749 -----CAGCA--GA-----AT-----TCCAG--TGGT----- 766
 DB 3648 AGGCTCTGCAGCACACGACCAAGGCAATGTTTTCACATCCAGATTTGTGCC 3707

767 ACAAG-----GAGCAGAAAAG-----ACT-----GA-----787
3708 ACATGGACCTGATGAGAGAGATCTCCATTTGGAACTTTTATTGGAACTTCCAGAAC 3767
788 ---TTGAGGAAAGAA-----A---GGGG-----TG-AA-----809
3768 AATTGAGGAAAGAGTTGATGGCCTATGGGGGCAAACTCAAGTATGCAATCTATTTCG 3827
810 AG--T--GGA--AAACAG-----ACCT--T--TCCTC-----TCA-----A 835
3828 AGCTCGGAGAGAACAGTTTCTCTACATATAATCTCCCTCAAGTGATCATTCGAGGTGGG 3887
836 -A---ACTCAT-CT-----TCTTCA-----ATG-----TC-TCTGA-----A 861
3888 CACCTACTCATGCTAGAAATATCGTCAGGCATATGGCTCTCTCTGATGGCCAAATGA 3947
862 C-----ATGAC-----TATGG-----872
3948 CAAGGCATGAATTGAATGACAGAGAAAGATGGAATATTTGGGGATGATCCTCGAG 4007
873 ---GAACT---AC-----ACTTGGCTG-----888
4008 TCCATAGACTGTGACCCGAGAGACTT-CTTGGATATATATATATGATTAATCAATTA 4066
889 ---GC--CT-----C-CAA-----CA-----898
4067 CTTATCAAGCTACTTATGGAATTTTCATGCGACAAAGCAGGATTTCTGAAATCTCAATG 4126
899 ---AGCTG-----GGCC-----ACACCAATG-----CCAGC-----921
4127 GAGGTAGCTGAACAAGGAGGTGGACACAAATGACTCTCTCCAGCTGACTTGTGATGAAAA 4186
922 ---AT-----CAT-GCTATT-TGG-----TCC-----AGGC-----GGCG-----T 947
4187 TGTGATTGCTCCCTGGCTTATCTGGCTCTCTCTGAGGCAATGCTTGGCGGATTTTAT 4246
948 C-A---GGC-----AGGT-----GAGCAAC-----GGCAC-----968
4247 CGACTGCGTTCTCAACAGGTGGCGGACCCCTGGACCAACCTGGGCACCTGTGTTCCA 4306
969 -GTGAGG--A-GG-----GCAAGGTGCGT-----CTG-----992
4307 TGTCAATGTAATGGACAGAGAGCTGTGTGACCTGAAACATGATGCGAGAAATGCT 4366
993 ---GCTG-----GCTG-----C-----CTCTT-----CT--G-----GTC 1011
4367 CAACATCACACTGCTGGTGAATCTTCTGAAACGATGTGCTCTTGGATACTATGGAATTGTC 4426
1012 ---TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030
4427 AAGGGATTGCCAATGACTGTGAGCAATGTGCTGCTGCTCTGATTTCTTCCAGTAACAT 4486
1031 TT 1032
4487 TT 4488

RESULT 15
US-09-562-702A-7
; Sequence 7, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenko, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198

; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 9419
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(9264)
US-09-562-702A-7

Query Match 43.0%; Score 445.5; DB 4; Length 9419;
Best Local Similarity 38.1%; Pred. No. 8.4e+02;
Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;
QY 1 ATGAAAAACCAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36
Db 2075 ATGG-AAGCATTCAGCAGCTGTAGAAGTGTGTCAAGTCCACCCAGCGGTATACTGGCTCC 2133
QY 37 TCTTGGGGCAATCTT-----CAC-GG-----GGC-----TGGC-- 62
Db 2134 TCTTGTG-AATCTTGTGGCTAGGCAAGCGGAGTTAAAGCGCACTATTTTGTGGCAT 2192
QY 63 -----TGCT-----CTGT-----GTCTCT-----T- 77
Db 2193 CTGTGAGCCATGTCAAGTCTTGGTTCATGCGGAGTCTCTGTGATGACGTCCTGGAGAATG 2252
QY 78 CC-----AAGGA-----GT-GCCC-----GTG-----C-- 94
Db 2253 CCTGAACCTGTAAAGGATCACACAGGTGGCCCAATTTGTGATAAATGTCTTCTCGTTCCTA 2312
QY 95 --GC-AGC-----GG-----AGA-TGCCA-----CCT-----T 113
Db 2313 TGGCGAGCTACTAAAGAACTCTGAAGACTGTCAACCTGTGCTGCTCCACTCAATAT 2372
QY 114 CC---CCAA-----AGC-----TA-----TGGA---CAAC-GTGA 136
Db 2373 CCCATCCAAATAACTTTAGCCCAACGTCGCAATTTAGACGGAGTCTTGGATTGATCTGTGA 2432
QY 137 -----CGGTCCGG-----CAGG-----GGAGA-----GC-----158
Db 2433 TGGATGCCCTGTGCGGTACACAGGACACGCTGTGAGAGGTGTGCAAGGCTATTTTGG 2492
QY 159 C-ACCCTC-----AGG---TG---CA---CTAT---TGACAAACGGG---187
Db 2493 ACAACCCCTCTGTACTGAGGATCAATGTCAGCCATGCCAATGCAATGCAATGCACTTGACTT 2552
QY 188 -T-CA-CCC-GG-----GTG---GC-----CTGGC-----TAAACC--G--C 213
Db 2553 CTCCTATCCCTGGCAGCTGTGACAGCTTGTCTGGCTCTCTGTGATATGTAACACAGGTAC 2612
QY 214 AGCA--CC---ATC-----CTCTATGCTG--GGA-AT-----GACA---AG-TGGTGC--249
Db 2613 AACAGCCGGTA-CTGTGAGCTCTGTCTGATGGATATTTTGGAGATGAGTGTGATGCA 2671
QY 250 -----CTG-GATCC---TGGC-----GTGG-TCCT--TCTGA-----GCAACACCC 283
Db 2672 AGAATGTGAGCCCTGTCTGTATGCGGTGGCTCTTCTCTGAGGTTTGCACAGTC 2731
QY 284 AAAC--G-CAGT--ACAGCATGAGATCCAGAACGT-----G-GATGTG---TAT 324
Db 2732 AAACCTGGACAGTGTGAGTGCA--GAG--CC--AACGTTCCAGGTCAGAGATGTGCAAAAT 2785
QY 325 GACGA---GGGCCCT-----TACA-----CCTGC-----345
Db 2786 G-CAAGGCTGGGACCTTTGGCCTTACAAATCAGCAAGGGGTGTGTTCCCTGCAACTGCAAT 2844
QY 346 -----TCG---GTGCAGACA---GACAA-----CCACCC---368
Db 2845 TCTTTTGGGTCTAAGTCAATTCGACTGTGAAGAGATGGACATGTTGTTGGTCCCACTGGA 2904

QY 369 -----AAA-----GACCTTAGGTCCAC-CTCATTGTGCAAGTATCTCCCA- 410
Db 2905 GTACAGGAGAAATGTGACCGCT-GTCCCAACGGCT-ATT-T-CAA-----CTTCCAAAG 2956
QY 411 AA-----TTGTAGAGAT-TTCT-T-CAG-----ATA-TCT-----CCATTAAAT 444
Db 2957 AAGGAGGTCACAGCTTGT-GA-ATGTTCTCATCTGGGTAAATATGTGACCCA-AA- 3011
QY 445 GA-AGGAAACAAT--ATTAGCTCAGCTG-ATAGCAACTGGTAGACCA--G-CTT- 495
Db 3012 GACTGGG--CGATGCATTTGCC-CACC--CAATA-CCATTGG-AG--AGAAATGTTCTA 3061
QY 496 ACGGT-----TACTTGAGACACATCTCTCCCAAGC-GGTT-----GGCTTTCTGTAG 542
Db 3062 AATGTGCACCAATACCTGGGGCCACAGCAATACCA--CTGGTTGTAGGC-TTGTAC 3117
QY 543 TGAAG-AC-----GAATACCTGG-----AAATTCAGS-----GCA-----T 572
Db 3118 TGCAGCACAGTGGGATCTTTGGATTTCCAAATGCAATGTAATACAGGCCAATGCAACTGT 3177
QY 573 CAGCC-----GG-----GA-GCAGTC-AGG-----GG-ACTA----- 596
Db 3178 CATCCAAAATCTCTGGTGCAAAATGTACAGAGTGCAGTCGAGGTCACTGGAATACCCT 3237
QY 597 CGAGTGCA-----GTG-----CTTC-----CA-ATG-----AC-GTG----- 621
Db 3238 CG-CTGCAATCTCTGTGACTGCTCTCTCCCTGGGACAGATGCCACCACTGTGATTCAGA 3296
QY 622 GCC-----GGCCCGTGGT-----AC--GG-AGAGTA-----AAGTCCAGGT-GA 658
Db 3297 GACTAAAAAATGCTCTGTAGTATGATCAAACTGGGCGAGTGCACCTTTGAAGGTGAATGGA 3356
QY 659 A-CTATCCAC-----CA-----T-----ACATT-----TCAGAGCCAG- 687
Db 3357 AGGC-ATCCACTGTGACAGATGCGCGCTGGCAATTCGGACTC-GATGCCAAGATCCA 3414
QY 688 -----GG-TACAG-----G-----TG-TC-----CCC-GTG-----GGA-CAAAAGG- 715
Db 3415 CTGGCTGAGCAGCTCTATTGCTTGGCAGTACTACCCAGTCTCTGGAAGCAAAAGGA 3474
QY 716 -----GGACACTGCAAGT-----TGAAGCTCAGCAG-----T-CCCT----- 748
Db 3475 CTGATCCGGAC-GTG-GGTGACTCTGAAGGTGAGCAGACCAATCTACCCCTGTAGATG 3532
QY 749 -----CAGCA--GA-----AT-----TCCAG-----TGCT----- 766
Db 3533 AGGCTCTGCAGCACGACCAACCAAGGCAATGTTTTTCAACATCCAGAGATTTGTCGCC 3592
QY 767 ACAAG-----GATGACAAAAG-----A-GGGG-----TG-AA----- 809
Db 3593 ACATGGACCTGATGAGAGAAGATCTCCATTTGGAACCTTTTATTGGAACCTTCCAGAAC 3652
QY 788 ----TTGAAGAAAGAA-----A-GGGG-----TG-AA----- 809
Db 3653 AATTGGAAGAAAGAAAGTTGATGGCTATGGGGGCAAACTCAAGTATGCAATCTATTTCG 3712
QY 810 AG--T--GGA-AAAAG-----ACCT-T--TCCTC-----TCA-----A 835
Db 3713 AGGCTCGGGAAGAAACAGGTTTCTCATATATATCTCAAGTATCATTCGAGGTGGGA 3772
QY 836 A--A--ACTCAT-CT-----TCTTCA-----ATG-----TC-TCTGA-----A 861
Db 3773 CACTCTACTGCTAGAAATTTCTGTCAGGCATATGGCTCTCTGATTTGGCCAAATGA 3832
QY 862 C-----ATGAC-----TATGG----- 872
Db 3833 CAAGGCATGAAATGAAATGACAGAGAAAGAAATATATATATATGGGAGATGATCTCGAG 3892
QY 873 -----GAACT--AC-----ACTTGGCGTG----- 888
Db 3893 TCCATAGAACTGTGACCCGAGAGACTTT-CTTGGATATATATATATATATATTCATTACATT 3951

QY 889 -----GC-CT-----C-CAA-----CA----- 898
Db 3952 CTTATCAAGCTACTTATGGAATTTTCATGCGACAAAGCAGGATTTCTGAAATCTCAATG 4011
QY 899 -----AGCTG-----GGCC-----ACACCAATG-----CCAGC----- 921
Db 4012 GAGGTAGCTGAACAAGGACGTGGAAACAACAATGACTCTCTCCAGCTGACTTTGATTGAAAAA 4071
QY 922 -----AT-----CAT-GCTATT-TGG-----TCC-----AGGC-----GCCG-----T 947
Db 4072 TGTGATTTCCCTCGGCTATTTCTGAGCTCTCTGAGGCATGCTTGCCTGGGATTTAT 4131
QY 948 C-A--GCG-----AGGT-----GAGCAAC-----GGCAC----- 968
Db 4132 CGACTGCGTTCTCAACAGGTGGCGGCACCCCTGGACCAACCCCTGGCACCTGTGTCCA 4191
QY 969 -GTCAGG--A-GG-----GCAGGCTGGT-----CTG----- 992
Db 4192 TGTCAATGTAATGGACACAGCAGCCTGTGTGACCTTGAAACATCGATATGCCAGATTTGT 4251
QY 993 -----GCTG-----CTG-----C-----CTCTT-----CT-----GTC 1011
Db 4252 CAACATCACTGCTGGTGACTTCTGTGAACGATGCTCTTGGATCTATGGAATTTGTC 4311
QY 1012 -----TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030
Db 4312 AAGGGATTGCCAAATGACTGTGCAAGATGTGCTGCTGCTGCTGATTTCTTCCAGTAAAT 4371
QY 1031 TT 1032
Db 4372 TT 4373

RESULT 16
US-09-562-702A-3
; Sequence 3, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 9420
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(9267)
US-09-562-702A-3

Query Match 43.0%; Score 445.5; DB 4; Length 9420;
Best local Similarity 38.1%; Pred. No. 8.4e+02;
Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;

QY 1 ATGAAACCAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36
Db 2075 ATGG-AAGCATTCAGCAGCTGTAGAGTGTGTCAGTGTGCCACCGAGGTATATGSGTCC 2133
QY 37 TCTTGGCAATCTTT-----CAC-GG-----GGC-----TGCG-- 62
Db 2134 TCTTGTG-ATCTGTGGCTAGGCACAGCGGAGTTTAACGGCACTATTTTTGTGGCAT 2192

2608 ACAACCCCTCTCTACTCTGGAGATCATGTGTCAGCCATGCCAATGCATGCAACCTTGGATT 2666

188 -T-CA-COC-GG-----GTG--GC-----CTGGC-----TTAAACC--G-C- 213

2668 CTCATCTCCCTGGCAGCTGTGACAGCTTGTCCTGGCTCCTGTCTGATATGTATAACCAAGTAC 2727

214 AGCA--CC--ATC-----CTCTATGCTG--GGA-AT-----GACA--AG-TGGTGC-- 249

2728 AACAGCCCGGTA-CTGTGAGCTCTGTGCTGATGATGATATTTTGGAGATGCAGTGTATCGGA 2786

250 ----CTG-GATCC---TCGC-----GTGG-TCCT--TCTGA-----GCAACACCC 283

2787 AGAACTGTGACGCCTGTGCTGTAAATGCCGGTGGCTCTTCTCTGAGGTTTGGCCACAGTC 2846

284 AAAC--G-CAGT---ACAGCATGAGATCCAGAACGT-----G-GATGTG---TAT 324

2847 AAACTGGACAGTGTGAGTGCA--GAG--CC--AAGCTTCAGGTCGAGATGTGACAAAT 2900

325 GACGA--GGGCCCT--TACA-----CCTGC-----CCTGC----- 345

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3020 GTCACAGGAGAAATGTACCGCT-GTGGCCACGGCT-ATT-T-CAA---CTTCCAAG 3071

411 AA-----TTGTAGAGAT--TTCT--TCAG--ATA--TCT--CCATTAAT 444

3072 AAGGAGGCTGCACAGCTTGT-GA-ATGTTCTCATCTGGGTAAATAATGTGACCCA--AA- 3126

445 GA-AGGGAACAT-ATTAGCCTCACCTGC-ATAGCAACTGGTAGACACAGA--G-CCT- 495

3127 GATGGG--CGATGATTTGCC-CACC--CAATA-CCAATTGG-AG--AGAAATGTTCTA 3176

496 ACGGT-----TACTTGGAGACACATCTCTCCAAAGC-GGTT----GGCTTTGTGAG 542

3177 AATGTGCCCCCAATACCTGGGGCCACAGCATTAACA--CTGGTTGTGAAGC--TTGTAAAC 3232

543 TGAAG-AC--GAATACTTGG-----AAATTCAGG-----GCA--T 572

3233 TGACGACACATGGGATTCCTGGATTCATATGCANATGTAATACAGGCCCATGCAACTGT 3282

573 CACCC-----GG-----GA-GCAGTC-AGG-----GG-ACFA----- 596

3293 CATCCAAAATTCCTGGTGCAAAATGTACAGAGTGCAGTGCAGGTCACTGGAACCTACCCCT 3352

597 CGAGTGGA-----GTG-----CCTC-----CA-ATG-----AC-GTG----- 621

3353 CG-CTGCAATCTCTGTGACTGCTCTCTCCCTGGACAGATGCCAACACTGTGATTCAGA 3411

622 GCC-----GGGCCCGTGGT-----AC--GG-AGAGTA-----AAGGTCAACCGT-GA 658

3412 GACTTAAAAATGCTCTCTGTAGTATCAAACTGGSCAGTCGACCTTGTAAAGTGAATGTGGA 3471

659 A--CTATPCAC-----CA-----T--ACATTT-----TCAGAGCCAG----- 687

3472 AGGC-ATCCACTGTGCAGATGCCGGCCTGGCAAAATTCGGACTC-GATGCCAAGAAATCCA 3522

688 --GG-TACAG--G---TG--TC-----CCC-GTG-----GGA-CAAAAGG- 715

3530 CTGGCTGCGAGAGCTGCTATTGTCTTCGGCACTACTACCAGTGTCTGNAGCAAAAGGA 3588

716 -----GGAACACTCGAGTG-----TGAAGCCTCAGCAG-----T-CCCC----- 748

3590 CTGATCCGGAC-GTG--GGTGACTCTGAAGGCTGAGCAGACCAATTCACCCCTGGTAGATG 3647

749 ---CHAGA--GA-----AT-----TCCAG-----TGGT----- 766

3648 AGGCTCTGCAGACACAGCACCAAGGGCATTTGTTTTTCAACATCCAGAGATGTTGCCCT 3700

767 ACAAG-----GATGACAAAG-----ACT-----GA-- 787
Db ACATGGACCTGATGAGAAAGATCTCCATTTGGAAACCTTTTATTGGAACTTCGAGAA 3767
788 ---TTGAGGAAAGAA---A---GGGG-----TG-AA-- 809
Db AATTGAGGAAAGAAAGTTGATGGCTATGGGGCAAACTCAAGTATGCAATCTATTTCG 3827
810 AG--T--GGA--AAACAG-----ACCT-T--TCCTC-----TCA-- 835
Db AGGCTCGGAGAAACAGGTTTCTACATATAATCTCTCAAGTATGATCATTCGAGGTGGG 3887
836 A---ACTCAT-CT-----TCATCA---ATG---TC-TCCTG---A 861
Db CACCTACTCATGCTAGAAATATTCGTCAGGCAATATGGCTCTCTGATTTGGCCAAATGA 3947
862 C-----ATGAC-----TATGG----- 872
Db CAAGGCATGAATTCGAATGACAGAGAAAGATGGAATATTTATGGGATGATCCTCGAG 4007
873 ---GAACT--AC-----ACTTGGGTG----- 888
Db TCCATAGAACTGTGACCCGAGAGACTT-CTTGATATATATATATATATATCAATTCAT 4066
889 ---GC--CT-----C-CAA-----CA-- 898
Db CTTATCAAGTACTATTGGAATTTTCATGCGACAAAGAGGATTTCTGAAATCTCAATG 4126
899 ---AGCTG-----GGCC---ACACCAATG----- 921
Db GAGGTAGCTGAACAGGAGCTGGAACAACATGACTCTCTCCAGCTGACTTGTGATTGAAAA 4186
922 ---AT-----CAT--GCTATT-TGG---TCC---AGGC-----GCCG--T 947
Db TGTGATTTGCTCCCTGGGCTATTCTGGCTCTCTCTGTGAGGCAATGCTTGGCCGGATT 4246
948 C-A--GCG-----AGGT-----GAGCAAC---GGCAC----- 968
Db CCACTGCTTCTCAACAGGTGGCGCCACCCCTGACCAACCCCTGGGCACTGTGTCCA 4306
969 -GTCGAGG--A--GG-----GCAGGTGCGT-----CTG----- 992
Db TGTCAATGTAATGGACAGAGCGCTGTGTGACCCCTGAAACATGATATGCGAGAAATGT 4366
993 ---GCTG-----CTG--C-----CTCTT-----CT--G-----GTC 1011
Db CAACATCACACTGCTGGTGAATCTCTGTGAACGATGTGCTCTTGGATATGGAATTTGTC 4426
1012 ---TTGC-----A-----CCTGC-----TTCT--CA-- 1030
Db AAGGATGCCAAATGACTGTGAGCAATGTGCTGCCCTCTGATTTCTTCCAGTAACAT 4486
1031 TT 1032
Db 4487 TT 4488

RESULT 18

US-09-561-709B-8
; Sequence 8, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champilaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949

; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 9534

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(9382)
US-09-561-709B-8

Query Match 43.0%; Score 445.5; DB 4; Length 9534;
Best Local Similarity 38.1%; Pred. No. 8.6e+02;
Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;

QY 1 ATGAAAACCAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36
Db 2190 ATGG-AAGCAATTGCAGCAGCTGTAGAAGTGTGTCAAGTGTGCCCCACCCAGGATATCTGGCTCC 2248
QY 37 TCTTGGGCAATCTT-----CAC-GG-----GGC-----TGGC-- 62
Db 2249 TCTTGTG-AATCTTTTGGCTAGGCACAGCGAGTTAAAGGCACTATTTTGTGGCAT 2307
QY 63 -----TGCT-----CTGT-----GTCTCT-----T- 77
Db 2308 CTGTGAGCCATGTCAGTCTTTTGGTCATGCGGAGTCTGTGATGACGTCACTGGAGATG 2367
QY 78 CC-----AAGCA-----GT-GCCC-----GTG-----C-- 94
Db 2368 CCGTGAATGTAAAGATCACACAGGTGGCCCATATTGTGATAAATGTTCTTCTGGTTTCTA 2427
QY 95 --GC-AGC-----GG-----AGA-TGCCA-----CCT-----T 113
Db 2428 TGGCGAGCTACTAAAGAACTCTGAAGACTGTCAACCTGTGCTGCTCCACTCAATAT 2487
QY 114 CC-----CCAA-----AGC-----TA-----TGGA--CAAC-GTGA 136
Db 2488 CCAATCAATTAATTTAGCCCAACGTGCACTTTAGACGGAGTCTTGTGATTGATCTGTGA 2547
QY 137 -----CGTCCGG-----CAGG-----GGAGA-----GC----- 158
Db 2548 TGGATGCCCTGTGGGTACACAGGACACCGCTGTGAGAGGTGTGCAAGGCTATTTTGG 2607
QY 159 -C-ACCCTC-----AGG--TG-----CA--CTAT-----TGACAAACCGGG--- 187
Db 2608 ACAACCCCTCTGTACCTGGAGGATCAATGTCAGCCATGCAATGCAATGCAATGCAAT 2667
QY 188 -T-CA-CCC-GG-----GTG--GC-----CTGGC-----TAAACC--G--C 213
Db 2668 CTCATCTCTGGCAGCTGTGACAGCTTGTCTGGCTCTGTCTGATATGTAAACAGGTAC 2727
QY 214 AGCA--CC--ATC-----CTCTATGCTG--GGA-AT-----GACA-----AG-TGGTGC-- 249
Db 2728 AACAGGCCGGA-CTGTGAGCTCTGTGTGATGATATTTTGGAGATGAGTTGATGGA 2786
QY 250 -----CTG-GATCC---TGGC-----GTGG--TCCT--TCTGA-----GCAACACCC 283
Db 2787 AGAATGTCAGCCCTGTGCTGTAATGCGGTGGCTCTTTCTCTGAGGTTTGGCAGCTC 2846
QY 284 AAAC--G-CAGT-----ACAGCATCGAGATCCGAACGT-----G-GATGTG---TAT 324
Db 2847 AACTGGACAGTGTGAGTGCA--GAG--CC--AACGTTCAAGGTCAGAGATGTGACAAAT 2900
QY 325 GACGA---GGGCCCT---TACA-----CCTGC----- 345
Db 2901 G-CAAGGCTGGGACCTTTGGCCTACAATCAGCAAGGGGCTGTGTTCCCTGCAACTGCAAT 2959
QY 346 -----TCG---GTGCAGACA--GACAA-----CCACCC-- 368
Db 2960 TCTTTTGGGTCTAAGTCAATGCACTGTGAAGAGAGTGGCAATGTTGGTGGCAACCTGGA 3019

369 QY -----AAA-----GACCTCTAGGCTCCAC--CTCATGTGCAAGTATCTCCCAA- 410
3020 Db GTACAGGGAAGAAATGTGACCGCT-GTGCCCAAGGCT-ATT-T-CAA-----CTTCCAAG 3071
411 QY -----TTCTAGAGAT-TTCT--TCAG-----ATA--TCT--CCATTAAT 444
3072 Db AAGAGGCTGCACAGCTTGT-GA-ATGTTCTCACTGGGTAAATATGTGACCCA-AA- 3126
445 QY GA-AGGGAACAAT--ATTAGCTTCACCTGC-ATAGCAACTGTGAGACCA--G-CCT- 495
3127 Db GACTGGG--CGATGCAATTGGC-CACC--CAATA-CCATTGG-AG--AGAAATGTCTTA 3176
496 QY -----TACTTGAGACACATCTCTCCAAAGC-GGTT-----GGCTTTGTGAG 542
3177 Db AATGTGCACCAATATCTGGGGCCACAGCAATTACCA--CTGGTTGAAGGC-TTGTAAAC 3232
543 QY TGAAG-AC--GAATACTTGG-----AAATTCAGG-----GCA-----T 572
3233 Db TGACGACAGTGGATCTTGGATTCCCAATGCAATGTAAATACAGGCCCAATGCAACTGT 3292
573 QY CACCC-----GG-----GA-GCAGTC-AGG-----GG-ACTA----- 596
3293 Db CATCCAAATCTCTGTGCAAAATGTACAGAGTGCAGTGCAGGTCACTGGAATACCCCT 3352
597 QY CGAGTGCA-----GTG-----CCTC-----CA-NTG-----AC-GTG----- 621
3353 Db CG-CTGCAATCTGTGACTGTCTTCTCCCTCGGACAGATGCCACACCTGTGATTCAGA 3411
622 QY GCC-----GGCCCGCTGGT-----AC--GG-AGAGTA-----AAGGTCACTGT-GA 658
3412 Db GACTAAAAATGCTCTGTGTAGTGTATCAATCAATGGGAGTGCACCTGTAAAGGTGGA 3471
659 QY A--CTATCCAC-----CA-----T--ACATT-----TCAGAACCAAG----- 687
3472 Db AGGC-ATCCACTGTGACAGATGCGCGCTGCGCAAAATTCGGACTC-GATGCCAAAGATCCA 3529
688 QY --GG-TACAG--G--TG--TC-----CCC-GTG-----GGA-CAAAAGG-- 715
3530 Db CTGGCTGACAGCTGCTATTGTTCTGGCACTACTACCCAGTCTCTGAGCAAAAGGA 3589
716 QY -----GGACACTGCAGTG-----TGAAGCTCAGCAG-----T-CCCT----- 748
3590 Db CTGATCCGAC-GTG-GTGACTCTGAAGGCTGAGCAGACCATCTTACCCCTGTAGATG 3647
749 QY -----CAGCA--GA-----AT-----TCCAG-----TGGT----- 766
3648 Db AGGCTCTGCAGCACACGACCAACCAAGGCAATGTTTTCACATCCAGAGATGTTGCC 3707
767 QY ACAAG-----GATGACAAAAG-----A--GGGG-----TG-AA----- 809
3768 Db AATTGGAAGAAAGATGTGATGGCTATGGGGCAAACTCAAGTATGCAATCTATTTCG 3827
810 QY AG--T--GGA--AAACAG-----ACCT-T--TCCTC-----TCA-----A 835
3828 Db AGGCTCGGGAAGAAACAGGTTTCTCATATAATATCTCAAGTATATTCGAGGTGGA 3887
836 QY A--A--ACTCAT-CT-----TCTTCA-----ATG-----TC-TCTGA-----A 861
3888 Db CACTCTACTCATGATGATTAATTCGTGAGCATATGCTGCTCTCTGATGGGCAATTTGA 3947
862 QY C-----ATGAC-----TATGG----- 872
3948 Db CAAGCATGAAATGAAATGACAGAGAAGAAATGGAATATATTATGGGATGATCTCTCGAG 4007
873 QY -----GAACT--AC-----ACTTGGCTG----- 888
4008 Db TCCATAGAACTGTGACCGAGAGAACTT-CTTGGATATATATGATATTCATTAATTT 4066

889 QY -----GC-CT-----C-CAA-----CA----- 898
4067 Db CTTATCAAGCTACTTATGGAAATTTATGCAAAAGCAGGATTTCTGAATCTCAATG 4126
899 QY -----AGCTG-----GGCC-----ACACCAATG-----CCAGC----- 921
4127 Db GAGGTAGCTGAACAAGGAGCGTGGAAACAACATGACTCTCCAGCTGACTTGTGATTGAAAA 4186
922 QY -----AT-----CAT--GCTATT-TGG-----TCC-----AGGC-----GCGC-----T 947
4187 Db TGTGATGTTCCCTGGCTATTCTGCTCTCTCTGTGAGGCAATGCTTGCCTGGGATTTAT 4246
948 QY C-A--GCG-----AGGT-----CAGCAAC-----GGCAC----- 968
4247 Db CGACTGGCTTCTCAACAGGTGGCGCCGACCCCTGGACCAACCCCTGGCAGCTGTGTCCA 4306
969 QY -GTGAGG--A-GG-----GCAGCTGGCT-----CTG----- 992
4307 Db TGTCAATGTAATGAGACACAGCAGCCTGTGTGACCCCTGAAACATCGATATGCCAGAAATGT 4366
993 QY -----GCTG-----CTG-----C-----CTCTT-----CT--G-----GTC 1011
4367 Db CAACATCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4426
1012 QY -----TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030
4427 Db AAGGATTCGCAATGACTGTCAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4486
1031 QY TT 1032
4487 Db TT 4488

RESULT 19
US-09-562-702A-1
; Sequence 1, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9535
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(9379)
; NAME/KEY: sig_peptide
; LOCATION: (50)..(115)
US-09-562-702A-1

Query Match 43.0%; Score 445.5; DB 4; Length 9535;
Best Local Similarity 38.1%; Pred. No. 8.6e+02;
Matches 892; Conservative 0; Mismatches 97; Indels 1353; Gaps 253;
QY 1 ATGAAACACCAT--C--CAGC--CAAAA-----A-TGCACA-----ATTCT--AT-C 36
Db 2190 ATGG-AAGCATTCAGCAGCTGTAGAGTGTGTCAGTCCCAAGGATATATGCTCC 2248
QY 37 TCTTGGGCAATCTT-----CAC-GG-----GGC-----TGCG-- 62

QY 1012 -----TTGC-----A-----CCTGC-----TTCT--CA-----AAT 1030
 Db 4427 AAGGATGCGCAATGACTGTGACAAATGTGCGCTCGCCCTGTGATTTCTTCCAGTAACAAT 4486
 QY 1031 TT 1032
 Db 4487 TT 4488

RESULT 20

US-08-457-273B-41/c
 ; Sequence 41, Application US/08457273B
 ; Patent No. 5849995
 ; GENERAL INFORMATION:
 ; APPLICANT: Hayden, Michael
 ; APPLICANT: Lin, Biaoyang
 ; APPLICANT: Nasir, Jamal
 ; TITLE OF INVENTION: Mouse Model for Huntington's Disease and
 ; TITLE OF INVENTION: Related DNA Sequences
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Virginia Bennett
 ; STREET: PO Box 37428
 ; CITY: Raleigh
 ; STATE: No. 5849995th Carolina
 ; COUNTRY: US
 ; ZIP: 27627
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/457,273B
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bennett, Virginia C.
 ; REGISTRATION NUMBER: 37,092
 ; REFERENCE/DOCKET NUMBER: 3477-85A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-854-1400
 ; TELEFAX: 919-854-1401
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10348 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; US-08-457-273B-41

Query Match 43.0%; Score 444.6; DB 2; Length 10348;
 Best Local Similarity 39.1%; Pred. No. 1e+03;
 Matches 875; Conservative 0; Mismatches 97; Indels 1264; Gaps 247;
 QY 2 TGAAG-----ACCA-----TCCAGCCAA-----AAATGCAC-----AA- 29
 Db 7715 TCAAACTGAGTACGACTGTGTCAGCCTAGTGTGTGATGCGGTAGTGAATCCTTTAAG 7656
 QY 30 --TTCTATCTTTGG-GCAATCTTCAGGGG--CT---G---GCTG-----C 65
 Db 7655 ACTTCCTTTTCTCGAGGAA-CTCCACGGGATCTCAGGGAATGCTGTGCCAAAATCCCC 7597
 QY 66 TC-----T--GTGTC--T-----CTTCCA--AGCAGTG-----CCCGTG----- 93
 Db 7596 TCCCGTTTGGGTACCACTCCAGCTTCCACACAGTGGGGGACACGTGTGTAGCTGTT 7537
 QY 94 -C-----GCA-GCG-----GA-GATGCCACCTTCCCAAAGCTATGGACAAGTG 135
 Db 7536 GACAAAGGGCAGCGGGCCAGGCTGATGATG--ATGTT--CCTGAGCAATGG-----CGTG 7485

QY 136 ----ACGTCCGCG-----AGG-----G-----GGAGAG 155
 Db 7484 AGAAAG--CCGCGACGCGCTATTCCTTTTATGACCCAGGCAACACCGACTGCAGAG 7427
 QY 156 -----C-GCCACC--CT--CAGG-TGC-----ACT-----ATT----- 177
 Db 7426 ACTCCACCATTTCTGCGCACCATCTCACAGGCTGCAGTGATATATCTAGGATTCGTGTGT 7367
 QY 178 ---GA-CAA-----CGGGT-CACC-CG--GGTGGC----- 200
 Db 7366 TTGGATCTACTTCCTCC--TCCTCTCGTGAATGCTTTTGGGTAATTTGCTCTCTTT 7310
 QY 201 CTGG-CTA-AA-----CC--GCAGCAC--CA---TCCTCTATGCTGGGAA-TG-AC 240
 Db 7309 CTGGACTAAGAGCTGCTCTCCAGGCTGCACCTCAACGGGCTCCAGAT--GAAGTGAC 7252
 QY 241 A-AGT-----GGTGC--C-TGGATC-----CTCGGTGG-----TC-CTTCTGA 274
 Db 7251 ACAGTAGATGAGGAGCAGCGCTGGGTCAAAATC-TGTGGAGGAGACCACTCCAG 7193
 QY 275 G--CA--A--CA-CCCA--AAC-GCAGTACA-----GCATCGAGATCCAGA--A 311
 Db 7192 GCCAGGAGCTCAGGGCCAGGAGCAGAGTCCAGCCCTGCTCGAGATCCAGACTCA 7133
 QY 312 -CGTGGATGTG-----T--AT-----GACGAGGGCC-----C--- 335
 Db 7132 GCG-GGATCTGCTCATGGATCAAAATGCCAGGAC-AGGGCTCAAGGTTGCCACCAAG 7075
 QY 336 -TT-ACA-----CCTGCTC-----GGTGA--GAC-----AGAC 360
 Db 7074 TTTCACAATGTCTCTCTTTCTCAGGAGGAAGTGCAAATGACTGGCAGTTTGGAGAC 7015
 QY 361 AACCAACCCAAAG-ACCT--CTAGGCTCC-----A-----C-----CTCAT--TGTG 396
 Db 7014 CACCACC---AGTA-CTGTGCCAGGGCCCGGCGCAGAGTGGCGAGGAGTATATACAGTG 6959
 QY 397 CAAGTATCTCCAAAATTGAGAGATTTTCTTCAGATATCTCCATTA----- 442
 Db 6958 C-AGCATC-CCCAA-----ACAGA--TCATTCACTTGTCTCCAGTAGCCCGGCTCT 6909
 QY 443 --ATGAAG-----GGAACA-AT-AT--TAGC-----CTCAGCTGA--TAG--- 475
 Db 6908 GCAGGAGCTCGGGCTGGAAGACATGATGACAGCAGGAGGAGCT--GCTGCAGGT-GCCG 6852
 QY 476 --CA-ACTGTAGACAGAG--CCT-ACGG-----TT-----ACT-----TGG-- 507
 Db 6851 CTCACAGGG--CCAGAGTCACTCAGGGCTGCTTCAAAGAGGCACTCTTCTGGCC 6796
 QY 508 ---AGACA--CATCTC-TCCC-A-----AAGC--GG--T---TGGCT---TTG---T 539
 Db 6795 ACCAGAAATTTCA-CTCATCCCTAGGCTTAAGCATGAGCTAGCAGGCTTAGGTTGAAT 6737
 QY 540 --GAG-----TGAAGACA--ATA-CTT-----GGAA-----ATTCAGGGA---T- 572
 Db 6736 CCAGTTTCATCATGAAGGC-ATTCTATCTTTCAGCAGGAATCCGATTC--CCAGCTCTG 6680
 QY 573 CAC---CCGGGAGCAGT-CAG-----GGGACT--ACGAG-TG-- 602
 Db 6679 CACTTCC--AGCAGTGCAGATCTGACCTGTGTCCACACACTGGGATTTGACAAGATGA 6623
 QY 603 ----CAGT---G-CC-----TCCAATG--ACGTGGCGCGCCCGT----- 632
 Db 6622 CGTACCAGTCTTTGTCTCGGACTCACTGTCTTCCAGTGACACGTCGCCCATCCCCCTCAGCG 6563
 QY 633 GGT-----AC-----GGAGAG--TAA----- 646
 Db 6562 GGTGGGAAGACTCGAGGAGAGGAGGACTAAGTGAATCTTGTGAGGAGAGAGAAACC 6503
 QY 647 ----AGG-----TC-----A-CCG-----TGAA----- 659
 Db 6502 TGTCCAGAGGAATAGAGCTTTGGTGTCTCTGAGGAGCCCGCTGCTCTGAAGTATT 6443
 QY 660 ----CT---A-----TCCA-----CCA-----TACATTT----- 676

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Db 6442 CCTGATCTGTGAGTCTTCCATTTGCAACTGGCCATCTGCTCTGTAAATTTGCG 6383
QY 677 -CAGAAGC-----CAAGGTAC-AGG-TGTC--CC--CGTG--GGACA 710
Db 6382 CCAGAAGCATTTCTACCGCGACAAAG---CAAGGATGTCACCATCGGACCCAGCACA 6327
QY 711 ---AAAGGG---ACA---CTG-----CAGTGTGAAGC---CTC--A--GC- 740
Db 6326 CGAAAGGGGTGCACAGAAGCCTGTCCACATACAGCGTG-AGCAGCTCCCGACTGGCT 6268
QY 741 -AG-----TCCCTC--AGCA--GAA-----TTC--CAG--TGCT- 766
Db 6267 GAGATGGATCCCTCCAGCACTGAAGATTTTCTTCAGCATGTTGGAGTTGAAGGTT 6208
QY 767 ---ACAA-----GATGA-----CA-----AAA 781
Db 6207 TTCACACAGAGACTGAATTTGCTGGATGAACAGGCGCTGGCAGCAGAGTTCCGATGAAC 6148
QY 782 G--ACTGATTGAAG--GAA--A-----GAAAGG-----G--GT 806
Db 6147 GGCACCTGA-TGAAGTCTGTACTGGAGGCTCGTGGAAAGGCTGATCAGATCTGAATGT 6089
QY 807 GA-----AAGTG-----GAAGT-----GA--AA--AC 819
Db 6088 GATTTACATGAGCCACGTTAAGTGTCTCGGAGTCTGAGGAGTCTTGACAGACATAATCAC 6029
QY 820 ACA-----CCT-TTC-----CTCT-----832
Db 6028 AGAAGAGAAATGAGAGCCCTCTTCGTACTATTCTATTGACATTCCAAGTTGGGTG 5969
QY 833 -CAA--AA-CTCATCTCTTCA--AT-----GT--CT-----CTGAACA 863
Db 5968 CCAAGTCAAGATCTCTCTTCTCCAGACATCTGGGACTAAGTAACCTTTGCTGGACA 5909
QY 864 TGACTAT-----GGG--AACTACACTTGGTGGCTCCA-----895
Db 5908 -GACTGTGTCTTTTCGGGGTCTGCTGCACTT-C-TGCCACACAGCGGTAGTCGGTGTGT 5852
QY 896 ---ACAGCTG--G-----G--CCA-----CACCA-----AT-- 915
Db 5851 TGACAGCAGCAGTATCTACACACAGCAGCAGCAGCGCGGTGGTGGTATCATGG 5792
QY 916 -----GCCAGCA--TCATGCTATTGGTCCAGG-----CGCC--G--TC 948
Db 5791 AACGAGCCCGCAGTTCAAGCT-----GTCCAGGGGTAGAAACTGCCCGCCACAGCCATC 5737
QY 949 A--GCG---AG-----GTGAGCA-----A-----CGGCAC-----G--TCGAGCA 976
Db 5736 ACTGGCGAACAGCCTAGTG-GCAGCTGTGTGATTTCTCCGGAACATTCAGACAGTTGAAGA 5678
QY 977 -G-GG--CAG-----GC---TGC---GT--CTGGC-----TGCTGC- 1000
Db 5677 TGTGGATCAGACATAGCAGTGTGCCCTAGTTCCTGGCAATAGAAAGTATGTTGCTGT 5618
QY 1001 --CT-----CTTCTG--GTCTTGACC--TG-CTTCTCAA-----TT 1031
Db 5617 CACTCATTTCCACCTTCAGCTGTTTGTAAACATGTTCTTAAAGATGTTCTTAAAGATACCAACAGTT 5558
QY 1032 -----TTGA 1035
Db 5557 GTAATAGAAACCTTTGA 5542
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RESULT 21

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US-08-556-419-13/c
; Sequence 13, Application US/08556419C
; Patent No. 6093549
; GENERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Shi-Hua
; APPLICANT: Sharp, Alan
```

```
; APPLICANT: Lanahan, Anthony
; APPLICANT: Worley, Paul
; APPLICANT: Snyder, Solomon
; TITLE OF INVENTION: Huntingtin-associated protein
; FILE REFERENCE: 01107.52271
; CURRENT APPLICATION NUMBER: US/08/556.419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 10348
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-556-419-13
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Query Match 43.0%; Score 444.6; DB 3; Length 10348;
Best Local Similarity 39.1%; Pred. No. 1e+03; 97; Indels 1264; Gaps 247;
Matches 875; Conservative 0; Mismatches 0;

QY 2 TGAAG-----ACCA-----TCCAGCCAA-----AAATGCAC-----AA- 29
Db 7715 TCAACTGAGTACGACTGTCCAGCCTAGTGTGTGATGCGGTAGATGAATCTCTTAAG 7656
QY 30 --TTCATCTCTTGG-GCAATCTTTCACGGGG--CT--G--GCTG-----C 65
Db 7655 ACTTCCTTTTCTGAGGAA-CTCCACGGGATCTCAGGGAATGCTGTGCCAAATCCCC 7597
QY 66 TC-----T--GTGTC--T-----CTTCCA-AGGAGTG-----CCCGTG----- 93
Db 7596 TCCCGGTTGGTGACCATCAAGCTTCCACACAGTGGGGGCACACCTGTGTAGTGT 7537
QY 94 --C-----GCA-GCG-----GA-GATGCCACTTCCCAAGCTATGTGACAACTG 135
Db 7536 GACRAGGGGCGAGCGGGCGGCGAGCTGATGATG-ATGTT--CCTGAGCAATGG---CGTG 7485
QY 136 ---ACGTTCCGGC-----AGS-----G---GGAGAG 155
Db 7484 AGAAACG--CGGCAACGCGGCTATTCTTTATGACCAAGGCCAACACCGACTGCAGAG 7427
QY 156 -----C-GCCACC--CT--CAGG-TGC-----ACT-----ATT----- 177
Db 7426 ACTCCACCATTTCTGCCACCATCTCACAGCTGCAAGTATATCTTAGGATCTGTGTGT 7367
QY 178 ---GA-CAA-----CGGGT--CACC-GG--GGTGGC-----200
Db 7366 TTGGATCTACTTCTCTCC--TCCTCTCGTGTGCTTTTGGGGTATTGTCTCTTT 7310
QY 201 CTGG-CTA-AA-----CC--GCAGAC--CA--TCCTCTATGTGGAA-TG-AC 240
Db 7309 CTGGACTAAGAGCTGTCTCTCCAGCTGCACTGCAACGCGCTCCAGGAT--GAAGTGAC 7252
QY 241 A-AGT-----GGTGC--C-TGGATC-----CTCGCTGG--TC-CTTCTGA 274
Db 7251 ACAGTAGATGAGGAGCAGCGGTGGGTCAAACTC-TGTGGAGAGACCGCTCCAGA 7193
QY 275 G--CA--A-----CA--CCCA--AAC-GCAGTACA-----GCATCGATCCAGA--A 311
Db 7192 GGCAGGAGAGCTGCGAGGCGCAGGCGAGCAGCAGTCCAGCGCTGCTGGAGATCCAGACTCA 7133
QY 312 -CGTGGATGTG-----T---AT-----GACGAGGGCC-----C--- 335
Db 7132 GCG-GGATCTGCTCATGGATCAATGCCAGGAC-AGGGCGCTCAAGGGTTGCCACCGAA 7075
QY 336 -TT-ACA-----CCTGCTC-----GGTGA--GAC-----AGAC 360
Db 7074 TTTCATATGCTCTTCTTCTCTCAGGAGGAGGTGCAATGACTGGGCGAGTTTGGAGAC 7015
QY 361 AACCAACCCAAAG--ACCT--CTAGGGTCC-----A-----C-----CTCAT--TGTG 396
Db 7014 CACCACC---AGGTA-CTGTGCCAGGCGCGGCGCAGAGTGGGGGAGGACTGATACAGTG 6959
QY 397 CAAGTATCTCCAAATTTGTAGAGATTTC-TTCAGATATCTCAATTA-----442
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6958 C-AGCATC-CCCAA-----ACAGA--TCATTCACTTGTCTCCAGTAGCGCGGCTCT 6909
443 --ATGAAG-----GGAACA-AT-AT--TAGC-----CTCAGCTGCA--TAG--- 475
6908 CGAGCAGCTCGGCTGAAGACATGATGGACAGCAGGAGCT--GCTGCAGGT--GCCG 6852
476 --CA--ACTGTTAGACCAAG--CCT-ACGG-----AT--TGG-- 507
6851 CTCACAGG-----CCAGAGTCACTCAGCGCTCTCAAAAGGACACTCTCTGCCC 6796
508 --AGACA--CATCTC--TCCC-A-----AAGC--GG--T--TGGCT-----TTG--T 539
6795 ACCGAAATTTCA--CTCATCCCTAGGCTTAAGCATGAGCTAGCAGGCTTAGGTTGA 6737
540 --GAG-----TGAGACGA--ATA--CTT-----GGAA-----ATTGAGGCA--T- 572
6736 CCGAGTTTCATCATGAAGGC-ATTCTATCTTTGAGCAGGAATCCGATTTCA--CCAGCTCTG 6680
573 CAC-----CGGAGCAGT--CAG-----GGGACT--ACGAG--TG-- 602
6679 CACCTTCC--AGCAGTCAGAACTGACCTGGTCCACACTGGGATTTGACAGATGAA 6623
603 -----CAGT--G-CC-----TCAATG--ACGTGGCGCGCCGCT----- 632
6622 CGTACCAGTCTTTGTCCGAGTCACTGTTTCCAGTGACACGTGCCCCATCCCGCTCCAGCG 6563
633 GGT-----AC-----GGAGAG--TAA----- 646
6562 GGTGGAGAGACTGGAGGAGGAGGACTAAGTGTGTCATGTTGATGGTGAGAGACGAAC 6503
647 -----AGG-----TC-----A--CCG-----TGAA----- 659
6502 TGTCCAGCAGGAATAGAGCCCTTTGGTCTCTGAGCGAGCCGCTGCTCTGAAGTATT 6443
660 -----CT--A-----TCCA-----CCA-----TACATT----- 676
6442 CTTGATTTCTGTTGATGTTCTTCCATVGGCACTGGGCCCATGCTCTGTAAATTTGCG 6383
677 --CAGAAGC-----CAAGGGTAC--AGG-TGTC--CC--CGTG--GGACA 710
6382 CCAGAGCAATTTACCCGGGACNAG--CAAGGATGTCACCATCGAGCCAGCAGCA 6327
711 --AAAGGG--ACA-----CTG-----CAGTGTGAAGC-----CTC--A--GC- 740
6326 CGGAAGGGGTGCAACAGAGGCTGTCCACATACAGCGTG--AGCAGAGCTCCGAGTGC 6268
741 --AG-----TCCCTC--AGCA--GAA-----TTC--CAG--TGCT----- 766
6267 GAGATGGATCCCTCAGACACTGAGAGTCTTCTCAGCATGTTGAGTGAAGGTT 6208
767 --ACAA-----GGATGA-----CA-----AAA 781
6207 TTCAACAGAGACTGAATGCTGATGAACAGCGCGCTGGCAGCAGAGTTCGGATGA 6148
782 G--ACTGATTGAAG--GAA--A-----GAAAG--G-----GT 806
6147 GGCAGTGA--TGAAGTCTGTACTGAGGCTCGTGGGAAAGGCTGATCAGATCTTGAATG 6089
807 GA-----AAGTG-----GA-----AA--AC 819
6088 GATTTCATATGAGCCAGCTTAAGTCTCGAGTCAATGAGGTTCTGACAGACATATCAC 6029
820 AGA-----CCT--TTC-----CTCT----- 832
6028 AGAAGAAATGAGAGCCCTCTCTGCTACTATTTCTTATTTGCATTTCCAAAGTTTGGCTG 5969
833 CAA-----AA--CTCATCTTTTCA--AT-----GT--CT-----CTGAACA 863
5968 CCAAGTCAGAAATCCCTCTCTTCTCAGACATCTGGGACTAAGTAATCTTGTGCTGGACA 5909
864 TGACTAT-----GGG--AACTACACTTTCGTTGGCTCCA----- 895
5908 -GACTGTGCTTTTCCGGGCTGTGCTGCACTT-C-TGCCACACGCGGTAGTCGGTGTGGT 5852

QY 896 --ACAGCTG--G-----G--CCA-----CACCA-----AT-- 915
Db 5851 TGACAAGCAGCAGTATCTGACACAGAGCAGCAGGCGCGGTGGTGTGATCAATGG 5792
QY 916 -----GCCAGCA--TCATGCTATTTTGGTCCAG--CGCC--G--TC 948
Db 5791 AACGAGCCGCAAGTTTCAAGCT-----GTCCAGGTTGTAGAAACTGCCGCCACAGCCATC 5737
QY 949 A--GCG-----AG-----GTAGCA-----A-----CGGCAC--G--TCGAGGA 976
Db 5736 ACTGCGGAACAGCCTAGTG--GCAGCTGCTGTGATTTCTCCGGAACATTTCCAGACTTGAAGA 5678
QY 977 -G-GG--CAG-----GC-----TGC--GT--CTGGC-----TGCTGC- 1000
Db 5677 TGTGGATCAGACATAGCAGTGTGCTAGTTCCTGGCAATAGAAAGTATGTTGCTGCT 5618
QY 1001 --CT-----CTTCTG--GTTTGCACC--TG-CTTCTCAAA-----TT 1031
Db 5617 CACTCAFTTCCACCTTCAGCTGTTTGTAAACATGCTCTTCTAAAGAAATACCAACCACTT 5558
QY 1032 -----TTGA 1035
Db 5557 GTAATAGAAACCTTGA 5542

RESULT 22

US-09-041-886-14/c
; Sequence 14, Application US/09041886
; Patent No. 6235872
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharoz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 316..9748
; US-09-041-886-14
Query Match 43.08; Score 444.6; DB 3; Length 10348;
Best Local Similarity 39.14; Pred. No. 1e+03;

Matches 875; Conservative 0; Mismatches 97; Indels 1264; Gaps 247;

Qy 2 TGAAA-----ACCA-----TCCAGCCTA-----AAATGCAC-----AA- 29
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Qy 30 --TTCTATCTCTGG-GCAATCTTCAGGGG--CT---G---GCTG-----C 65
Db 7655 ACTTCTCTTCTCTGGAGAA-CTCCACGGGGATCTCAGGATGCTGTGGCAAAATCCCC 7597
Qy 66 TC-----T-GTGTCT-T-----CTTCCA-AGGAGTG-----CCCGTG----- 93
Db 7596 TCCCGTTTGGGTGACCATCAAGCTTCCACACGAGTGGGGGCACACGTGTGTAGCTGTT 7537
Qy 94 --C-----GCA-GGG-----GA-GATCCACCTTCCCAAGCTATGACAAAGCTG 135
Db 7536 GACAAGGGGAGGGCGGGCCAGGCTGATGATG-ATGTTT--CCTGAGCAATGG-----CGTG 7485
Qy 136 ---ACGGTCCGGC-----AGG-----G-----GGAGAG 155
Db 7484 AGAAACG--CCGGCAGCGCGCTATTCTTTTATGACCAAGGCCAACACGACTGCAGAG 7427
Qy 156 -----C-GCCACC-CT--CAGG-TGC-----ACT-----ATT----- 177
Db 7426 ACTCCACCAATTCTGCCACCACTCTCACAGGCTGCAGTGAATATCTTAGGATTTCTGTGT 7367
Qy 178 ---GA-CAA-----CCGGGT-CACC-CG--GGTGGC-----G----- 200
Db 7366 TTGATCTACTTCTTCC--TCCTCTCTGCTGATGGCTTTTGGGGTATTTGTCTCTTCTTT 7310
Qy 201 CTGG-CTA-AA-----CC--GCAGCAC--CA---TCCTCTATGCTGGGAA-TG-AC 240
Db 7309 CTGGACTAAGAGCTGCTCTCCAGGCTGCACCTGCAACGGGCTCCAGGAT--GAAGTGAC 7252
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Db 7192 GGCCAGGAGCTGCAGGGCCAGGAGCAGCAGTCCAGGCTGCTTGGAGATCCAGACTCA 7133
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Db 7132 GCG-GGATCTGCTCATGATCAAAATGCCAGGAC-AGGGCTCAAGGGTTGCCACCAGAA 7075
Qy 336 --TT-ACA-----CCTGCTC-----GGTGCA--GAC-----AGAC 360
Db 7074 TTTCATATGTCTTCTCTTTCTCAGGAGGAAGGTGCAAAATGACTGGGCGAGTTTGGAGAC 7015
Qy 361 AACCAACCAGAG--ACCT--CTAGGGTCC-----A-----C-----CTCAT--TGTTG 396
Db 7014 CACCAACC--AGGTA-CTGTGCAAGGGCCGGCCAGAGTGGGAGGAGTATATACAGTG 6959
Qy 397 CAAGTATCTCCAAAATTTAGAGATTC-TTCAGATATCTCCATTA----- 442
Db 6958 C-AGCATC-CCCAA--ACAGA--TCATTAATCTGCTCCAGTAGGCCCGCGCTCT 6909
Qy 443 --ATGAG-----GGNACA-AT-AT---TAGC-----CTCAGCTGCA---TAG--- 475
Db 6908 GCAGGAGCTCGGGCTGGAGAGCATGATGGACAGCAGGGAGCT--GCTGACGGT-GCGG 6852
Qy 476 --CA-ACTGGTAGACCAGAG--CCT-ACGG-----TT-----ACT-----TGG-- 507
Db 6851 CTCACACGGG-----CCAGAGTCACTCAGGGCTGCTTCAAAAGGGCACTCTTCTGGCC 6796
Qy 508 ---AGACA---CATCTC-TCCC-A-----AAGC--GG--T---TGGCT---TTG--T 539
Db 6795 ACCAGAAATTTCA-CTCATCTCTAGGCTTAAGCATGGAGTACAGGCTTAGGTTGAAT 6737
Qy 540 --GAG-----TGAAGAGA--ATA-CTT-----GGAA-----ATTGAGGCA--T- 572
Db 6736 CCGAGTTTCATGTAAGGCG-ATTTCATATCTTCCAGCAGGAATCCGATTCA--CCAGCTCTG 6680

Qy 573 CAC---CCGGAGCAGT-CAG-----GGGACT--ACGAG-TG-- 602
Db 6679 CACTTCC---AGCAGTGCAGATCTGACCTGGTCCACACTGGATTTGACAGATGAA 6623
Qy 603 ---CAGT---G-CC-----TCCAATG--ACGTGGCCCGCGCGT-- 632
Db 6622 CGTACCACTCTTTGTCCGGACTCACTGTTTCCAGTGACAGTGCCTATCCCGTCCAGCG 6563
Qy 633 GGT-----AC---GGAGAG--TAA----- 646
Db 6562 GGTGGGAAGAGACTGGAGGAGGAGGACTAAGTGTGATCTTGCATGTGGAGAGAGCAAAACC 6503
Qy 647 ---AGG-----TC-----A-CCG-----TGAA----- 659
Db 6502 TGTCCACAGGAATAGAGCCTTTGGTGTCTCTGAGCGAGCCCGCTCTCTGAAGTATT 6443
Qy 660 ---CT---A-----TCCA-----CCA-----TACATTT----- 676
Db 6442 CTTGGATTTCTGTGAGTTCTTCCATTGGCAACTGGGCACTGCTCTCTGTAATTTGCAG 6383
Qy 677 CAGAGC-----CAAGGTAC-AGG-TGTG--CC---CGTG--GGACA 710
Db 6382 CCAGAGCATTTCTACCCGGCGCAAG-----CAAGGATGTCGACCATGCGAGCCAGCACA 6327
Qy 711 ---AAAGGGG---ACA-----CTG-----CAGTGTGAAGC---CTC---A---GC- 740
Db 6326 CGGAAGGGGTGCACAGAGCCTGTCCACATACAGCGTG-AGCACAGTCCCGACTGGCT 6268
Qy 741 AG-----TCCCTTC--AGCA--GAA-----TTC--CAG--TGGT----- 766
Db 6267 GAGATGATCCCTTCCAAAGCACTGAGAGTTTCTTTCAGCATGTTGGAGTTGAAGGTT 6208
Qy 767 ---ACAA-----GGATGA-----CA-----AAA 781
Db 6207 TTCACACGAGACTGAATGCTGGATGAACAGCCCGCTGGCAGCAGATTCGATGAC 6148
Qy 782 G--ACTGATGAAG---GAA---A-----GAAAGG-----G---GT 806
Db 6147 GGCATGA-TGAAGTCTCTGTACTGGAGCTGCTGGGAAAGGCTGATCAGATCTTGAATGT 6089
Qy 807 GA-----AAGTG----- 819
Db 6088 GATTTACATGAGCCAGCTTAAGTGTCTCGGAGTCAAGGTTCTGACAGACATAATCAC 6029
Qy 820 AGA-----CCT-TTC-----CTCT----- 832
Db 6028 AGAAGAGATGAGAGCCCTCTTCTGATCTTCTTATTCACATTCGAAGTTGGCTG 5969
Qy 833 -CAA-----AA--CTCATCTTCTTCA--AT-----GT-----CTGAACA 863
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Qy 864 TGACTAT-----GGG--AACTACATTCGCTGGCTCCA----- 895
Db 5908 -GACTGTGTTCTTTGGGGTCTGTGCACTT-C-TGCCACCAGCGGTAGTGGTGGT 5852
Qy 896 --ACAAGCTG--G-----G-CCA-----CACCA-----AT-- 915
Db 5851 TGACAGCAGAGTATCTGACACAGCAGCAGCCGCGGTGGTGGTGTGATCATGG 5792
Qy 916 ---GCCAGCA--TCATGCTATTTGGTCCAGG-----CGCC--G---TC 948
Db 5791 AACGAGCCCGCAAGTTCAAGCT---GTCCAGGGTGTAGAAACTGCCGCCACAGCCATC 5737
Qy 949 A--GGG--AG---GTGAGCA-----A-----CGGCAC-----G--TCGAGA 976
Db 5736 ACTGCGGAACAGCCCTAGTG-GCAGTGTGTGATTTCTCCGGAACATTCAGACTTGAAGA 5678
Qy 977 -G-GG--CAG-----GC-----TGC--GT--CTGGC-----TCTGTC- 1000
Db 5677 TGTGATCAGACATGATGAGTGTGCTGTGCTGCTGCAATAGAAATGATGTTGCTGCT 5618


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QY 660 -----CT-----A-----TCCA-----CCA-----TACATTT----- 676
Db 6442 CCTGGATTCTGTTGAGTCTTCCATGCGCACTGGCCACTGCTCTGTGTAAATTTGCGAG 6383
QY 677 -CAGAAGC-----CAAGGGTAC-AGG-TGTC--CC-----CGTG--GGACA 710
Db 6382 CCAGAAGCATTTCTACCGCGGACAAAG-----CAAGGATGTGCGACCATGCGAGCCAGCACA 6327
QY 711 ---AAAGGG---ACA-----CTG-----CAGTGTGAAGC-----CTC--A---GC- 740
Db 6326 CGAAAGGGGTGCGACAGAAGCCTCTCCACATACAGCGTG-AGCACAGCTCCCGACTGGCT 6268
QY 741 -AG-----TCCCTTC--AGCA--GAA-----TTC--CAG--TGCT----- 766
Db 6267 GAGATGATCCCTTCCAAAGCACTGAAGAGTTTCTTTCAGCATGTTGGAGTTGAAGGTT 6208
QY 767 ---ACAA-----GGATGA-----CA-----AAA 781
Db 6207 TTCACACAGACTGAATTGCTGGATGAACAGGCGGCTGGCAGCAGAGTTCCGATGAAC 6148
QY 782 G--ACTGATTGAAG--GAA--A-----GAAAG--G-----G---GT 806
Db 6147 GGCACCTGA-TGAAGTCTGTACTGGAGGCTCGTGGAAAGGCTGATCAGATCTTTGAATGT 6089
QY 807 GA-----AAGTG-----GA-----AA--AC 819
Db 6088 GATTACATGAGCCAGCTTAAGTGCTCGGAGTCATGAGGTTCTGACAGACATAATCAC 6029
QY 820 AGA-----CCT-TTC-----CTCT----- 832
Db 6028 AGAAGAGAATGAGAGCCCTCTTCTGTAATTTCTTATTTGCACATTCGAAGTTTGGCTG 5969
QY 833 -CAA-----AA--CTCATCTTCTCA--AT-----GT--CT-----CTGACA 863
Db 5968 CCAAGTCAAGATCTCTCTCTTCTCCAGACATCTGGGGACTAAGTAATCTTGTGCTGGACA 5909
QY 864 TCACTAT-----GGG--AACTACACTTGCCTGGCTCCA----- 895
Db 5908 -GACTGTGTCTTTTCGGGGTCTGTGCACTT-C-TGCCACACCGGTAGTGGTGGTGT 5852
QY 896 -ACAAGCTG--G-----G--CCA-----CACCA-----AT-- 915
Db 5851 TGACAAGCAGCAGTATCTGACACACAGCAGCAGCAGCGCGGGTGGGTGTGATCATGG 5792
QY 916 -----GCCAGCA--TCATGCTATTGTGTCAGG-----CGCC--G--TC 948
Db 5791 AACGAGCCCGCAAGTTCAAGCT-----GTCAGGGGTGTAGAACTGCGCGCCACAGCCATC 5737
QY 949 A--GCG-----AG-----GTGAGCA-----A-----CGGCAC-----G--TCGAGGA 976
Db 5736 ACTGCGGAACAGCTTAGTG-GCAGCTGTGTGATTTCTCGGAACATTCAGACTTGAAGA 5678
QY 977 -G-GG--CAG-----GC-----TGC--GT--CTGGC-----TGCTGC- 1000
Db 5677 TGTGATCAGACACATTAAGCAGTGTGCGCTAGTTCCTGGCAATAGAAAGTATGTTGCTGCT 5618
QY 1001 --CT-----CTTCTG--GTCTTGACC--TG-CTTCTCABA--TT 1031
Db 5617 CACTCATTTCCACCTTACGCTGTTTGTGAACATGCTCTTAAGAAGATACCAACCAAGTT 5558
QY 1032 -----TTGA 1035
Db 5557 GTAATAGAAACCTTGA 5542
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RESULT 24

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US-08-453-265-5/c
; Sequence 5, Application US/08453265
; Patent No. 5693757
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Marcy E.
; APPLICANT: Ambrose, Christine M.
; APPLICANT: Duyao, Mabel P.
```

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; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Huntington DNA, Protein And Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,265
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3880003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 316..9748
; US-08-453-265-5
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Query Match

Best Local Similarity 43.0%; Score 444.6; DB 1; Length 10366;
Matches 875; Conservative 0; Mismatches 97; Indels 1264; Gaps 247;

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QY 30 --TTCTATCTCTGG-CCAATCTTCAGGGG--CT---G---GCTG-----C 65
Db 7655 ACTTCTTTTCTCTGGAGAA--CTCCAGGGGATCTCAGGGATGCTGTGCCAAATCCCC 7597
QY 66 TC-----T--GTGTC--T-----CTTCCA--AGGAGTG-----CCGCTG----- 93
Db 7596 TCCCGGTTTGGGTGACCATCCAAAGCTTCCACACGAGTGGGGGCACAGTGTGTAGCTGTT 7537
QY 94 --C-----GCA-GCG-----GA-GATGCCACCTTCCCAAGCTATGGACAACGTG 135
Db 7536 GACAAGGGCAGCGCGGCCAGGCTGATGATG--ATGTT--CCTGAGCAATGG-----CGTG 7485
QY 136 ---ACGGTCCGCG-----AGG-----G---GGAGAG 155
Db 7484 AGAAACG--CCGGCAGCGCGCTATTCTTTATGACCCCAAGGCCAACACCACTGCAGAG 7427
QY 156 -----C-GCCACC--CT--CAGG-TGC-----ACT-----ATT----- 177
Db 7426 ACTCCACCATTTCTGCCACCATCTCAGAGGTGCAAGTATATACTTAGGATTCGTGTGT 7367
QY 178 ---GA-CAA-----CCGGGT-CACC-CG--GGTGGC----- 200
Db 7366 TTGGATCTACTTCTCTCC---TCTCTCTCGGTGATGCGCTTTTGGGGTATTTGCTCTCTTT 7310
QY 201 CTGG-CTA-AA-----CC--GCAGCAC--CA---TCCTCTATGCTGGAA-TG-AC 240
Db 7309 CTGGACTAAGAAAGCTGTCTTCCAGGCTGCACTGCAACCGGCTTCCAGGAT--GAAGTGAC 7252
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QY 241 A-AGT-----GGTGC--C-TGGATC-----CTGCGTGG-----TC-CTTCTGA 274
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QY 7251 ACAGTAGATGAGGAGCAGCGGTGGGTCAAACTC-TGTGGAGGAGACACACGCTCCAGA 7193
Db      |||||
QY 275 G--CA--A--CA--CCCA--AAC-GCAGTACA-----GCATCGAGATCCAGA---A 311
Db      |||||
QY 7192 GGCACGACAGCTGACGGGCCAGGCAGCAGCAGTCCAGCCCTGCTCGAGATCCAGACTCA 7133
Db      |||||
QY 312 -CTGGATGTG-----T--AT--GACGAGGGCC-----C--- 335
Db      |||||
QY 7132 GCG-GGATCTGCTCATGTATCAATGCCAGGAC-AGGGCCTCAAGGGTTGCCACACGAA 7075
Db      |||||
QY 336 -TT-ACA-----CCTGCTC-----GGTGA--GAC-----AGAC 360
Db      |||||
QY 7074 TTTCACAATCTCTCTTCTCAGGAGGAGGTGCAATGACTGGCGAGTTTGGAGAC 7015
Db      |||||
QY 361 AACACCCAAAG--ACCT--CTAGGGTCC-----A-----C-----CTCAT--TGTC 396
Db      |||||
QY 7014 CACCACC--AGSTA-CTGTGCCAGGGCCCGGCCAGAGTGGGCAGGGACTGTATACAGTG 6959
Db      |||||
QY 397 CAGATATCTCCAAATTTAGAGATTTC-TTCAGATATCTCCATTA----- 442
Db      |||||
QY 6958 C-AGCATC-CCAA-----ACAGA--TCATTCACTTGTCTCAGTAGGCCGCGCGCTCT 6909
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QY 443 -ATGAAG-----GGAAACA-AT-AT--TAGC-----CTCACCTGCA--TAG--- 475
Db      |||||
QY 6908 GCAGGCAGCTCGGCTGGAGACATGATGGACAGCAGGGAGCT--GCTGCACGGT-GCCG 6852
Db      |||||
QY 476 --CA-CTGTAGACACAGAG--CCT-ACCG--TT-----ACT--TGG-- 507
Db      |||||
QY 6851 CTCACACGGG--CCAGATGTCACCTCACGGGCTGCTTCAAAAGGGCACTCTTCTGGCC 6796
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QY 508 ---AGACA--CATCTC-TCCC-A-----AAGC-GG--T--TGGCT--TTG--T 539
Db      |||||
QY 6795 ACCAGAAATTCA-CTCATCCCTAGGCTTAAGCATGGAGTAGCAGGCTTAGGTGACT 6737
Db      |||||
QY 540 --GAG-----TGAAGACGA--ATA-CTT-----GGAA--ATTACGGCA--T- 572
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QY 6736 CCGAGTTTCATCATGAAGGC-ATTCAATCTTCAGCAGGAATCCGATTCA--CCAGCTCTG 6680
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QY 573 CAC--CCGGGAGCAGT-CAG-----GGGACT--ACGAG-TG-- 602
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QY 603 ---CAGT--G-CC-----TCCATG--AGTGGCCGCGCCCTG----- 632
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Db      |||||
QY 677 -CAGAAGC-----CAAGGTAC-AGG-TGTC--CC---CGTG--GAACA 710
Db      |||||
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Db      |||||
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Db      |||||
QY 6326 CGGAAGGGGTGCAGAGAGCTTCTCCACATACAGCGTG-AGACAGCTCCCGACTGGCT 6268
Db      |||||
QY 741 -AG-----TCCCTTC--AGCA--GAA-----TTC--CAG--TGCT-- 766
Db      |||||
QY 6267 GAGATGGATCCCTCCAGGACCTAAGAGTTTCTTTCAGCATGTTGGAGTTGAAAGTT 6208
Db      |||||
QY 767 ---ACAA-----GGATGA-----CA-----AAA 781
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Db 5207 TTCACAAACAGACTGAATTGCTGGATGACAGGCGCTGGCAGCAGATTCCGATGAC 6148
QY 782 G--ACTGATTAAG--GAA--A-----GAAAG-----G--GT 806
Db 5147 GGCACCTGA--TGAAGTCTCTGACTGAGGCTCGTGGAAAGGCTGATCAGATCTTGAATGT 6089
QY 807 GA-----AAGTG-----GA--AA--AC 819
Db 5088 GAATTACAAATGAGCCACGTTAAGTGTCTGGAATCATGAGGTTCTGACAGACATATCAC 6029
QY 820 AGA-----CCT-TTC-----CTCT----- 832
Db 5028 AGAAGAGATGAGAGCCCTCTCTGACTATTTCTATTGACATTCCAAGTTTGGCTG 5969
QY 833 -CAA-----AA--CTCATCTTCTCA--AT-----GT--CT-----CTGAACA 863
Db 5968 CCAAGTCAAGATCCTCTCTCTCCAGACATCTGGGAGCTAAAGTAACCTTGTGCTGGACA 5909
QY 864 TGAATAT-----GGG--AACTACACTTCCGTGGCTCCA----- 895
Db 5908 -GACTGTGCTTTTCGGGCTCTGCTCACTT-C-TGCCACACGCGGTAGTGTGTGTGT 5852
QY 896 --ACAAGCTG--G-----G--CCA-----CACCA-----AT-- 915
Db 5851 TGACAAGCAGCAGTATCTGACACAGCAGCACACAGGCGCGGTGGTGTGTGATCATGG 5792
QY 916 -----GCCAGCA--TCATGCTATTTGGTCCAGG-----CGCC--G--TC 948
Db 5791 AACGAGCCCGCAAGTTCAAGCT-----GTCCAGGGTGTAGAAACTGCCGCCACAGCCATC 5737
QY 949 A-GCG-----AG--GTGAGCA-----A-----CGGCAC-----G--TCGAGA 976
Db 5736 ACTGCGGAACAGCCTAGTG-GCAGCTGCTGTGATTTCTCGGAACATTCAGACTTGAAGA 5678
QY 977 -G-GG--CAG-----GC-----TGC-----GT--CTGGC-----TGTGTC- 1000
Db 5677 TGTGATCAGACACATTAGCAGTGTGCTAGTTCTCTGGCAATAGAAAGTATGTGTGTCT 5618
QY 1001 --CT-----CTTCTG--GTCCTGCACC--TG-CTTCTCAA--TT 1031
Db 5617 CACTCATTTCCACCTTCAGCTGTTTGTAAACAATGTCTTCTAAAGAATACCAACAGTT 5558
QY 1032 -----TTGA 1035
Db 5557 GTAATAGAACCTTGA 5542
```

RESULT 25

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US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
```


APPLICATION NUMBER: US/08/414.657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 base pairs
TYPE: nucleic acid
STRAINEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...924
OTHER INFORMATION:
US-08-414-657D-7

Query Match 42.9%; Score 444.5; DB 2; Length 924;
Best Local Similarity 61.3%; Pred. No. 13;
Matches 656; Conservative 0; Mismatches 166; Indels 249; Gaps 87;

1 AT--GAAACCAATCCAGCCAAATGACAAATCTCTCTTTGGGCAATCTTTCACGGGGC 58
2 ATCGGAAA-----CAG-----TTGC-CA-----CT---GG-----TCCT-ACTGAGA 33
59 TGGCTGCTCTGTCTTTT-CCA-AGGAGTCCCGTGGCGAGCGGAGATGCCACCTTCCC 116
34 T---TGCTCTGCTCT-TCTTCCACAGGACTGCTGCTTCCGACGCTGGAT-----TTTAAAC 84
117 CAAGCTATGACACACGTCAGGTCGCGCAGCGGGGAGAGCCACCTCAGGTGC--ACT 174
85 CGAGGC-ACGGACAACATCACCCTGAGGCGAGGAGACACGCCATCTCAGGTGGTCT 143
175 A-TTGACAAACCGGG---TCAACCGGGTGGCTGCTAAACCG---CAGCACCATCTCTAT 228
144 AGAAGACAA-----GAATCA--AAGGTGCTGTTGAACCGTTCTG--GCATCATTTT 195
229 GCTGGATGACAGTGTGCTGATCCTCGCTGGTCTCTTCTGAGC-----AACAC-C 282
196 GCTGGACATGACAGTGTGCTCTGACCCACG---GGT-----TGAGCTGGAGAA-AGGC 246
283 CAAC-CCGAGTACAGCAT-CGAGATCCAGAACTGATGATGACGAGGG--CCCT 336
247 CATCTCTGGATACAGCTCCGA-ATCCAGAGTGTGATGATGATGAGGGTTCC-- 303
337 TACACCTGCTCGTGCAGACAGACACCA-----CCCAAGACCT--CTAGGGTCCACCTC 390
304 TACACTTGTCTAGTTCAGAC--AC-AGCATGAGCC--AAGACCTCCCAA--GTTTACTTG 357
391 ATTGTGCAAGTATCTCCCA--AAATGTAGAGATTTCTTCAGATATCTCC-----AT 440
358 ATCGTACAAG-----TCCCAACCAA-----AGA--TCTCCA-ATATCTCTCGGATGCA 403
441 ---T-AATGAAGGGAACAAATATTAGCTC--ACCTGCATAGCACTGGTAGACAGAGCC 494
404 CTGTGAATGAGGCGAGCAACGT--GACTCTGTCTGATGGCAATGGCCGCTCTGAACC 461
495 TACGGTT---ACTTGGAGACATCTCTC-CCAA-----AGCGTGTGGCTTTGTGA--GT 543
462 T---GTTATCACTCGAGACAC--CTTACACCAACTGGGAAG-----GGAATT-TGAAGA 510
544 GAAGACGAATCTTGGAAATTCAGGGCATCACCGGAGCAGTACAGGAGCTACAGATGC 603
511 GAAGAAGAATATCTGGAGATCTTGGCATCACACAGGAGCAGTACAGGCAAAATATGATGC 570

QY 504 AGTGCCTCCATGACGTGGCGCGCCGTGCT---ACGGAGGTAAAGGTACCGTGAAC 660
Db 571 AAAGTGCCTCCAAACGAGGTCTCTCTGGCGGATGTCAAAC--A-AGTCAAGGTCACTGTGAAC 627
QY 661 TATCC-ACCA-TA-CATTTTCAAGAGCCAAAGGTACA--GGTGTCCCGTGGGACAAAAGG 715
Db 528 TATCTCTCCACTATCA---CAGATCCAAG--CAATGAAGCCACC-----ACA-----G 673
QY 716 G--GACA--CTGC-----AGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGT 766
Db 674 GACGACAAAGCTTCACTCAATGTGAGGCTCGGCGAGTCCCTGACCTGACTTTGAGTGGT 733
QY 767 ACAAGGATGACA-----AAAGACTG---A-----TTGAAGGA--AAGA--AAGGGGTG 807
Db 734 ACCGGATGACACTAGGATAAATAGTCCAAATGGCCCTTGA--GATTAAGAGCAGG--- 787
QY 808 AAGTGGAAAACACAGACCTTTCTCTCAAAAC--TCATCTTTCTTCAATGTCTCTGAAACATG 865
Db 788 --AG-GG---CCAGTC--TTCC-CT---GACGGTGA---C--CAACGTCACTGAGGAGC 829
QY 866 ACTATGGGAACACTACTTGGTGGCTTCCAAAGCTGGGCGCACCAATGCCAGCATCA 925
Db 830 ACTACGGCAACTACACCTGTGTGGCTGCCAACAAAGCTGGGGGTCCACCAATGCCAGCCTAG 889
QY 926 TGCTATTGTTCCAGGCGCGCTCAGCGAGGTGAGCAACGCGACGTGCGAGGA 976
Db 890 TCCTTTTCAGACCTGG---GTC-----GGTGA-----GAGGA 918

RESULT 26

US-09-369-364A-1
; Sequence 1, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3002
; TYPE: DNA
; ORGANISM: mus musculus ADAMTS-5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(2810)
US-09-369-364A-1

Query Match 42.9%; Score 443.9; DB 4; Length 3002;

Best Local Similarity 37.7%; Pred. No. 1,2e+02;

Matches 889; Conservative 0; Mismatches 103; Indels 1363; Gaps 247;

QY 1 ATG-----AAAACCA-TCCAGC-----CA-AAAATGCAC-AAATTC 32
Db 502 ATGGCGGTACACTCTTAAGCCACTCTCTGCTGGGTCTCTGGGCGAGATATGAACAAATT- 560
QY 33 TATCTCTTTGGCA---ATCTTTACG-----GGGCT----- 59
Db 561 TA-----TGGGATGATCTTCCGCATCTCTGTCATGCTTACACCGCGAGGCTTTAGCT 615
QY 60 ---GGC-----TG-----CT-CTGTGTC-----TCT-----TCCAG 82
Db 616 TCGAGGCGCTCCGCCACGCGCCAGTTCGAGACTCTCTGATCCCATCTGGGCCCAA- 674
QY 83 GAGTGGCC---GTGGCCAG-----C--GGAGATGC-CA-C-CT-TCCCAAGCT-ATG 126
Db 675 GAGAGCCCTCGGTGCGACAGTAGATCTAGGAGAGCGCTCAGCGCTGGCCCCCGAGCTGCTG 734

127 GACAA---CG---TG---ACGGTCCGG---CAG---GG-GGAG--- 153
128 TACCGCCATTGTAATAACCTCTGACCACTGAAACAGTGGCCGCTACTGTGACAGGGAGAGG 1847
129 TAC---TAC---GGAGAGT---AAAG---TCACC--- 654
130 GCCATATACCGTCTCTGCACTGTTTACACCTCTGCCACCAATGTAATCTTTTCGCCAT 1907
131 GTGAA---GTGAA---CTATC---CA---CCATACATTT-CA 678
132 GAGCAGTGTGAAGCCAAAATGGCTATCAGTCTGATGCAAGAGGTCAAAACATTTGTA 1967
133 GAA---G---CAAAGGTA---CAGGTGCC---CC---GTGGGACAA--- 711
134 GAATGGTTCACAA---ATATGCAAGTGTCTCTGCCGACAGATGTGTG---CAAGCTTACCTGC 2024
135 AAGGGACA---CTGCA---GT---G---TCGA 732
136 AGAGTAAAGGGACAGAGTCTATGTGTCTTTTCTCAAAGGTTACGGATGGGACTGAA 2084
137 GCC-T-CAGCA---GTCC--- 745
138 TCCAGGCCGTACAGCAACTCTGTGTGTCCGAGGACGGTGTGTGAGACTGTGATGAC 2144
139 C---CTCA---GC---AG---AATTCC 760
140 GGCATTATTGGCTCAAAGCTACAATATGACAAGTGTGGAGTGTGCGGAGGGGATACTCC 2204
141 AGTGTACAGAGTATTCGAACTT---GA---CAA---AAG---ACTG--- 786
142 AGTTGTACAGAGTATTCGAACTT---GA---CAA---AAG---ACTG--- 786
143 TGAAGGA---AA---GAAAG---G---GGTGAAG--- 811
144 AGGATCCCTGAGGAGCAACCCACATAAAGTCCGACAGTTCAAGCCAAAGACCACT 2324
145 TG---GAAAAC---AG-ACC--- 824
146 AGATTCCCTGCTACTTAGCCCTGAAAGAAACCTGGCGAGTACTTTATCAATGGCAAG 2384
147 TTTCTTC-TCA-AAAC---TCATCTTCTCAAT-GT---C-TC-TGAAC--- 862
148 TACATGATTTCCATTTCCAGTTCAGAGACCATCATGACATCAATGGTACCGTCAATGACTACAGT 2444
149 ATGACT---ATGACT---ATGGGA---ACTA---CAC---T- 882
150 GGATGGAGCCACAGAGATGATTTTATCATGGATGGGCTATTTCAGCCACAAAGAAATC 2504
151 TG---G---CCT---CCAAC---AAGC--- 901
152 CTGATCGTGCAGATCTTTGCCACAGACCACTAAAGCGCTAGGCGTCCGTTACAGCTTT 2564
153 TG---GGCCAC---AC---ATGCCAGCATCA--- 925
154 TTTGTTCCCAAGAGACCACTCAAAAGATAACTCTGTCTATCAGCCATGGCAGCAACAG 2624
155 TG---CTA---T---T---T---GGTCCA-GGC---GCC-G-T-CAGC 951
156 GTGGACCACTCTTACACAGCTGCAGTGGGTGACAGGTCCATGGCTGGCTGCTCCAG- 2683
157 GA---GGTGAACA-A---C---GGCAGCTCGAGGA---GGCAGGGTGC---GTCTG--- 992
158 GACCTGTGA-CACAGCTGGCAC-CTAGGACCGGTGCAG--TGCCAGGATGGAACAGGA 2739
159 GCT---GCTGCC-TCT-TCT---GGTCT--TGACCT--GC-T-TCT-C--- 1026
160 AATTAGCTAAAGGATGCTCTCTCTCAGAGCCCTTCTGCATTTAAGCAATGCTGTGCTGA 2799
161 AAAT-TT---TG 1034
162 AGAATGTTAGCCTG 2814

RESULT 27

US-08-179-481-1
 : Sequence 1, Application US/08179481
 : Patent No. 5624816
 : GENERAL INFORMATION:
 : APPLICANT: CARRAWAY, KERMIT L.
 : APPLICANT: CAROTHERS CARRAWAY, CORALIE A.
 : APPLICANT: FREGIEN, NEVIS L.
 : TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
 : NUMBER OF SEQUENCES: 125
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CUSHMAN, DABY & CUSHMAN
 : STREET: 1100 NEW YORK AVENUE, N.W.
 : CITY: WASHINGTON
 : STATE: D.C.
 : COUNTRY: U.S.A.
 : ZIP: 20005-3918
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/179,481
 : FILING DATE: 28-DEC-1993
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/922,521
 : FILING DATE: 30-JUL-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: KOKULIS, PAUL N.
 : REGISTRATION NUMBER: 16,773
 : REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202) 861-3000
 : TELEFAX: (202) 822-0944
 : TELEX: 6714627 CUSH
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2603 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: both
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : US-08-179-481-1
 :
 : Query Match 42.9%; Score 443.7; DB 1; Length 2603;
 : Best Local Similarity 42.0%; Pred. No. 30;
 : Matches 848; Conservative 0; Mismatches 112; Indels 1061; Gaps 231;
 :
 : 1 ATGA-AAAC-----CATCCAGC-CA-AAAA--TGCA-ATTTCTAT--- 35
 : 290 ATAACCAACGGTGGCCCTTTAAACA-CCAGCAGACACTGAAGACTTGCCTGATTTCAATGCC 348
 : 36 -CT-----CT--TG-----GG-----CAA--TC-----TTACGGGGC--TG 60
 : 349 ACTGGTGCTTACTGATCCAAATGGCTCCCAAGTCTCAGCCAACTTTGATGGGACAGTG 408
 : 61 GC--TGCTCTGTG-----TCTCT-----TCCA-----AGGA 84
 : 409 ACCAT-CTCTGTGATGCTCTCTCCAAATCCTTCACGCTCTCCAGCCTGTGAGGA 467
 : 85 GT---GC---CC-----GTGC-----GCAG-C-GG-----AGATG----- 106
 : 468 GTACCGCAACACACAAAGGGCTTCTGGAGTCTGGAATGACATCCAGAGATGACTT 527
 : 107 -----CCACCTTC-----CCNA-----AG-----CTA 124
 : 528 CAGATGCCCAATGCTCCACCATCCCTCCAAACAGCTCCGAGGAGACTCTTTTCCACTA 587
 : 125 TG---GACACG-----TGACGG-----TCC--GGCAGG-G-GGAGAGGCCACCC 163
 : 588 TGGATGACATCGGAACTAACGGATAGGCTCTCTTGG--GGTAGGACAG-----ACCC 641

Qy 164 TCAGGTGC-----ACT--A-----TTG-----AC-----AAC-----CGGTC 189
 Db 542 TC-----TGCTTCTGAGTTTACTCCCATCTTCTTGTCCCACTGTGGACAGAGCGG--C 696
 Qy 190 ACCGGGTG-----G--C-CTGGCT-AAAC-----CGCA-----GCA-----CCATCC 223
 Db 697 GCC--GGTGAAGACTTGTATCTCTGGGTGCAACGAGGACGACAGTCAAGTTTGACATCC 754
 Qy 224 T--CTATGCTGG-----GA-AT--GACAAGTGGTC-----CTGATCCT----- 258
 Db 755 TGGCCA--CAGGAAACAGAGACATCGACAA-----AGCACCAACTCAATCTTTAGACAT 808
 Qy 259 --CG--CGTG-----GT-----CCT-T--CT--G-AGCAACA 280
 Db 809 TCCGCACGTGAATGGCACGCTCAACCAGTACCCACCCCTATCCACTACAGCAGCAAGA 868
 Qy 281 CCCAA-----AC-----GC-AGTACAG-----CATGAGAT--CCAG-AACGT--GGATG 319
 Db 869 TTCAAGCCTACAGGGCGAGAAACAGTGGCCATTGAGATCACCAGCAAC-TCTAAGGATG 927
 Qy 320 T-GTAT--G-----ACGAGGC-----CCTTACACCTGCT-----CGG-----T 350
 Db 928 TCGTAITCAGCCTCTCCAAACAGTGCAGTGGCCTTTGAGCT-CTTTGAAAACGGGAGTTT 986
 Qy 351 GCA-----GACAGACAACCA--CCCA-AAG-----ACC-----TCTA-----GG--GTC 384
 Db 987 GCAGGTGGACA-CCAA--CATCCCAGAGAAACGTACCTGGAGATTCTAGCAAGGGGATGTC 1044
 Qy 385 CA-CCTCA-TTGTGCA--AGTATCTC--CCAAATTTGTAGA-----GATTTCTTCAAT 432
 Db 1045 AAGACTAACTTGT-CATCGGTA-CTCCAGCC-----TG-AGCGGTGGCTTGTCTTC----- 1092
 Qy 433 ATCTCCATTAAATGAAGGGAACAATATT-----AGCCTCACTGCATA-----GCAAC 479
 Db 1093 -TGT--AGTAAGGA--GGAAACAGTGTTTGTACAAGAG-----ACCAGAAAGAGGGCAAC 1143
 Qy 480 T-----GGTAGACCAG-----AG-----CCTACGG-----TT----- 501
 Db 1144 TCTTCCACTGAGGT-GACCAGCTGCAAGTGGATGGGAACCTCTTCGCGCGCTTGTGTA 1202
 Qy 502 -ACT-----TG-----GAGACA-----CAT----- 515
 Db 1203 AACTCTAAGGACCTCTGCACCTGAGCCATCTTCCCTAATGTGAGACTGCATTCCTGGAA 1262
 Qy 516 --CTCTC-----CCAAA--G-C-GG--TTGGC-T--TTGTG-A--GTCAA 546
 Db 1263 GGGCTGTGAGCCTGCCCTCAAAACATGACTGGAGATGGCGTCATTTGTAGCTGTGGA 1322
 Qy 547 GA---C-GAATACTTG--GAA--ATT-----CAGGGCATCAC-----CC--GG-- 579
 Db 1323 GATCTCTGAATTC-TGCCAGAACCATCTCTGTCTGTGTAATTACTGTTATAACCATGCC 1381
 Qy 580 -----GAGCA-GTCAGG-----GACTACGAG-----TGCA-----G-----TGCTTC 612
 Db 1382 ATTGCGA-CATCTCTGGGCTCCAGACTGCCAGCCACTTGCACCTCGCCCCCTGCCTTC 1440
 Qy 613 AATGACCTGGCCG-CG--CGTGGTACGAGAGTA-AAGTCA-----CCGTGAACTAT-- 663
 Db 1441 ACTG--GTAACCGCTGTCTC-TGG-CCGG-GA--ACAATTTCACTCCCATCATATAA 1493
 Qy 664 -----CC-----ACCATACA-----TTTCAG-----AA-GCC--AAG 688
 Db 1494 AGAGTTTCCCTTGAGGACCAT-CACGCTCTCTCAGGGAGGAGCAAAAGCCTCTAACG 1552
 Qy 689 GT-ACAGGTGC-----CC-C-GTGGGACAAA-----AG-G-----GGACA----- 720
 Db 1553 CTGAC-----GTCAATGCTCGGTGG--CAAACTACTAGAGAACTTGACATCGGGCTT 1606
 Qy 721 ----CT-----GC--AGTG-----TGA-----AGCTC-----AG--CAGTC----- 744
 Db 1607 TTCTCTCAACAGCTTGTAGTGAAGCTGATCGAACCTCTCCGGAGGACCACTCTTGGCA 1666
 Qy 745 --CCC--TCAGCA---GAA-----TTCCAGT--GGTACAAGG----- 772

DB 1667 AGCCATTCATCACTGGAAGTGGCTCTCCCACTTCAAGTACCGTCCAGGGGAGCCCTCA 1726
QY 773 -----A--TG-ACAA--AAGACTGAT-----TGAAGGA----- 795
DB 1727 TCACATATCTGAACACCA--ACTGATAAGCGCGTGGATGGAGGCTTCTCTCTCCAGGC 1784
QY 796 -----AAGAAAGGGGTGA--AGTGAAGA--CAG-----AC-----CT--TTCC--- 829
DB 1785 TCGGAGGAGAGCG--GAAGAGAGTGGAGAGCCAGAGAACGTCCCGCTTCTTCCCA 1843
QY 830 TTTC-A-----AAAC-TCATCTTTCTTCA-----ATGTCTCTGAACATGACTATG--GGA 874
DB 1844 TCTCGAGGGCAGACGTC-----CAGGACGGGATGGCCCTGAACCTTAAGTATGCTGA 1895
QY 875 -----ACTACACTTGG--TGGC-----CT--CCA-----ACA-----AG----- 900
DB 1896 CGAGTACTTCACTGGGATGGCTTACAAAGCTACCACTTGGTCTACAGCCGCCAGGATGG 1955
QY 901 -----CT-----GGGC-----CACA-----CCAAATGCCAGCA 922
DB 1956 CGTCACTGTGTCTCCCATGTAGTGGGCTACTGTCAATGGAGGCCAATGCAGCA 2015
QY 923 TCATGCTATTGG--TCCAG-----GCG-----CCGTCA-----GCG 952
DB 2016 -CCTGCCAGATGGGCCCCAGTGCCAGCGCAACCTTCAAGCATCTACACATCTCTGGGGCG 2074
QY 953 A--G--GTGAGC-----AAC-----GGCA--CGTC--GA-----GGAGGCG 980
DB 2075 AACGCTGTGAGCATTAAGCGTGAACCTTGGGCGATCTTTCGGGATTCCTTTGGAGCCC 2134
QY 981 AGGCTG-CGTGTGGCTGT--GCC-TCTT--C-----TGGTCTTGCAC-----CTGCT 1022
DB 2135 TGGTGCCTCTTGTCTACTTGGCACTTAGCATGTGTGTCTTCTACTTCTGCGGCTGCT 2194
QY 1023 -----T-----CTCA-AATTTGA 1035
DB 2195 CCATGAACAAGTTCTCTACCTCCCTCTGGACTCAGAACTGTGA 2235

RESULT 28

US-08-179-481-97

Sequence 97, Application US/08179481

Patent No. 5624816

GENERAL INFORMATION:

APPLICANT: CARRAWAY, KERMIT L.

APPLICANT: CAROTHERS CAPREWAY, CORALIE A.

APPLICANT: FREGIEN, NEVIS L.

TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESS: CUSHMAN, DARBY & CUSHMAN

CITY: WASHINGTON

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

APPLICATION DATA:

FILING DATE: 30-JUL-1992

APPLICATION NUMBER: US/08/179,481

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/922,521

FILING DATE: 30-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:

LENGTH: 2232 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2232

US-08-179-481-97

Query Match 42.9%; Score 443.5; DB 1; Length 2232;
Best Local Similarity 42.4%; Pred. No. 69;
Matches 845; Conservative 0; Mismatches 113; Indels 1037; Gaps 230;

QY 1 ATGA-AAAC-----CATCCAGC-CA-AAAA--TGCAC-AATTCTAT--- 35
DB 290 ATAACCAACCGTGGCCCTTTAAACA-CCAGCGACACTGAAGACTTGCCTGATTCATATGCC 348
QY 36 -CT-----CT--TG-----GG-----CAA--TC-----TTCAAGGGGC--TG 60
DB 349 ACTGTGTCTTACTGATCCAAATGGCTCCCAAGTCTCAGCACTTTGATGGGACAGTG 408
QY 61 GC--TGCTCTGTG-----TCTCT-----TCCA-----AGGA 84
DB 409 ACCAT-CTCTGTGATGTCTCTCCACATCTTTCAGCCTCTCCAGCTGTCAAGGA 467
QY 85 GT--GC--CC-----GTGC-----GCAG-C-GG-----AGATG--- 106
DB 468 GTACCGCAACACACAAAGGGCCTTCTGGAGTCTGGAATGCAATCCAGAAGATGACT 527
QY 107 -----CCACCTTCC--CCAA-----AG-----CTA 124
DB 528 CAGATGCCCATGGCTCCACCTCCCAACGCTCCAGGAGAGACTCTTTCCACTA 587
QY 125 TG-----GACAAAG-----TGACGG-----TCC--GGCAGG-G-GGAGAGCGCCACC 163
DB 588 TGGATGACATCGGAAACTAACGGGATAGGCTCTCTGG--GGTGAGGACAG--ACCC 641
QY 164 TCAGGTGC-----ACT--A-----TTG-----AC-----ACG--CGGTC 189
DB 642 TC--TGCTCTGAGTTTACTTCCCATCTTCTTGTCCCACTGTGGAACAAGAGCGG--C 696
QY 190 ACCCGGCTG-----G--C--CTGGCT-AAAC-----CGCA-----GCATCC 223
DB 697 GCC--GGTGAAGACTTGATCTCTGGGTCAACGAGGACGACAGTGAAGTTGACATCC 754
QY 224 T--CTATGCTGG-----GA-AT--GACAGTGTGTC-----CTGGATCTCT-- 258
DB 755 TGGCCA--CAGGAACAGAGACATCGGACAA--AGCACCACCACTCAATCTCTTAGAATC 808
QY 259 --CG--CGTG-----GT-----CCT-T-----CT--G-AGCAACA 280
DB 809 TCCGGCAGTGAATGGCAGCTCAACAGTACCCACCCCTATCCACTACAGCAAGA 868
QY 281 CCCAA--AC-----GC-AGTACAG-----CATCGAGAT--CCAG-AACGT---GGATG 319
DB 869 TTCAGGCTTACAGGGGCGAGAACAGTGGCCATTGAGATCACCAGCAAC-TCTAAGGATG 927
QY 320 T-GTAT--G-----ACGAGGC-----CCTTACACTGTCT-----CGG-----T 350
DB 928 TCGTATTCAGCCTCTCCAAACAAGTGCAGTGGCCTTTGAGCT-CTTTGAAAACGGGAGTTT 986
QY 351 GCA-----GACAGACAAACA--CCCA-AAG-----ACC-----TCTA-----GG--CTC 384
DB 987 GCAGGTGACA-CCAA-CATCCCCAGAAGAGTACCTGGAGATTTCTAGCAGGATGTC 1044
QY 385 CA-CCTCA-TTGTGCA--AGTATCTC-----CCAAAATTGTAGA-----GATTCTTCAGAT 432

Db 1045 AAGACTAACTTGT-CATCGGTA-CTCCAGCC-----TG-AGAAGGTGCTTCTTC----- 1092
QY 433 ATCTCCATTAAAGAGGAAACAATATT-----AGCCTCACCCTGNTA-----GGAAC 479
Db 1093 -TGT-AGTAAGGA--GGAACAGTGTGTTGTACACGAG--ACCAGCAAGAGGGCAAC 1143
QY 480 T-----GGTAGACCAG-----AG-----CCTACCG-----TT----- 501
Db 1144 TCTTCCACTGAGGT-GACCAGCTCAAGTGGGATGGGAACCTCTTCGCGCTTGTGTGA 1202
QY 502 -ACT-----TG-----GAGACA-----CAT----- 515
Db 1203 ACACCTTAAGGACCTCTGCACGTAGCCATGCTTCCCTAAATGTGAGCTGCATCTCTCGGAA 1262
QY 516 -CTCTC-----CCAAA--G-C-GG---TGSC-T---TTGTG-A---GTGAA 546
Db 1263 GGGCTGTGAGCCCTGCCCTCAACATGACTGGAGATGGGCGTCATTGTGTAGCTGTGGA 1322
QY 547 GA---C-GAATACTTG--GAA-ATT-----CAGGCACTAC-----CC--GG-- 579
Db 1323 GATCTCTGAATTC-TGCCAGAACATTTCTCTCTCTGTGAATTACTGTATAACCATGGCC 1381
QY 580 -GAGCA-GTCAGG-----GACTACGAG-----TGCA-----G-----TGCTTCC 612
Db 1382 ATTGCGA-CATCTCTGGGCTTCCAGACTGCCAGCCCACTTGCACTGGCGCCCTGCTTC 1440
QY 613 AATGACGTGCCGCG-GC--CCGTGGTACGAGAGTA-AAGGTCA--CCGTGACTAT-- 663
Db 1441 ACTG--GTAAACCGTCTCTCC-TGG-CCGG-GA--ACAATTTCACTCCCATCATCTATAA 1493
QY 664 -CC-----ACCATAA-----TTTCAG-----AA-GCC-----AAGG 698
Db 1494 AGAGCTTCCCTTGAGGACCAT-CACGCTCTCTCAGGAGGAGGAGAAAGCCTCTACG 1552
QY 689 GT-ACAGGTGC--CC-C-GTGGGCAAA-----AG-G-----GGACA----- 720
Db 1553 CTGAC-----GTCAATGCTCGGTGG--CAAACTGCTAGAGAACTTGCAATCGGGCTT 1606
QY 721 -CT-----GC--AGTG--TGA-----AGCTTC-----AG--CAGTC----- 744
Db 1607 TTCTCTCCAACTGAGTGTAGTGTGATGATGAGACCTCTCCCGAGAGCACTGCTTGGCA 1666
QY 745 -CCC--TCAGCA--GAA-----TTCCAGT--GGTACAAG-- 772
Db 1667 AGCCATTCTACTGGAAGTGTCTCTCCCACTCAAGTACCGTCCAGGGGACCCCTCA 1726
QY 773 -A-----TG-ACAA--AAGACTGAT-----TGAAGGA----- 795
Db 1727 TCCACTATCTGAACAACCA--ACTGATAAGCGCGGTGATGAGGCGCTTCTCTCCAGGC 1784
QY 796 -AAGAAAGGGGTGAA--AGTGAATAA--CAG-----AC-----CT--TTCC-- 829
Db 1785 TCGCAGGAGAGCGG-GAAGAGGAGTGGAGAGCCAGGAGAGAGAGTCCGCTTCTTCCCA 1843
QY 830 TCTC-A--AAAC-TCATCTTCTTCA-----ATGCTCTGAACATGACTATG--GGA 874
Db 1844 TCTCGAGGAGAGCGT-C-----CAGGAGGAGTGGCCCTGAACCTAAGTATGCTGGA 1895
QY 875 -ACTACACTTGGG-TGGC-----CT-CCA-----ACA-----AG----- 900
Db 1896 CGAGTACTTCCAGTGGATGGCTACAAAGGCTACCACTTGTGTCTACAGCCCGCCAGGATG 1955
QY 901 -CT-----GGGC-----CACA-----CCAATGCCAGCA 922
Db 1956 CGTCACCTGTGTGCCCATGTAGTGAAGGGTACTGTCAATGAGGCGCAATGCAAGCA 2015
QY 923 TCATGCTATTGG--TCCAG-----GCG--CCGTCA-----GCG 952
Db 2016 -CTGCGAGATGGGCCCGAGTGCAGTGCAGTGCAGCACTTTCAGCATCTACATCTCTGGGGCG 2074
QY 953 A-G--GTGAGC-----AAGC-----GGCA--CGTC--GA-----GGAGGC 980

Db 2075 AACCGTGTGAGCATCTAAGCGTGAAACTTGGGCACTTCTTCGGGATCCTCTTTGGAGCCC 2134
QY 981 AGCGTG-OGTCTGCTGCT-GCC-TCTT--C-----TGCTCTTGAC-- 1022
Db 2135 TGGGTGCCCTCTTGTCTACTGCGCATCTAGCATGTGTGTGCTTCTTCACTTCTGCGGCTGT 2194
QY 1023 TC-T--CAAATTTT 1033
Db 2195 CCATGAACAAGTTCT 2209

RESULT 29
US-07-596-467-1
; Sequence 1, Application US/07596467
; Patent No. 5308862
; GENERAL INFORMATION:
; APPLICANT: Chappell, J.
; APPLICANT: Saunders, Court A.
; APPLICANT: Cuellar, R.
; APPLICANT: Wolf, Fred R.
; TITLE OF INVENTION: Method and Composition for Increasing
; TITLE OF INVENTION: Sterol Accumulation in Higher Plants
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & Milhamow
; STREET: 180 N. Stetson St.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; APPLICATION NUMBER: US/07/596,467
; FILING DATE: 19901012
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; TELEPHONE: 312 616-5400
; TELEFAX: 312 616-5400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4768 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 164..2827
; US-07-596-467-1

Query Match 42.8%; Score 443.4; DB 1; Length 4768;
Best Local Similarity 38.5%; Pred. No. 2.7e+02;
Matches 888; Conservative 0; Mismatches 107; Indels 1314; Gaps 249;

QY 1 ATGAA-----A---ACCATCC---AGC---CA--A--AA 21
Db 528 ATGAAGCTTTGGCCCTTTTCTGCTTTTCTAGAGCGAGTGCACATAGCA 587
QY 22 A---TGCAC-AA-TTCTATCTCT-----T---GGG-CAATCT---TCACGG---GG 57
Db 588 AGTTTCCCTTAAGTTCAAACCTCTCAGGATGAAGTGAAGAAATATAGCTCGCGAATGG 647
QY 58 -CTGG-----C-----TGCTC-TGTG---TCTCTTCCAA--GGAGT-- 86
Db 648 CAATTCGGGGCCCCCACTTACCCCTGTGCTCTTGTGGAATGTCTGTAAATGGAGTTG 707
QY 87 GC-CC-----GTGCG-CAGC-GGAGAT-----GC--CA---C-----C 111

Sequence 1, Application US/07934374
Patent No. 5349126
GENERAL INFORMATION:
APPLICANT: Chappell, J.
APPLICANT: Saunders, Court A.
APPLICANT: Cuellar, R.
APPLICANT: Wolf, Fred R.
TITLE OF INVENTION: Process and Composition for Increasing
TITLE OF INVENTION: Sterol Accumulation in Higher Plants
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & Milnamow
STREET: 180 N. Stetson St.
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,374
FILING DATE: 19920814
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 616-5400
TELEFAX: 312 616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4768 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 164..2827
US-07-934-374-1
Query Match 42.8%; Score 443.4; DB 1; Length 4768;
Best Local Similarity 38.5%; Pred. No. 2.7e+02;
Matches 888; Conservative 0; Mismatches 107; Indels 1314; Gaps 249;
QY 1 ATGAA-----A---ACCATCC---AGC-----CA--A--AA 21
Db 528 ATGAAGCTTTGGCCCTTTTCTGCTGCTTTTGTGATGACCTTTCTAGAGCGAGTGCACTAGCAA 587
QY 22 A---TGAC-AA-TTCTATCTCT-----T---GGG-CAATCT---TCACGG---GG 57
Db 588 AGTTTGCCCTAAGTTCAACTCTCAGATGAAGTAAGGGAATAATATAGCTGCGGGAATGG 647
QY 58 -----CTGG-----C---TGCTC-TGTG---TCTCTTCCAA--GGAGT-- 86
Db 648 CAATTCCTGGGCCCCACATTCACCTTGTGATGCTCTGTGGATGCTCTGTAAATGGAGTTG 707
QY 87 GC-CC-----GTGCG-CAGC-GGAGAT-----GC-CA---C---C 111
Db 708 GCACCATGTACGGGGTGGCTGAGCTTGAAATCATGTGCTGTTGGCTGCAATGCTGTGC 767
QY 112 TTCCCCAAAGCTA---TG-----GACA-----A---CCTGAGGTCC---GG---C--- 145
Db 768 TTGCC--AA-TACTTCTGTTCATGACATTTTCCAGCGCTGTGTCTCCTGCTCTCTTG 824
QY 146 AG-----GGG-----GAGAG---CG-CCA-----C-CCTCAG-----GTCC---AC 173
Db 825 AGCTTCTCGGGAAGTCGAGAGGGTGTCTCAATTTGTCAGCTTAGCCATTTTCCCGAG 884
QY 174 TATTG-----AC--AACCGGGTCACCC---GGG----- 196

Db 385 TTTTGAAGAGAGAGAGATAAACCACCTGTAAACCACAAAGGTCAAGATGATATGT 944
QY 197 -----TGG---CCTG-----GCTAA-----A-----CCGC--- 213
Db 945 CTTTAGGTTTGGTTCTTTGTTTCATGCTCACAGTCGATGATGATGATCCCTCCCTCAGA 1004
QY 214 --AGCAC-----CATCCTCTA-----TG---CTGG-----G 234
Db 1005 ATAGCACACAGAACAT--TCTAAAGTCTCTTGGGACTGGATGAAGATGTGTCACAGAG 1062
QY 235 AA-TGA--CAAGTGGTGC---CTGG-----ATC-CTC-----GC----- 261
Db 1063 AATTGAACCAAGTGTCTCTCTGGCAGTTTATCTCTCCAGATGATCAGCATGGACAT 1122
QY 262 -----GTGGT---CCT-----TCTG-----AG-----C---A 277
Db 1123 TGAACAGTGTGTACCTCTGAGCTTAGCTTTCTGTTGGCTGTCAAGTACATTTCTTTGA 1182
QY 278 ACACCCA-A-ACGAGT--ACA-G-----CA-----TCG----- 301
Db 1183 ACAAGCAGACAGAGTCCACATCTGCTTTAAAAAATCCTATCACGTCTCTGTGTGAC 1242
QY 302 -----AGA---TCCAG--AAC---GT-----GGA-----TG---TGT---ATGA--CGA 329
Db 1243 CCCAAGAAAGCTCCAGACAACTGTTGTAGACGGAGCCTCTGCTTGTGAGAGGAGCGA 1302
QY 330 G--GGCCCTTACA-----CCTGCTGGTG--C-AGACAG----- 358
Db 1303 GAAG---CTTTTCATCGGTTGAGGAGAGCCTG--GGGTGAGCCCAAGATAGAAAAGTTGAG 1357
QY 359 -----ACAACC-----AC-----CCAA--AGA----- 373
Db 1358 GTTATAAACCATTAGTGTGGAACTGAGAGTGCAGAGAGCTACATTTGCTTGGC 1417
QY 374 -CCTTAGGGTCCA--CCT--CATTTGTGCA-----AG--T---AT---CTCC 407
Db 1418 GCCTCT--GGGACCAGCCCTCCAGTG--GCAGCGAGGACACAGGAGCTTGAATTTGAACCTCC 1475
QY 408 CAA-----AATTGTAGAGATTTCTCAGATATCT-----CC-ATTAAT 444
Db 1476 CCAGTGAGCCTCGGCCCTAA--TGAAGA--ATGCTGCGAGATA--CTGGAGAGTCCGA-- 1527
QY 445 GAAGGAAACAATATTAGCCTCAC--TGCAATAG--CAAC---TGCT---AG-AC 487
Db 1528 GAAAGTGCAGAGTT--CCTTAGGATGCAGAGATCATCCAGTTGGTCAATGCCAGCAC 1585
QY 488 --CAGAGCCTAC-----GG-----TTACTTTGGAGACACAT----- 515
Db 1586 ATCCAGCCTACAAATGGAAACCTTA--ATGAAACTCATGAACGTGGTGTATCTATTCTG 1644
QY 516 -----CTCTCC--CAAGC----- 527
Db 1645 CCGGAGCTCTCTCCACAAAGCTTCCAGAGCCTTCTCTCTGAGTACCTGCTTACAG 1704
QY 528 -----GGT--TG---GCTT--TGTAGTGA--GA--CGAATA--- 554
Db 1705 AGATTATAATTTCCTGCTGTGATGGAGCTTGTCTGTA--GAATGTGATCGGATATG 1762
QY 555 -----CT---TGG-AAA-----TTC--- 565
Db 1763 CCCATCCTGTCGAGTAGCAGGCGCTCTGTGCTGGATGGTAAAGAGTACCAGGTTCCA 1822
QY 566 AGGCGATCACCCTGGGA--GCAGTCAG--GG-----A-CTAC-CAG--TGCGAG----- 605
Db 1823 ATGCAACAAC--GGAAGGCTGTCTGGTGCCAGCACCAACAGAGGCTGCGGGCAATAG 1880
QY 606 -----TGCC-----TCC-----A-----ATGA--CGTGGCC----- 624
Db 1881 GTCTTGTGTGAGGTGCCAGCAGCGGGTCTCTTCAGATGGGATGACCCCGGGCCAGTGG 1940
QY 625 -GCG---CC-CGTG---GT-A--C--GGAG-AGTAAGG-----T---CACC----- 654

Db 1941 TCGGTCTTCTCGTCTGTGATTCTGCAGAGTGAAGCCCTGGCTTGAACACCCGAG 2000
QY 655 -----GTGA-----A-----CTATC-----CACCATTA C-AATT-----CAGA 680
Db 2001 GGTTCGGGTGATAAAGGAGCGCT-TCGATAGCAC--TAGCAGATTTCACCGCTTACAGA 2057
QY 681 AG-----CCA-----AGG-----GTACA-----GGT-----GTCC----- 700
Db 2058 AGCTTCATGTGACCATGGCAGGGCGCAACTGTACATCCGTTTCCAGTCCAAGACAGGGG 2117
QY 701 ----CCGTGG-----ACA-A-----AAGGGGACACTGCAAG-----TGTAAGCCTC 737
Db 2118 ATGCCATGGGGATGAACATGATTTCGAAGG--CACTG-AGAAAGCACTTCTGAAGCTTC 2174
QY 738 AGCAGTCC--CCTCA--GCAGATTC--C-----AGTGGT-ACAA--GGA-TGACAA- 779
Db 2175 AGGAGTCTTTCTGAAATGCGAG-ATTCTGGCAGTTAGTGGTAACACTGCACTGACAAG 2233
QY 780 AA-----G-----ACT-GATTGA-----AGGAAAGAAAG-----GGGTGA----- 808
Db 2234 AAACCTGCCGCCATAAAGTGGATCGAGGGAAGAGGAAAGACAGATTGTGTGAAGCTGTT 2293
QY 809 -----AA-----GTG-----GAA-----AAGAGC--CTTTC-----CTCTCA----- 834
Db 2294 ATTCCAGCCCAAGGTGTGAGAGAGTATTAA-AGACAAC-TACGGAAGCTATGATTGACG 2351
QY 835 -AAAC--T--C-----ATC-----TTCTTCAATGTCTCTGAACAT--GA--CT----- 868
Db 2352 TAACATTAACAAGATCTTGTGGGTCTTCCCATGGCTGGGACATAGGAGGCTACAATG 2411
QY 869 ---ATG--GGAA-----CTACACTTGC--GTGGCC----- 891
Db 2412 CCATGCAGCAACATCGTCACGTCTATCTACA-TTGCATGTGGCCAGGATGCAGCACAG 2470
QY 892 -----TCCBAC-----AAGC---TGGGCCACACCAATG----- 916
Db 2471 AATGTGGGAGTTCAAACTGTATTACTTTAATGGAAGCAAGTGGTCC-CACGAATGAAGA 2529
QY 917 C-----CA--GCATCATG-----CTAT-----T-----TGGT----- 936
Db 2530 CTTGTATATCAGCTGCACCATGCCATCTATAGATAGGAACTGTGGGTGGTGGGACCAA 2589
QY 937 -----CCA-GGC--GCC-GTC-----A-GCAGGTGAGCAACGGCAAGT-C--GA-- 973
Db 2590 CCTCCTACCACACAGAGCGCTGTCTGCAGATGCTAGTGTTCAA-GGAGCGGTGCAAGACA 2648
QY 974 -----GGAG-----GGCA-GGC-----TGC-----GTCTGG--CT-----GCTG--- 999
Db 2649 ATCCTGGAGAAATGCACGGCAACTTGCAGAAATTGTGTGTACTGTAAATGGCTGGGG 2708
QY 1000 -----CCT-----C-TT-----CTTG-----TCTTG-----CACCTGCTTC--- 1024
Db 2709 AGTTGTCTTGTATGGCAGCATTTGGCAGCAGGACATCTTGTAGAACTCACATGGTTCATA 2768
QY 1025 -----TC-----AAATTT-----TG 1034
Db 2769 ACAGATCGAAGATAAATTTACAAAGATCTG 2797

Search completed: May 28, 2004, 21:13:39

Job time : 143.237 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2004, 15:19:20 ; Search time 2977.63 Seconds
(without alignments)

10379.861 Million cell updates/sec

Title: US-10-017-084a-522_COPY_134_1168

Perfect score: 1035

Sequence: 1 agaaaaccatccagcga.....acctgtctcattttga 1035

Scoring table: IDENTITY NUC

Gapop 1.0 , Gapext 0.1

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estom:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	878.2	84.9	1808	11	AK045973
2	878.2	84.9	1808	11	AK046377
3	866.4	83.7	874	29	AY406347
4	802.5	77.5	1039	10	BE798585
					BE798585 601581610

5	757.6	73.2	773	29	AY406348
6	756.8	73.1	856	13	BUI55617
7	724	70.0	874	29	AY406349
8	679	65.6	1085	9	AL533026
9	650.8	62.9	765	14	CD354474
10	639.2	61.8	979	12	BG261691
11	636	61.4	865	12	BI666583
12	585	56.5	3166	11	AK042854
13	580	56.0	759	14	CF737474
14	560.4	54.1	784	12	BI549918
15	541.3	52.3	545	10	BE263639
16	540.8	52.3	732	12	BI551784
17	535.1	51.7	2798	11	AK028345
18	514.6	49.7	580	12	BI548566
19	513.2	49.6	953	12	BM423716
20	503.7	48.7	861	12	BM009450
21	501.7	48.5	1033	12	BM807426
22	500.1	48.3	1083	12	BM809227
23	499.6	48.3	890	12	BI755360
24	497.3	48.0	849	14	CD327172
25	494.1	47.7	1138	12	BM556708
26	485.5	46.9	2768	11	AK030681
27	481.3	46.5	840	13	BU320256
28	479.8	46.4	1017	29	AY406973
29	476.8	46.1	740	13	BU368328
30	476.5	46.0	896	13	BO890272
31	476.4	46.0	1017	29	AY406971
32	475.6	46.0	663	12	BM724307
33	474.7	45.9	2467	11	AK044845
34	473.6	45.8	1015	29	AY406972
35	472.9	45.7	768	9	AU080629
36	467.3	45.1	601	14	CS582386
37	466.7	45.1	1304	12	BM911516
38	460.1	44.5	1953	11	AK030503
39	458.1	44.3	2096	11	AK035218
40	457.4	44.2	524	10	BE014142
41	454	43.9	553	10	BE864555
42	454	43.9	806	9	AU051132
43	445.8	43.1	14278	11	AY318958
44	445.8	43.1	14278	11	AY321317
45	445.6	43.1	5118	11	AK036018
46	445.3	43.0	2650	11	AK044093
47	444.7	43.0	4483	11	AK031352
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50	443.8	42.9	3447	11	BC034177
51	443.8	42.9	3657	11	AK088000
52	443.7	42.9	3678	11	BC023964
53	443.4	42.8	3626	11	BC051109
54	443.2	42.8	4035	11	AK044634
55	443.1	42.8	2650	11	AK044093
56	443.1	42.8	6081	29	AY414808
57	443	42.8	633	12	BG706987
58	442.8	42.8	2892	29	AY412595
59	442.8	42.8	4362	11	AK083908
60	442.7	42.8	4346	11	AK046357
61	442.6	42.8	4014	11	AK049365
62	442.5	42.8	2866	11	AK033729
63	442.5	42.8	3167	29	AY413771
64	442.5	42.8	3525	11	BC015070
65	442.5	42.8	4463	11	AK083374
66	442.5	42.8	7886	11	BC034956
67	442.4	42.7	3473	11	AK051488
68	442.4	42.7	3991	11	AK047198
69	442.3	42.7	3364	11	AK036850
70	442.3	42.7	3971	11	AK054393
71	442.2	42.7	3670	11	AK052437
72	442.2	42.7	4379	11	AK086942
73	442.1	42.7	4013	11	AK014400
74	442.1	42.7	4035	11	AK044634
75	442	42.7	2677	11	AK082284
76	442	42.7	2952	11	AK053804
77	441.9	42.7	2963	11	AK082337

78	441.9	42.7	3178	11	AK0541179	Mus muscu
79	441.9	42.7	3647	11	AK0481100	Mus muscu
C 80	441.8	42.7	3589	11	AK052257	Mus muscu
C 81	441.8	42.7	3991	11	AK0471198	Mus muscu
C 82	441.7	42.7	3326	11	AK039444	Mus muscu
C 83	441.7	42.7	3731	11	AK089450	Mus muscu
C 84	441.7	42.7	7529	29	AY406124	Mus muscu
C 85	441.5	42.7	754	12	BI550038	603192502
86	441.5	42.7	3473	11	AK030985	Mus muscu
87	441.4	42.6	3299	11	AK040388	Mus muscu
88	441.4	42.6	3316	11	AK004900	Mus muscu
89	441.4	42.6	3955	11	AK054356	Mus muscu
90	441.4	42.6	4728	11	AK087828	Mus muscu
91	441.3	42.6	2586	11	AK044240	Mus muscu
C 92	441.3	42.6	3584	11	AK030952	Mus muscu
C 93	441.2	42.6	3459	11	BC042640	Mus muscu
94	441.1	42.6	3041	11	AK038097	Mus muscu
95	441.1	42.6	3677	11	AK019471	Mus muscu
C 96	441.1	42.6	4153	11	AK083675	Mus muscu
97	441	42.6	3041	11	AK038097	Mus muscu
98	441	42.6	3633	11	AY383690	Rattus no
99	441	42.6	4356	11	AY352516	Rattus no
100	441	42.6	4477	11	AK037730	Mus muscu

RESULT 1	
AK045973	
LOCUS	AK045973 1808 bp mRNA linear HTC 20-SEP-2003
DEFINITION	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230328N06 product:NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.
ACCESSION	AK045973
VERSION	AK045973.1 GI:26337738
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 9279253
MEDLINE	10349636
PUBMED	10349636
REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374
JOURNAL	20499374
MEDLINE	211042159
PUBMED	211042159
REFERENCE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913
JOURNAL	20530913
MEDLINE	11076861
PUBMED	11076861
REFERENCE	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	
PUBMED	

REFERENCE	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
JOURNAL	563-573
MEDLINE	563-573
PUBMED	563-573
REFERENCE	6 (bases 1 to 1808) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/
COMMENT	Location/Qualifiers 1. 1808 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM:DB:B230328N06" /db_xref="MGI:2411356" /db_xref="taxon:10090" /clone="B230328N06" /sex="male" /tissue_type="corpora quadrigemina" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 204. 1238 /notes="unnamed protein product; NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus] (SWISSPROT Q62718, evidence: FASTY, 99.4%ID, 92.1%length, match=951) putative" /codon_start=1 /protein_id="BAC32555.1" /db_xref="GI:26337739" /translation="MTKIQAQKNSISWAIFTGLAALCLFQGVVPSGDAFPKAMDN VTRQESATLRCTIDNRVTRVAVLNRSTILVAGNDKCLDPRVLLSNTQTOYSIEI QNVVDYEGPYTCVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISITCIAT GREPVTWRHISGPKAVGVSEDEYLEIGITRQSGEYECASNDVAAPVRRVKVT VPPYISRAHSGVPVQKGTQCEASAVPSAFQWFKDKLVKSGKGVKVRNRPFL LSKLTFPNVSEHDYNGYTCVASNKLGTNASIMLFGVAGVSEVNNSTSRAGCIWLLP LVLVHLLKPF"
FEATURES	Source 1. 1808
ORIGIN	84.9% Score 878.2; DB 11; Length 1808; Best Local Similarity 90.5%; Pred. No. 3.5e-10; Matches 937; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
Qy	1 ATGAACACCATCCAGCCAAATGCAATTCATCTCTTTGGCAATCTTCACGGGCTG 60
Db	204 ATGAACACCATCCAGCCAAATGCAATTCATCTCTTTGGCAATCTTCACGGGCTG 263

RESULT 4	LOCUS	DEFINITION
BE798585		

QY 439 ATTAAATGAAGGAAACAATATTAGCCTCAGCTAGCACTGGTAGACGAGCCTACG 498
 Db 339 ATTAAATGAAGGAAACAATATTAGCCTCAGCTAGCACTGGTAGACGAGCCTACG 398
 QY 499 GTTACTTGAGACACATCTCTCCAAAGCGGTGGCTTGTGAGTGAAGCAATCTTG 558
 Db 399 GTTACTTGAGACACATCTCTCCAAAGCGGTGGCTTGTGAGTGAAGCAATCTTG 458
 QY 559 GAAATTCAGGCAATCACCGGAGCAGTCAAGGGGACTACAGTGCAGTGCCTCCCAATGAC 618
 Db 459 GAAATTCAGGCAATCACCGGAGCAGTCAAGGGGACTACAGTGCAGTGCCTCCCAATGAC 518
 QY 619 GTGGCGCGCCCGTGTGAGTGAAGGTAAAGGTCAACGTTGAATATCCACATACATTTCA 678
 Db 519 GTGGCGCGCCCGTGTGAGTGAAGGTAAAGGTCAACGTTGAATATCCACATACATTTCA 578
 QY 679 GAAAGCCAGGTTACAGTGTCTCCCGTGGGACAAAGGGGACACTGAGTGTGAAGCCTCA 738
 Db 579 GAAAGCCAGGTTACAGTGTCTCCCGTGGGACAAAGGGGACACTGAGTGTGAAGCCTCA 638
 QY 739 GCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAAGACTGATTGAAGGAA-A 797
 Db 639 GCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAAGACTGATTGAAGGAA-A 698
 QY 798 GAAAGGGGTGAA-AG-TGGAAACAGACG--TTTCCT-CTCAAACACTCAT--CTTC-TTC 849
 Db 699 GAAAGGGGTGAA-AG-TGGAAACAGACG--TTTCCT-CTCAAACACTCAT--CTTC-TTC 758
 QY 850 AATGT-CTCTGAA-CAT-GACTAT--GGGAACATACACTTGGCGCTCCCAACAGCTGGG 905
 Db 759 AATGTCTCTGAAACATGACTTGGGAACTACACTTTGGC--GGGCTCCCAACAGCTGGG 817
 QY 906 CACACCAATGCCAGTATCTAT--TTCGCT--TTCGCT--TTCGCT--TTCGCT--TTCGCT 937
 Db 818 -CACACCAATGCCAG-ATCATCTATTACGCTAAATAGAGCAGTACAGAAAGTTGTGAC 875
 QY 938 CAG--GC--GCGG--T-CAG--CGAG-GTGAG-----T-CAG--CGAG-GTGAG----- 959
 Db 876 CAGTGAGAGCACAATGCCGATAGGACAGTCCAGTCTACAGCCCGGAGTGTGAGCGAGC 935
 QY 960 CAACG-----GCA-----GCTCAG--GAGGCGAGGCT-----GCGTCTGGCTGCTCCCTCT 1004
 Db 936 CAAAGAAGCAGCAGGCGCG--CGAGTGA--GCAAGCTAGAGGCG--GCTTGGTGCC--- 986
 QY 1005 TCTGTCTTGTGACCTGCTCTTCAATTTTG 1034
 Db 987 TCTGG---TGC-CGCG---TCAATTGTTG 1008

RESULT 5
 LOCUS AY406348
 DEFINITION Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY406348
 VERSION AY406348.1 GI:39762322
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 773)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 PUBLISHED
 2 (bases 1 to 773)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
 Direct Submision
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES
 Location/Qualifiers
 source 1..773
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
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 /locus_tag="HCM2527"
 ORIGIN
 Query Match 73.2%; Score 757.6; DB 29; Length 773;
 Best Local Similarity 98.4%; Pred. No. 2.6e-08;
 Matches 761; Conservative 0; Mismatches 6; Indels 6; Gaps 1;
 QY 168 GTGCACATATTACAAACCGGFTCAACCGGTGGCTGGCTAACCAGCAGCACCATCTCTA 227
 Db 1 GTGCACATATTACAAACCGGFTCAACCGGTGGCTGGCTAACCAGCAGCACCATCTCTA 60
 QY 228 TGCTGGGAATGACAAGTGGTGCCTGGATCTCTGGCTGGCTCTCTGAGCAACACCCAAAC 287
 Db 61 TGCTGGGAATGACAAGTGGTGCCTGGATCTCTGGCTGGCTCTCTGAGCAACACCCAAAC 120
 QY 288 GCAGTACAGCATCAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACCTGCTC 347
 Db 121 GCAGTACAGCATCAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACCTGCTC 180
 QY 348 GGTGCAGACAGCAACCAACCAAGACCTCTAGGCTCCACCTCATTTGCAAGTATCTCC 407
 Db 181 GGTGCAGACAGCAACCAACCAAGACCTCTAGGCTCCACCTCATTTGCAAGTATCTCC 240
 QY 408 CAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTC 467
 Db 241 CAAATTTGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTC 300
 QY 468 CTGCATAGCACTGTTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAA-- 524
 Db 301 CTGCATAGCACTGTTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCAA-- 360
 QY 525 ---AGCGGTTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGCGCATCCCGGA 581
 Db 361 CGCAGCGTTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGCGCATCCCGGA 420
 QY 582 GCAGTACGGGACCTACAGTGCAGTGCCTCCATGACGTGGCGCGCCGCTGGTACGGAG 641
 Db 421 GCAGTACGGGACCTACAGTGCAGTGCCTCCATGACGTGGCGCGCCGCTGGTACGGAG 480
 QY 642 AGTAAAGTCAACGTTGAACCTATCCACATACATTTCAAGACCAAGGTTACAGTGTCCC 701
 Db 481 AGTAAAGTCAACGTTGAACCTATCCACATACATTTCAAGACCAAGGTTACAGTGTCCC 540
 QY 702 CGTGGGCAAAAGGGGACACTGCGAGTGTGAAGCTCTCAGCAGTCCCTTCAGCAAGATTCCA 761
 Db 541 CGTGGGCAAAAGGGGACACTGCGAGTGTGAAGCTCTCAGCAGTCCCTTCAGCAAGATTCCA 600
 QY 762 GTGGTACAGGATGACAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAG 821
 Db 601 GTGGTACAGGATGACAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAG 660
 QY 822 ACCTTTCTCTCAAACTCATCTTTCTCAATGCTCTGACATGACTATGGAAGTACAC 881
 Db 561 ACCTTTCTCTCAAACTCATCTTTCTCAATGCTCTGACATGACTATGGAAGTACAC 720
 QY 882 TTGCGTGGCTCCAAACAGCTGGGCCACCAATGCCAGCATCATGCTATTG 934
 Db 721 TTGCGTGGCTCCAAACAGCTGGGCCACCAATGCCAGCATCATGCTATTG 773

ORIGIN

Query Match 70.0%; Score 724; DB 29; Length 874;
Best Local Similarity 89.1%; Pred. No. 3.4e-07;
Matches 779; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

QY 168 GTGCACATATGACACCGGGTACCCGGGTGGCTGGCTAAACCGCAGCACCACATCTCTTA 227
Db 1 GTGCACAAATTTGACACCGAGTACCCGGGTGGCTGGCTAAACCGCAGTACCATCTCTTA 60
QY 228 TGCTGGGAATGACAACTGGTGGCTGGATCTCGGTGGTCTCTGAGCAACACCCAAAC 287
Db 61 TGCTGGAAATGACAACTGGTGGCTGGATCTCTGGTGGTCTCTGAGTAAACACCCAGAC 120
QY 288 GCAGTACAGCATCGAGATCCAGAACCTGGATGTGTATGACGAGGGCCCTTACACCTGCTC 347
Db 121 CCAGTACAGCATCGAGATCCAGAACTGGATGTGTATGAGGGCCCTTATACCTGCTC 180
QY 348 GGTGCAGACAGCAACCAACCCAGACCTCTAGGTGCCACCTCATTTGTGCAAGTATCTCC 407
Db 181 GGTGCAGACAGCAACCAACCCAGACCTCTAGGTGCCACCTCATTTGTGCAAGTATCTCC 240
QY 408 CAAAATTGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCTCAC 467
Db 241 CAAAATTGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGGAACAAATATTAGCTCAC 300
QY 468 CTGCATAGCACTGGTGTAGACCGAGCCTACGTTACTTGGAGACACATCTCTCCCAA --- 524
Db 301 TTGCATAGCCACAGGTAGACCGAGCCTACGTTACTTGGAGACACATTTCTTCCCAAGCC 360
QY 525 ---AGCGGTGGCTTTGTGAGTGAGACCAATCTTGAAGTGGGATCGAGGATCCAGGGCATCACTCGGGA 581
Db 361 CGCAGCGGTGGCTTTGTGAGTGAGATGAGTACCTGGAGATCCAGGGCATCACTCGGGA 420
QY 582 GCAGTCAAGGAGTACGAGTGCAGTGCCTTCCAAATGACGTGGCGCGCGCTGGTACGAG 641
Db 421 ACAGTCAAGGAGTACGAGTGCAGTGCAGTGCCTTCCAAAGCTGGCGCGCGCTGGTACGAG 480
QY 642 AGTAAAGTCAAGTGAATCTATCCACATATCCATTTCAAGGACCAAGGTTACAGGTGTCCC 701
Db 481 AGTGAAGTCAAGTGAATCTATCCACATATCCACATATCCAGAGCTAAGGGCACAGGTGTCCC 540
QY 702 CTTGGGACAAAAGGAGACATCTCAGTGTGAGGCTCAGAGTCCCTCAGCAGATTTCA 761
Db 541 CTTGGGACAAAAGGAGACATCTCAGTGTGAGGCTCAGAGTCCCTCAGCAGATTTCA 600
QY 762 GTGGTCAAGGATGACAAAGACTGATTAAGGAAAGAGGGGTGAAGTGGAAACAG 821
Db 601 ATGGTTCAAGGATGACAAAGACTGATTAAGGAAAGAGGGGTGAAGTGGAAACAG 660
QY 822 ACCTTTCTCTCAAACTCTCTTCTCAATGTCTCTGAACTGATGGAATCTGAGTCAAC 881
Db 661 ACCTTTCTCTCAAACTCTCTTCTCAATGTCTCTGAACTGATGGAATCTGAGTCAAC 720
QY 882 TTGGTGGCTCCAAAGAGTGGGACCAACCAATGCCAGCATCATGCTATTGTTGGTCCAGG 941
Db 721 ATGTGTGGCTCCAAAGAGTGGGACCAACCAATGCCAGCATCATGCTATTGTTGGTCCAGG 780
QY 942 CGCGTCAAGGAGTGAAGCAAGCACTGTGAGGAGGAGGAGGCTGCTGCTGCTGCTGCC 1001
Db 781 TGCTGTGAGTGAAGTGAAGCACTGTGAGGAGGAGGAGGAGGCTGCTGCTGCTGCTGCC 840
QY 1002 TCTTCTGCTGTGACCTGCTCTCAAAATTTGA 1035
Db 841 TCTTCTGCTGTGACCTGCTCTCAAAATTTGA 874

RESULT 8
AL533026

LOCUS

DEFINITION AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone

CSODN005YD20 5-PRIME, mRNA sequence.

ACCESSION

AL533026

VERSION
KEYWORDS
SOURCE
ORGANISM

AL533026.2 GI:31070858

EST.

Homo sapiens (human)

Homo sapiens

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1085)

J. W. B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:12796519.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 6387.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CSODN005DB100P1&cluster=6387.f. Contact :

Peng Liang Email: fliang@lifetech.com URL: invitrogen Corporation 1600

http://fulllength.invitrogen.com/

Paradise Avenue Genoscope sequence ID: CSODN005DB100P1.

Location/Qualifiers

1..1085

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODN005YD20"

/tissue_type="ADULT BRAIN"

/dev_stage="adult"

/clone_lib="Homo sapiens ADULT BRAIN"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo (GT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

ORIGIN

Query Match

Best Local Similarity 65.6%; Score 679; DB 9; Length 1085;

Matches 772; Conservative 1; Mismatches 19; Indels 364; Gaps 50;

QY 2 TGAACCAATCCAGCCAA-AAA--TGACAAATTTCTATCTCTGGCAGTCTTTCAGGGGC 58
Db 2 TGAAC--AT--AG--AACAAATTTGACAA---A-----AAAC--CA---NGC 35
QY 59 TGGCTGTCTGTGTCTCTTCCAGGAGTCCCGTGCAGCGAGATGCCACCTCAGGTGCACTATTG 118
Db 36 TNNTTAC---NNGTC---CNNA--ATT--CC-----CGG-GATG----- 63
QY 115 AAGCTATGGAACAAGTCAAGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTG 178
Db 64 --GCTA-----GGAGA-----A-----CAG-----CTATT-- 81
QY 179 ACAACCGGTCACCCGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATG 238
Db 82 ---C---CA---GTG---T---T---GCG------TA-----GAAAT-- 99
QY 239 ACAAGTGGTGGTGGATCTCGGTGGTCC--TTCTGAGCAACACCCAAACGAGTACAGC 297
Db 100 ---T---T---AT--TC-----CCATTCGGA-----C 115
QY 298 ATCGAGATCCAGAACGTTGATGTATGACGAGGGCCCTTACACCTGCTCGGTGACACA 357
Db 116 -TC-----CTTG-ACTT---TGIGT-----TTAAA-----TAGG---AG--- 141
QY 358 GACACCAACCAAGACCTTAGGCTCCACCTCATTTGTGCAAGTATCTCCAAAATTTGA 417
Db 142 GA-AA-----TCAAAG---CTA-----A---ATT---AAAGTATCTCCAAAATTTGA 179
QY 418 GAGATTTCTTCAGATATCTCATTAATGAAGGAAACAAATATTAGCTCCTCAGTCAAGCA 477

180 GAGATTCTTCAGATATCTCCATTATGAAGGAACAATATTAGCTACCTCCATCAGCA 239
QY
478 ACTGGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTT 537
Db
240 ACTGGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTT 299
QY
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QY
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658 AACTATCCACCATACATTTTCAGAAAGCAAGGTCACAGGTGTCCCGTGGGACAAAAGGG 717
Db
420 AACTATCCACCATACATTTTCAGAAAGCAAGGTCACAGGTGTCCCGTGGGACAAAAGGG 479
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778 AAAA----- 781
Db
540 AAAAGAGCTGMAATCTCAATTCACAGTTTGGTTATGATGGGAAGCTTCTCCCATGGTG 599
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782 ----- 781
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600 GAGCAATGGTGTCAAAGCGCCAGTGGGATCAATCAGCCTGACTTGTCTGGCAGAACTCTC 659
QY
782 --GACTGATTGAAGGAAGAAAGGGGTGAAGTGAAGGAAGGAGTGAAGTGAAGTGAAGT 839
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1020 GCTTCTCAAAATTTGA 1035
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900 GCTTCTCAAAATTTGA 915

RESULT 9
CD354474
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD354474 765 bp mRNA linear EST 15-JUL-2003
UI-N-GMO-cydg-16-0-UI.r1 NIH BMAP_GMO Mus musculus cDNA clone
IMAGE:30361215 5', mRNA sequence.
CD354474
CD354474.1 GI:31146975
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 765)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-rc@mail.nih.gov
Tissue procurement: Dr. Jim Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouseefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pyX-5.

FEATURES
source

Location/Qualifiers
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/mol_type="mRNA"
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/tissue_type="whole brain"
/dev_stage="1, 5 and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_GMO"
/note="Organ: Brain; Vector: pyX-Asc; Site:1: EcoR I;
Site:2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was size
selected according to mRNA size fraction, ligated with EcoR
I adaptor, digested with NotI and then cloned
directionally into pyX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAATCTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 62.9%; Score 650.8; DB 14; Length 765;
Best Local Similarity 90.4%; Pred No. 1.9e-05;
Matches 697; Conservative 0; Mismatches 68; Indels 6; Gaps 6;
QY 15 GCCAAAATGCAATTTCTTCTTGGGCAATCTTCAGCGGGCTGGTCTCTGTCT 74
Db 1 GGCAAAATGCAATTTCTTCTTGGGCAATTTTCAGCGGGCTGGTCTCTGTCT 60
QY 75 CTTTCAAGAGTGGCGGTGGCGGAGATGCCACCTTCCCAAGCTATGCAACGT 134
Db 61 CTTTCAAGAGTGGCGGTGGCGGAGATGCCACCTTCCCAAGCTATGCAACGT 120
QY 135 GACGCTCCGCGAGGCGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGCTCACCG 194
Db 121 GACGCTCAGGCGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGCTCACCG 180
QY 195 GGTGGCTGGCTAAACCGGAGCACCCTCTCTATCTGGGAATGACAAGTGGTCTGGA 254
Db 181 GGTGGCTGGCTAAACCGGAGCACCCTCTCTATCTGGGAATGACAAGTGGTCTGGA 240
QY 255 TCCTCGCTGGTTCCTTCTGAGCAACACCCAGCAGTACAGCATCGAGATCCAGAACT 314
Db 241 TCCTCGTGGTTCCTTCTGAGTAACCCAGCAGTACAGCATCGAGATCCAGAACT 300
QY 315 GATGTGTATGACGAGGCGCTTTACACCTGCTCGGTGAGATGACAAGTGGTCTGGA 374
Db 301 GATGTGTATGAGGCGCTTTACACCTGCTCGGTGAGATGACAAGTGGTCTGGA 360
QY 375 CTCAGGTCACCTCATGTTGCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATAT 434
Db 361 CTCAGGTCACCTCATGTTGCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATAT 420
QY 435 CTCATTAATCAAGGGAACAATATTAGCTCAGCTGATGCACTGCTAGCAGAGGCC 494
Db 421 CTCATTAATCAAGGGAACAATATTAGCTCAGCTGATGCACTGCTAGCAGAGGCC 480
QY 495 TACGGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGCAATA 554
Db 481 TACAGTAACTGGAGACATATTTCTCCCAAGCGGTGGCTTTGTGAGTGAAGTGAATA 540

QY 555 CTTGGAAATTCAGGGCATACCCGGAGCAGTCAAGGGGACTACAGTGCAGTGCCTCCAA 614
 Db 541 CTTGGAGATCCAGGGCATACTCGGGAACTAGTCAAGGGGAGTGCAGCGCTCCAA 600
 QY 615 TGACGTGGCGCGCCCGTGGTACGGAGAGTAAAGTCAACCGTGAACCTATCCACCATACAT 674
 Db 601 CGAGTGGCGGCGCCAGTGGTACGAGAGTGAAGTCAACCGTGAACCTATCCACCATACAT 660
 QY 675 TTCAAGACCAAGGTTACAGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGC 734
 Db 661 CTCAAGAGCTAAGGGCACAGTGTCCCGTGGGCGACAGAGGACTCTGCAGTGTGAAGC 720
 QY 735 CTCAAGAGTCCCTCAGCAGAAATTCAGTGTGATCAAGGATGACAAAGACT 785
 Db 721 TTC-GCAGT-CCTTCAGCAGAAATTTCA-TGGT-C-NGGATGAC-AAAGACT 765

RESULT 10

LOCUS BG261691 979 bp mRNA linear EST 13-FEB-2001
 DEFINITION 602373361F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4480983 5',
 mRNA sequence.

ACCESSION BG261691

VERSION BG261691.1

KEYWORDS GI:12771416

SOURCE EST.

ORGANISM Mus musculus (house mouse)

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 1 (bases 1 to 979) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10315 row: i column: 16

High quality sequence stop: 715.

FEATURES

source

1. 979

/organism="Mus musculus"

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/clone="IMAGE:4480983"

/tissue_type="retina"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_94"

/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dr primed.

Average insert size 3.3 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

ORIGIN

Query Match 61.8%; Score 639.2; DB 12; Length 979;
 Best Local Similarity 73.3%; Pred. No. 0.0001;
 Matches 792; Conservative 0; Mismatches 88; Indels 200; Gaps 80;

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 Db 39 GAGAAATGGGGTCTGTGGTACCTGTCTCTCCCTCGGAAAGTGC-----CTCGTG 88
 QY 43 ----GCAATCT-TCAAGGGGCTGCTGTCTGTCTCTT-----CCA-AGGAGTGCCTG 92
 Db 89 TCGTG---TCTCTCA-----GGCTGTAT---TC-CTTGATCCCAAGAGTGCCTG 134
 QY 93 GCGCAGCGGAGATGCCACCTTCCCAAGCTATGGAACAGCTGACGCTCCGGCAGGGGGA 152

Db 135 GCGTACGCGAGATGCCACCTTTCCCAAGCTATGGAACAGTGCAGCGTCAGCAGGGGGA 194
 QY 153 GAGCGCCACCTCAGTGCAGTATTGACAACCGGGTCAACCGGGTGGCTGGCTAAACCG 212
 Db 195 GAGCGCCACCTCAGTGCAGTATTGACAACCGGGTCAACCGGGTGGCTGGCTAAACCG 254
 QY 213 CAGCAACCTCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCCTCGCGTGGTCTTCT 272
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 QY 273 GAGCAACCCCAACCGCAGTACAGCATCGAGATCCAGAACGTTGATGTATGACAGGG 332
 Db 315 GAGTAAACCCAGAGCCAGTACAGCATCGAGATCCAGAAATGATGATGATGATGAGGG 374
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 Db 375 CCCTTATACCTGCTCGGTGACAGACAGCAACACCCAAAGACCTCTAGGGTCCACTCAT 433
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 QY 513 CATCTCTCCCAAGCGTGGCTTGTGAGTAGAGCAACAACTACTTGGAAATTCAGGGCAT 572
 Db 554 TATTTCTCCCAAGCGTGGCTTGTGAGTAGAGTTCCTTCAGATATCTCCATTAATGAAGGGA 613
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 QY 860 AACATGACTATGGAACTACACTTGGCTGGCTCCCAACAGCTGGGCGCACCAATGCCA 919
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RESULT 11

BI666583

LOCUS

DEFINITION

603291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5',

mRNA sequence.

ACCESSION BI666583

VERSION BI666583.1

KEYWORDS GI:15580816

SOURCE Homo sapiens (human)

BI666583 865 bp mRNA linear EST 12-SEP-2001
 603291469F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310833 5',
 mRNA sequence.

BI666583

GI:15580816

EST.

Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 865)
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: rstraub@xmail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Pietro Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLAM11787 row: j column: 18
 High quality sequence stop: 742.
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 (gtcgag); Oligo-dT primed using primer
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 insert size 2.3 kb and normalized to 10^5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this is
 a NIH_MGC Library."
 ORIGIN
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 Best Local Similarity 96.3%; Pred. No. 7.7e-05;
 Matches 658; Conservative 0; Mismatches 11; Indels 14; Gaps 14;
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 QY 121 GCTATGGAACAGTCAAGTCCGGGAGGAGAGCGCCACCTCAGGTGCATTTGAC 180
 DB 303 GCTATGGAACAGTCAAGTCCGGGAGGAGAGCGCCACCTCAGGTGCATTTGAC 362
 QY 181 AACCGGTCACCGGGTGGCTGCTTAACCGCAGACCATCTCTATGCTGGGAATGAC 240
 DB 363 AACCGGTCACCGGGTGGCTGCTTAACCGCAGACCATCTCTATGCTGGGAATGAC 422
 QY 241 AAGTGGTCTGGATCTCTGGGTGTCTTCTGAGCAACCCCAACCGCAGTACGATC 300
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 DB 483 GAGATCCAGAGAGTGTGTATGACGAGGCGCTTACACCTGCTCGGTGACAGACAC 542
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 RESULT 12
 AK042854 3166 bp mRNA linear HTC 19-SEP-2003
 LOCUS Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 DEFINITION enriched library, clone:A73031E08 product:NEUROTRIMIN PRECURSOR
 (GP65) homolog (Rattus norvegicus), full insert sequence.
 ACCESSION AK042854.1 GI:26089310
 VERSION HTC; CAP trapper.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 REFERENCES High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
 MEDLINE Genome Res. 10 (10), 1617-1630 (2000)
 PUBMED 20499374
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yanamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 JOURNAL sequencing pipeline with 384 multicapillary sequencer
 MEDLINE Genome Res. 10 (11), 1757-1771 (2000)
 PUBMED 20530913
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 JOURNAL of 60,770 full-length cDNAs
 MEDLINE Nature 420, 563-573 (2002)
 PUBMED 6 (bases 1 to 3166)
 6
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Onno, M., Ohsato, N.,
 Okazaki, Y., Saico, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
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 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan [E-mail:genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
 Fax:81-45-503-9216]
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL:http://genome.gsc.riken.go.jp/
 URL:http://fantom.gsc.riken.go.jp/
 Location/Qualifiers
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				Gaps	158;
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QY	61	GTCGTCTGTGTCCTTCC	AAGAGTGC	CGCGAGATGC	CACTTCCCAA
DB	266	GCGGTCTGTGCTCTTCC	AAGAGTGC	CGCGAGATGC	CACTTCCCAA
QY	121	GCTATGGCAACGTGAC	CGGTCCG	CAGGGGAG	CGCCACCTCAGTTC
DB	326	GCTATGGCAACGTGAC	CGGTCCG	CAGGGGAG	CGCCACCTCAGTTC
QY	181	AACCGGGTCACCCGGT	CGCTTAA	CCGAGAC	CAATCTCTATGCTGG
DB	386	AACCGAGTCACCCGGT	CGCTTAA	CCGAGATC	CAATCTCTATGCTGG
QY	241	AAGTGGTGCCTGCAT	CTCTCG	GTGGTCTT	CAGCAACCCAGTAC
DB	446	AAGTGGTGCCTAGAT	CTCTCG	GTGGTCTT	CAGCAACCCAGTAC
QY	301	GAGATCCAGAACGTG	GTATGAC	GAGGGCC	TTACACCTGCTCGGTG
DB	506	GAGATCCAGAA	TGTGATG	ATGAGG	CCCTTTATCTGCTCGGTG
QY					
DB					

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365	Db	AAACACCTTAAGACCTCCAGGGTCCACCTCATTTGCAAGGGTGGGCTTGGCTGGG	525
401	QY	-----TATC-----TC-----C	407
626	Db	AGGCCTGAGTGGGTGGCTGGGAATATCAACATTACTGATTTTTTCCACAATCCTAATC	685
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686	Db	CAAGCTAGGTTGGCTGTTCTCCCGACGAGTCTCTCTGGTGGTCACTTTGAAGCTAGAC	745
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473	QY	T-----A-G-----CAACT-----G-GT-----AGACAGA-----G-492	
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527	QY	-----CGG--TTGGCTT-----TG-----TG--AGTGAA	546
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547	QY	GAC-----GA-----ATACTT-----GG--AA	561
1104	Db	GACTGGATTACAGAGTCTCTTCTCCTATGTTCTCTTGTATTACTTTGTAGGCTTAA	1163
562	QY	-----ATT-----CAGG-----568	
1164	Db	TGTTTCTTTGGGTCTCCCGTTGTTTTGTGGGCTTTGTGGCAATTTCTCCAGTCTTCA	1223
569	QY	-----GC-----ATCAC-----CCGG-G--AGC-----AGTCAG-----589	
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590	QY	---GG-----GACTAC-----G-AG-TG-----C-AGTCCCTCCAATGAC-G--T	620
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621	QY	GGCCGC-----GCCCGTGGT--ACGGAGAGTAAAGTCACGTGAACAT-T--C--CAC	667
1343	Db	GG--GCTACATTGTCTGTTTTCTGACGGAGAG-AAAGG--CC-TCAAAATATTACTGCA	1395
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708	QY	-----ACA--A-AAG--GGGACACT--GC-----AGTGTGAA-GCCTCAGCAGT-----	743
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763	QY	TG-----GT--ACA--AG-GATG-----ACA--AAAGAC-TGATT-----789	
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Db      1734 GCATGATGGCAGGTGTCCAGCAGAGCCATGAAGTTCTCTTGCACAGCCCTGCTTCTCTG 1793
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Db      1794 GAATACACTTGAAGTAGATGAATGAACCTGAGTGACTCGAGAGAGACAAAGAATAG 1853
QY      901 -----C-----TGG-----GCCAC-----ACC 912
Db      1854 GGGATTGAGAAGACAAATTTGGAGAGTGAGCGAGGCCACTGTGAGCAGAGAGGAAGC 1913
QY      913 --AATGCCAGCAT-----CA-TGCTA-----T---TTGGTCAGGC-GCC----- 945
Db      1914 AGAATGCCATCATGAACCAACAGAGCTACGAGGAGTAGAATGGGGCAAGCAGCCATGAG 1973
QY      946 -----GTCAG--CGAGG-----TGAGCA-ACG---GCAGCTCGAGG---AGG- 978
Db      1974 ATGAGACTATGTTAGATGAGGGGACACTTGAGCATATGTTAG-AGG--GAGGTGAAGGT 2030
QY      979 -GCAG--G-CT-GC--G-TCTGGCTGCTG-----CCTC-----TTCTGGTC 1011
Db      2031 AGCAGCTGACTGGCAATGATCAGCTG-TGGTAGATGATGTTGACCTCAGGTTT-TTATC 2088
QY      1012 ---TTGCAC-CTGCT-----CTCT-----AAATTGCA 1035
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RESULT 13

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LOCUS      759 bp mRNA linear EST 10-OCT-2003
DEFINITION UI-M-HD0-cks-o-09-0-UI.r1 NIH BMAP_HD0 Mus musculus cDNA clone
IMAGE:30614264 5', mRNA sequence.
CF737474
CF737474.1 GI:37633810
EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      NIH-MGC http://mgi.nci.nih.gov/
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouseefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5

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FEATURES

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Location/Qualifiers
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Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTTATGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

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ORIGIN

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Best Local Similarity 83.5%; Pred. No. 0.0015;
Matches 642; Conservative 0; Mismatches 71; Indels 56; Gaps 15;

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QY      93 GGCAGCGAGATGACACTTCCCAAAAGCTATGACACACGTGAGCGTCCGGCAGGGGA 152
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QY      153 GAGCGCCACCTCAGTGCATATTGACAAACGGGTGACCCGGGTGCTGGCTAAACCG 212
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QY      213 CAGCACCATCTCTATGCTGGGAATGACAAAGTGGTGGCTGGATCTCGGCTGGTCTTCT 272
Db      233 CAGTACCATCTCTATGCTGGGAATGACAAAGTGGTGGCTGGATCTCGGCTGGTCTTCT 292
QY      273 GAGCAACACCCAAACCGAGTACAGCATCCAGATCCAGAACTGGATGTGTATGACGAGG 332
Db      293 GAGTAACACCCAGACCCAGTACAGCATTTGAGATCCAGAACTGGATGTGTATGACGAGG 352
QY      333 CCCTTACACCTGCTCGGTGACAGACAGCAACCCAGACCTTAGGCTCCACTCAT 392
Db      353 CCCTTATACCTGCTCGGTGACAGACAGCAACCCAGACCTTAGGCTCCACTCAT 412
QY      393 TGTGCAAGTATCTCCAAAATTGTAGAGATTTCCTCAGATATCTCATTAATGAAGGAA 452
Db      413 TGTACAAGTATCTCCAAAATTGTAGAGATTTCCTCAGATATCTCATTAATGAAGGAA 472
QY      453 CAATATTAGCTCCTCATGATAGCACTGGTAGACAGCCTACGGTTACTTTGAGAGACA 512
Db      473 CAACATCAGCTCCTCATGATAGCACTGGTAGACAGCCTACAGTAACCTGGAGACA 532
QY      513 CATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGACGACTTGGAAATTCAGGGCAT 572
Db      533 TATTTCTCCAAAGCGTTGGCTTTGTGAGTGAAGTACCTGGAGATTCAGGGCAT 592
QY      573 CACCGGAGCAGTACAGGGACTACGAGTGCAGTGCCTTCCAAATGACGTGGCGGCCCGT 632
Db      593 CACTCGGAAACAGTCAGGAGTACGAGTGCAGGCTCCAAACGAGCTGGCGGACCACT 652
QY      633 GGTACGAGAGTAAAGTCACTCCGTTGAATCCACCATATATTTCAGAAAGCCAGGGTAC 692
Db      653 GGTACGAGAGTAAAGTCACTCCGTTGAATCCACCATATATTTCAGAAAGCCAGGGTAC 712
QY      693 AGGTGTCTCCCGTGGGACAAAGGGGACACTGCACTGAGTGTGAGCTCAGCA 741
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RESULT 14
BI549918
LOCUS
DEFINITION
603194765F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5274161 5',
mRNA sequence.
ACCESSION
BI549918
VERSION
BI549918.1 GI:154337230
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
CDNA library Preparation: Miklos Palkovits, M.D., Ph.D.
Toshnyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHMil692 row: b column: 18
High quality sequence stop: 726.
Location/Qualifiers
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/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH MGC 95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dr primed using primer
5'-TTTTTTTTTTTTTTN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."
ORIGIN
Query Match 54.1%; Score 560.4; DB 12; Length 784;
Best Local Similarity 96.5%; Pred. No. 0.0059;
Matches 577; Conservative 0; Mismatches 5; Indels 16; Gaps 12;
QY 1 ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTTGGCAATCTTCACGGGGCTG 60
DB 193 ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTTGGCAATCTTCACGGGGCTG 252
QY 61 GTCGCTCTGCTCTCTCCAGGAGTCCCGTGGCGAGCGGAGATGCCACTTCCCCAAA 120
DB 253 GTCGCTCTGCTCTCTCCAGGAGTCCCGTGGCGAGCGGAGATGCCACTTCCCCAAA 312
QY 121 GCTATGACCAACGTGACGGTCCGCGAGGGGAGAGCCACCTTCAGTGCATATTGAC 180
DB 313 GCTATGACCAACGTGACGGTCCGCGAGGGGAGAGCCACCTTCAGTGCATATTGAC 372
QY 181 AACGGGTACCCGGGTGGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
DB 373 AACGGGTACCCGGGTGGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGAATGAC 432
QY 241 AAGTGGTGCCTGGATCTCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAATC 300
DB 433 AAGTGGTGCCTGGATCTCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAATC 492

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QY 301 GAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTTACCTGCTCGGTGACAGAC 360
DB 493 GAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTTACCTGCTCGGTGACAGAC 552
QY 361 AACCAACCAAGACCTCTAGGTCACCTCATTGTGCAAGTATCTCCCAAAATTCAGAG 420
DB 553 AACCAACCAAGACCTCTAGGTCACCTCATTGTGCAAGTATCTCCCAAAATTCAGAG 611
QY 421 ATTCTTCAGATATCTCCATTAAATGAAGGAACAATATTAGCTCA-CCTCATAGCAAC 479
DB 612 ATTCTTCAGATATCTCCATTAAATGAAGGAACAATATTAGCTCA-CCTCATAGCAAC 671
QY 480 TGGTAGACAGAGCTCAGGTTACTTGGAGACA-CATCTCTCCC--AAAGCGTTGGCTT 536
DB 672 TGGTAGACAGAGCTCAGGTTACTTGGAGACA-CATCTCTCCC--AAAGCGTTGGCTT 731
QY 537 TGTGA-GTGAAGA-CGAATACCTT-GGA-AAATCAGGGC-ATCA-CCCGGGAGCACTCA 588
DB 732 CGGACATGAAGACCGAATCTTGGACAATTC--GGCGATCACCCCGGAAC---CA 784

RESULT 15
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LOCUS
DEFINITION
601192064F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536127 5',
mRNA sequence.
ACCESSION
BE263639
VERSION
BE263639.1 GI:9137183
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 545)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Plate: LHM217 row: p column: 16
High quality sequence stop: 545.
Location/Qualifiers
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/db_xref="taxon:9606"
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="NIH MGC 7"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Query Match 52.3%; Score 541.3; DB 10; Length 545;
Best Local Similarity 99.6%; Pred. No. 0.0049;
Matches 543; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 271 CTGAGCAACACCCAAACGAGTACAGATCGAGATCCAGACGTGATGTATGACGAG 330
DB 1 CTGAGCAACACCCAAACGAGTACAGATCGAGATCCAGACGTGATGTATGACGAG 60
QY 331 GGCCCTTACCTGCTCGGTGCGAGACACACCCAAAGACTCTTAGGTCCACCTC 390
DB 61 GGCCCTTACCTGCTCGGTGCGAGACACACCCAAAGACTCTTAGGTCCACCTC 120

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586 QY -----TCAG-----GGGA---CT-----595
 777 DB AAAATTACCTAAATATCTGCTCAGCTTTCTTTTCATGACTTGGGAAGCCTTTGTTTCA 836
 596 QY -----CAGTG---CAGT-GC---CTCCATG---AC-----G-TG 621
 837 DB AACTGAAGGAAGAGTGTGTGAGTAGCTTTTGTGTGATGATGAATCTTGTGTGAGATG 896
 622 QY GCGCGGCC-----GTGTACGAGA-GT-AAAGGTCA---CC---GTGAAC---661
 897 DB GATGTGCCCTTTCTTATGTGGT---GTTGATGTGAG---CATGCCCTGGGAACCTTTG 952
 662 QY --AT--C-----ACATAC-----A-TTTCAGAAGCCA-----685
 953 DB ACATTAATGTATGTACTAAAGAAACCATACCTGCTTGTATTTTCAGAA---CAGTTT 1010
 686 QY AG-G-----GTA-CAGTG---TCCCC---GTGGGACAA---A---GGGA---718
 1011 DB AGAAGACTGTATCTGTTGAT---CTGATGTGGGGAAGGTGAGTGGGGGATTTG 1067
 719 QY CA---CTGCA-----GTGTGAAGC-----CTCAGCAGT---CC---745
 1068 DB CACTGTGCATGACCTTGTCTGGGTGTTTCAGCAATTTGTTAATACATCAGTACTACAT 1127
 746 QY C-CTCA-----GCAG---AAT-----TCC-----A 761
 1128 DB CTCTCAATAATGAAGGAATCTAAAGCAGATGGGTTCTTATCTCTTGGAAATAAA 1187
 762 QY -GTGGT-----A---CAAGGATG-----ACA-----778
 1188 DB TTGGTCCCACTTGAATTTCAAGATGGGCACAGACCATCTGATATATTACATGTTG 1247
 779 QY -----AAA---GACTGAT---GA-----AGGAAGAA-----AGG-----803
 1248 DB CCAGCAAACTATGATTTGATTTTGTGATATACAGGAATCAAGTGTCTCCCTCAGGATTA 1307
 804 QY G-----GTGAA---AGT-----GGAACACAGACT-TTCTCT-----CAA 835
 1308 DB GAAACACAAACGTGAACACGACTAGTAGGAATAACATATGCTGTGTGAATGTA 1367
 836 QY AACT-----CATCT-----TCTTCAATGTC-T---CT---GAA---CA 863
 1368 DB AACTAATGACATCTCAAGAAGCAGGAGCTT-AATCTCAGTAACTTTGAGAAGGCA 1426
 864 QY TGA---CT-----AT-----GGG-----AAC---TA-C---ACTT 883
 1427 DB -GAGATCTCCAAATACAAAATTCCTCCTCCGAGGAAGGAAAGAAACAAATAGCAGACTT 1485
 884 QY GGTG-GCTCCACA-AGCTGGCC--ACACCAATGC-----CAGCA---TCATG---927
 1486 DB GCTTGAAGCTTCC--CAGGCT--GCCTAGCCAGTGCAAAAATAGAAAATTTTCATGAA 1541
 928 QY -----CTATT---TGCTCAGGC---GCCGTGAGGAGTGGAGCAATCTTGTCCATCTCT 1652
 1542 DB AATAATGGAATGTACTCTCTCTTCTGCTGG---AGGCTGTG-TGTCA---AAGGT---C 1592
 961 QY AA--C--GG-CAGTGA-----G-GAGGG-----979
 1593 DB AATCATGCGCAGGTTGATTTCTCTCTTAGCTGTGATGAGCAATCTTGTCCATCTCT 1652
 980 QY -----CAGGC-TGCCCTGGC-----TGCTGCC 1001
 1653 DB TCCCTCCCTCCTCTTTTCTTATCAGTATG-GTATGGCTTGGTTTGTAAATG-TGTC 1710
 1002 QY TTTCTGTGCT-TG---CA-CCT-----GC-TTCT-----CAAA---1029
 1711 DB TCTT-AGGTCTGCTTCTCATCTCAGTAGCATTTCTCTTATGTGTGACTTATGCAACT 1769
 1030 QY -----TTTTGA 1035
 1770 DB TCCCTTTTGA 1780

RESULT 18

BI548566

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BI548566 580 bp mRNA linear EST 05-SEP-2001
 603189502F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5260753 5',
 mRNA sequence.
 BI548566
 BI548566.1 GI:15435878
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 580)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11657 row: d column: 02
 High quality sequence stop: 580.

Location/Qualifiers
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 /clone="IMAGE:5260753"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /clone_lib="NIH MGC 95"

note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site1: BamHI; Site 2: SalI-XhoI
 (gcgag); Oligo-dr primed using primer
 5'-TTTTTTTTTTTNN-3', size-selected for average
 insert size 2.5 kb and normalized to R0T 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI, National Institutes of Health). Note: this
 is a NIH_MGC Library."

ORIGIN

Query Match 49.7%; Score 514.6; DB 12; Length 580;
 Best Local Similarity 99.2%; Pred No. 0.033; 2; Indels 2; Gaps 2;
 Matches 518; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTGGCAATCTTCACGGGGCTG 60
 DB ATGAAACCATCCAGCCAAAATGCAATTTCTATCTTGGCAATCTTCACGGGGCTG 119
 QY GCTCTCTGCTCTTCCCAAGGAGTGCCTGTGGCAGCGAGATGCCACCTTCCCAAA 120
 DB GCTCTCTGCTCTTCCCAAGGAGTGCCTGTGGCAGCGAGATGCCACCTTCCCAAA 179
 QY GCTATGAC-AACTGACGGTCCCGCAGGGGAGAGCGCCACCTCAGGTGCTATTGA 179
 DB GCTATGACAACTGACGGTCCCGCAGGGGAGAGCGCCACCTCAGGTGCTATTGA 239
 QY CAACCGGTCACCGGGTGGCTGGCTTAAACCGCAGCACCATTCTTATGCTGGGAATGA 239
 DB CAACCGGTCACCGGGTGGCTGGCTTAAACCGCAGCACCATTCTTATGCTGGGAATGA 299
 QY CAAGTGTGCTGTGATCTCTGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCAT 299
 DB CAAGTGTGCTGTGATCTCTGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCAT 359

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QY 300 CGAGATCCAGAACGCTGGATGTGTATCAACGAGGCGCCCTTACACCTGCTCGGTGCGAGACAGA 359
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QY 360 CAACACCCCAAGACCTCTAGGCTCACTTATGTCAGAGTATCTCCCAAAATTGTAGA 419
Db 420 CAACACCCCAAGACCTCTAGGCTCACTTATGTCAGAGTATCTCCCAAAATTGTAGA 478
QY 420 GAATTTCTTCAGATATCTCCATTAATGAAGGGAACATATTTAGCTCCTCAGCTGCATAGCAAC 479
Db 479 GAATTTCTTCAGATATCTCCATTAATGAAGGGAACATATTTAGCTCCTCAGCTGCATAGCAAC 538
QY 480 TGGTAGACAGAGCCTACGGTACTTGGAGACACATCTCTCC 521
Db 539 TGGTAGACAGAGCCTACGGTACTTGGAGACACATCTCTCC 580

RESULT 19
BM423716
LOCUS
DEFINITION
AGENCOURT_G39987 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5516929
5', mRNA sequence.
ACCESSION
BM423716
VERSION
BM423716.1 GI:18391928
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 953)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2018 row: f column: 02
High quality sequence start: 10
High quality sequence stop: 571.
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Location/Qualifiers
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/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Query Match 49.6%; Score 513.2; DB 12; Length 953;
Best Local Similarity 87.9%; Pred. No. 0.23;
Matches 529; Conservative 0; Mismatches 3; Indels 70; Gaps 7;
QY 467 CCTGATAGCAACTGGTAGACAGAGCCTACGGTACTTGGAGACACATCTCCCAAG 526
Db 2 CCTG-----GGTGG-----CGATTAC--GG-----CAC-----GAG 25

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QY 527 CGTTTGGCTTTGTGAGTGAAGCAATACTTGGAAATTCAGGGCATCACCGGAGAGCAGT 586
Db 26 -GTTTGGCTTTGTGAGTGAAGCAATACTTGGAAATTCAGGGCATCACCGGAGAGCAGT 84
QY 587 CAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCCGCTGTACGGAGAGTAA 646
Db 85 CAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCCGCTGTACGGAGAGTAA 144
QY 647 AGTCAACCTGAATATCCACATACATTTCAAGAGCCAAAGGTTACAGGTGTCCCGCTGG 706
Db 145 AGTCAACCTGAATATCCACATACATTTCAAGAGCCAAAGGTTACAGGTGTCCCGCTGG 204
QY 707 GACAAAAGGGGACACTGTCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGT 766
Db 205 GACAAAAGGGGACACTGTCAGTGTGAAGCTTCAGCAGTCCCTCAGCAGAAATTCAGTGGT 264
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Db 265 ACAAGGATGACAAAAGACTGATTGAAGGAAAGAGGGGTGAAAGTGAAAACAGACCTT 324
QY 827 TCCTCTCAAAACTCATCTTCTCAATGTCTGTGAACATGACTATGGGAACATACCTTGG 886
Db 325 TCCTCTCAAAACTCATCTTCTCAATGTCTGTGAACATGACTATGGGAACATACCTTGG 384
QY 887 TGGCTTCCAAACAAGCTGGGCCACACCAATGCGCAGCATCATCTATT----- 933
Db 385 TGGCTTCCAAACAAGCTGGGCCACACCAATGCGCAGCATCATCTATTGAAAGTGAAGTAA 444
QY 934 -----GGTCCAGGCGCGCTCAGCGAGGTGAGCAACGCGCAGTCTGA 973
Db 445 CAGCCCTGACCCCTTGGAAAGGTCAGGCGCGCTCAGCGAGGTGAGCAACGCGCAGTCTGA 504
QY 974 GGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1033
Db 505 GGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
QY 1034 GA 1035
Db 565 GA 566

RESULT 20
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LOCUS
DEFINITION
603629962F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5443743 5',
mRNA sequence.
ACCESSION
BM009450
VERSION
BM009450.1 GI:16523804
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 661)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1921 row: 1 column: 16
High quality sequence stop: 659.
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Location/Qualifiers
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/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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ORIGIN

Query Match 48.7%; Score 503.7; DB 12; Length 661;
Best Local Similarity 93.9%; Pred. No. 0.11;
Matches 508; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 528 GGTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCGGAGCAGTC 587
Db 1 GGTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCGGAGCAGTC 60
QY 588 AGGGGACTAGAGTCAGTGCCTTCCATGACGTGGCGCGCGCGTGTGACGAGAGTAA 647
Db 61 AGGGGACTAGAGTCAGTGCCTTCCATGACGTGGCGCGCGCGTGTGACGAGAGTAA 120
QY 648 GGTCCCGTGAACCTACCACTACATTTTCAGAGCCAAAGGTACAGGTGTCCTCGTGG 707
Db 121 GGTCCCGTGAACCTACCACTACATTTTCAGAGCCAAAGGTACAGGTGTCCTCGTGG 180
QY 708 ACAAAGGGGACACTGCTGAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGT 767
Db 181 ACAAAGGGGACACTGCTGAGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGT 240
QY 768 CAGGATGACAAAGACTGATTTGAAGGAAGAAAGGGGTGAAGTGAAGTGAAGTGA 827
Db 241 CAGGATGACAAAGACTGATTTGAAGGAAGAAAGGGGTGAAGTGAAGTGAAGTGA 300
QY 828 CCTCTCAAACTCATCTTCTCAATGTCTCTGAACATGATGATGGAATCACTACCT 887
Db 301 CCTCTCAAACTCATCTTCTCAATGTCTCTGAACATGATGATGGAATCACTACCT 360
QY 888 GGCCTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTT----- 933
Db 361 GGCCTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTTGAAGTGAAGTGA 420
QY 934 -----GGTCCAGGCGCGTCCAGGCGCGTCCAGGAGTGAAGTGAAGTGAAGTGA 480
Db 421 AGCCCTGACCCCTTTGAAAGGTCCAGGCGCGTCCAGGAGTGAAGTGAAGTGAAGTGA 974
QY 975 GAGGCGAGGCTGGCTGTGGCTGTGCTTCTGTCTTGTGCTTGTGCTTGTGCTTGTGCT 1034
Db 481 GAGGCGAGGCTGGCTGTGGCTGTGCTTCTGTCTTGTGCTTGTGCTTGTGCTTGTGCT 540
QY 1035 A 1035
Db 541 A 541

RESULT 21
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LOCUS
DEFINITION
AGENCOURT 6581928 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471935
5', mRNA sequence.
ACCESSION
BM807426
VERSION
BM807426.1 GI:19124249
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1033)
NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE
JOURNAL
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM1981 row: c column: 08
High quality sequence stop: 639.

FEATURES
source

1..1033
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/db_xref="taxon:9606"
/clone="IMAGE:5471935"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 48.5%; Score 501.7; DB 12; Length 1033;
Best Local Similarity 93.9%; Pred. No. 0.64;
Matches 506; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 530 TTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCGGAGCAGTCAG 589
Db 1 TTGGCTTTGTGAGTGAAGACGAATCTTGGAAATTCAGGGCATCACCGGAGCAGTCAG 60
QY 590 GGGACTAGAGTCAGTGCCTTCCATGACGTGGCGCGCGTGTGACGAGAGTAAAGG 649
Db 61 GGGACTAGAGTCAGTGCCTTCCATGACGTGGCGCGCGTGTGACGAGAGTAAAGG 120
QY 650 TCACCGTGAATCTCCACCATACATTTTCAGAGCCAAAGGTACAGGTGTCCTCGTGGAC 709
Db 121 TCACCGTGAATCTCCACCATACATTTTCAGAGCCAAAGGTACAGGTGTCCTCGTGGAC 180
QY 710 AAAAGGGGACACTGCACTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGATCA 769
Db 181 AAAAGGGGACACTGCACTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGATCA 240
QY 770 AGGATGACAAAGACTGATTTGAAGGAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGA 829
Db 241 AGGATGACAAAGACTGATTTGAAGGAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGA 300
QY 830 TCTCAAAACTCATCTTCTCAATGTCTTGAACATGATGGAAGTGAAGTGAAGTGAAGTGA 889
Db 301 TCTCAAAACTCATCTTCTCAATGTCTTGAACATGATGGAAGTGAAGTGAAGTGAAGTGA 360
QY 890 CTTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTT----- 933
Db 361 CTTCCAAAGCTGGGCGCACCAATGCCAGCATCATGCTATTTTGAAGTGAAGTGAAGTGA 420
QY 934 -----GGTCCAGGCGCGTCCAGGCGCGTCCAGGAGTGAAGTGAAGTGAAGTGAAGTGA 976
Db 421 CCGTGAACCCCTTTGAAAGGTTCAGGCGCGTCCAGGAGTGAAGTGAAGTGAAGTGAAGTGA 480
QY 977 GGGCAGGCTGGCTGTGGCTGTGCTTCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 1035
Db 481 GGGCAGGCTGGCTGTGGCTGTGCTTCTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 539

RESULT 22

BM809227
 LOCUS
 DEFINITION
 AGENCOURT 6582414 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5468221
 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue procurement: DCTD/DP

cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM1971 row: h column: 14
 High quality sequence stop: 656.

FEATURES

source
 1. 1083
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5468221"
 /tissue_type="amelanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC 41"
 /note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GCACGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 48.3%; Score 500.1; DB 12; Length 1083;
 Best Local Similarity 93.7%; Pred. No. 0.85;
 Matches 505; Conservative 0; Mismatches 1; Indels 33; Gaps 1;
 QY 530 TTGGCTTTGTGAGTGAAGAGCAATCTTGGAAATTCAGGGCATCACCCGGAGAGTCAG 589
 Db 1 TTGGCTTTGTGAGTGAAGAGCAATCTTGGAAATTCAGGGCATCACCCGGAGAGTCAG 60
 QY 590 GGGACTACGAGTCAGTGCCTCCAAATGACCTGGCGCGCCGGTGGTACGGAGAGTAAGG 649
 Db 61 GGGACTACGAGTCAGTGCCTCCAAATGACCTGGCGCGCCGGTGGTACGGAGAGTAAGG 120
 QY 650 TCACCGTGAATATCCACCAATATTTCAAGACCAAGGGGTACAGGTGTCCCGTGGGAC 709
 Db 121 TCACCGTGAATATCCACCAATATTTCAAGACCAAGGGGTACAGGTGTCCCGTGGGAC 180
 QY 710 AAAAGGGGACATGCACTGTAAGACCTCAGCACTCCCTCAGCAGATTCAGTGGTACA 769
 Db 181 AAAAGGGGACATGCACTGTAAGACCTCAGCACTCCCTCAGCAGATTCAGTGGTACA 240
 QY 770 AGGATGCAAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCC 829
 Db 241 AGGATGCAAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCC 300
 QY 830 TCTCAAACTCATCTTCTTCAATGTCTTGAACATGACTATGGGAACTACACTTGGGTGG 889
 Db 301 TCTCAAACTCATCTTCTTCAATGTCTTGAACATGACTATGGGAACTACACTTGGGTGG 360

QY 890 CCTCAACAGCTGGCCACACCAATGCCAGCATCATGCTATTT----- 933
 Db 361 CCTCAACAGCTGGCCACACCAATGCCAGCATCATGCTATTTGAAAGTGAATACTACAG 420
 QY 934 -----GTTCCAGGCCCTGCAGGAGGTGAGCAACGGCAGCTCGAGGA 480
 Db 421 CCCTGACCCCTTGAAAGGTCAGGCCGCTCAGGAGGTGAGCAACGGCAGCTCGAGGA 480
 QY 977 GGGCAGGCTGCTGCTGCTGCTCTTCTGCTGCTTCTGCTGCTTCTCAAAATTTGA 1035
 Db 481 GGGCAGGCTGCTGCTGCTGCTCTTCTGCTGCTTCTGCTGCTTCTCAAAATTTGA 539

RESULT 23

BI755360 849 bp mRNA linear EST 25-SEP-2001
 603024964F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5195750 5',
 mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM11489 row: o column: 15
 High quality sequence stop: 848.

FEATURES

source
 1. 849
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5195750"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC 114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dr
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 48.3%; Score 499.6; DB 12; Length 849;
 Best Local Similarity 75.3%; Pred. No. 0.35;
 Matches 622; Conservative 0; Mismatches 118; Indels 86; Gaps 43;
 QY 2 TGAAGA--ACCATCCAGC--CAAAATGACAAATTCATCTTGGGCAATCTTCACGGGG 57
 Db 65 TGAGAGACCC--GCAGCGTC--GAGATGACCACTCTGCTACTGCTGCTCTCTCGGG 121
 QY 58 ----CTG-GCTGCTGTGTCTTCTTCCAGGAGTCCCGTGGCAGCGAGATGCCACT 112
 Db 122 ACAACTGCCCTGCTCT-----TCATCCAGGAGTCCCGTGGCAGCGAGATGCCACT 176
 QY 113 TCCCAAGACTATGGACAACTGACGTCCTCCGAGGGGAGAGAGCCCTTCAGGTGCA 172

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177 TCCCAAGCTATGACACAGCTGCGTCCGCGAGGGGAGAGCGCCACCTCAGGTGTA 236
173 CTATTGCAACCGGGTCAACCGGGTGGCTGGCTTAAACCGCAGCACCACCTCTATGCTG 232
237 CCATAGATGACCGGGTAAACCGGGTGGCTGGCTTAAACCGCAGCACCACCTCTACGCTG 296
233 GGAATGCAAGTGGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 290
297 GGAATGCAAGTGGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 354
291 GTACAGCATCGAGATCAGAACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 350
355 GTACAGCATCATGATCAGAACGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 414
351 GCAGACAGACACCA-CCCAAGACCTTGAAGGTTCACCTCATTTGCAAGTATCTCC-C 408
415 GCAGACAGACAAATCATCCCAA-ACGTCCCGGGTTCACCTTAATGCAAGTTCCTCTC 473
409 AAA-ATTGTAGAGATTCT--TCAGATATCTCATTAATGAAGGAA-CAATATTAGCC 463
474 AGATCAT-----GA-ATATCTCTCAGACATCACTGTGAATG-AGGGAAGCAGTGTGACCC 527
464 TCACCTG---CATAGCAACTGTGTAGACAGAGCTACGGTTACTTGCAGACATCTC-- 518
528 T--GCTGTGTC-TTGCTATTGGCAGACAGAGCAACTGTGATGATGAGACATCTGTCAG 584
519 TC--CCAAAGC--GGTTGGCTTTGAGTGAAGCAAGTATCTTGAAT--TCAGGGCATC 573
585 TCAACGAAGGCCAG--GGCTTTGTAAGTGAGGATGAGTACCTGGAGATCTC-TGACATC 640
574 ACCCGGAGCAGTCCAGGCACTACGAGTGCAGTGCAGTGCCTTCAATGACGTGGCGGCCGTG 633
641 AAGCGAGACAGTCCCGGAGTACGAATGACGCGCTTGAACGATGCTGCTGCGCCGAT 700
634 GTACGGAGAGT---AAAGGTTCACCGTGAATCTACCACTATACATTTTCAAGACCAAGGT 690
701 GTGCGGAAGTACAAA--TCAGTGTCACTATCTCTCCCTATATCTCAAAAGCCAA--GA 756
691 ACA--GGTGTCCCGT--GGGCAAAAGGGGACA--CTGAG-TGTGAAGCCTCAGCACT 743
757 ACACGTGGTGTTCAGTCCGG--CAGAAGGG--CATCTG-AGCTGTGAAGCCTCAGCT 811
744 CCCCTCA--GCAGAAATTCAGTGGT--AC-AGGATGACAAA--AG 782
812 CCC--CATGCTGAATTCAGTGGTTCAGAA--AAACCAG 849

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RESULT 24
CD327172
LOCUS
DEFINITION
AGENCOURT_14148239 NICHD_XGC_Eyel xenopus laevis cDNA clone
IMAGE:6949575 5', mRNA sequence.
CD327172
CD327172.1 GI:31091503
EST.
Xenopus laevis
Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 890)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM14565 row: k column: 14
 High quality sequence stop: 757.
 Location/Qualifiers
 1. .890
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:6949575"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NICHD_XGC_Eyel"
 /note="Organ: eye; vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: This is a Xenopus Gene Collection
 (XGC) library."

ORIGIN

Query Match	48.0%;	Score	497.3;	DB	14;	Length	890;
Best Local Similarity	73.3%;	Pred. No.	0.48;				
Matches	637;	Conservative	0;	Mismatches	151;	Indels	81;
Gaps	41;						

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QY 1 ATGAAAACCAT---C--CAGCCAAA---TGCACAAATTC--TATCTCTGGGCAATCT 49
DB 57 ATGGA---CATCGGGTCGACGCAAGGATGCTGCAC---TCGGT-TC-CTTGGGTTATCT 108
QY 50 TCACGGGGCTGGCTGCTGTCTCTTCCAAAGGAGTGCCTGGCGAGGAGATGCCA 109
DB 109 TCAGTGGGCTGGCTGTCTTTCCTCTCTCAAGAGTGCCTGGTGCACGGGGATGCCG 168
QY 110 CTTTCCCAAGCTATGACAAAGTGAAGTCCGCGAGGGGAGAGCGCCCTCAGGT 169
DB 169 GCTTCCCTAAAGCCATGGACAACTGACGGTTCGCAAGGGGACAGCGCCATCTCAGGT 228
QY 173 GCAC--TATTGACAAACCGGTCACCGGGTGGCTGGCTTAACCCGAGACCATCTCTA 227
DB 229 GCACAGTA--GACAAACAGAGTACACGAGTGCCTGGCTTAATCGTAGTACCATCTGTA 286
QY 228 TGCTGGGAATCAAGTGGTGC--TGGATCCTCGGTGGTCTTCTGAGCAACACCCAA 285
DB 287 CACTGGCAATCACAAGTGGT--CGATAGACCCCGTGTGGTCTTCTGGCCNACA--CAA 342
QY 286 ACG---CAGTACAGATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACC 342
DB 343 A-GAGTCAGTACAGATTCGATCCAAATGTGGACATTTATGATGAGGACCCCTACACC 401
QY 343 TGCTCGGTGACAGACAAACCCCAAGACCTTAGGTCCACCTCATTTGTGCAAGTA 402
DB 402 TGCTCTGTGACAGACAGACATCACCCCAAAACCTCTGCTGTACATCTCATTTGTCAAGT- 460
QY 403 TCTCCC-AAAATTGTAGAGATTTCTTCAGATAT--CTCCATTAATGAAGGAAACAATATT 459
DB 461 TCCCGCTCGAATTTGTGATATTTCTTCAAAATATTGCT--GTTAATGAAGGACGTAATGTC 518
QY 460 AGCCTCACCTGCATAGCAACTGGTAGACAGAGCCTACG--GTTACTTGGAGACACATCT 517
DB 519 AGCCTGATTTGCAATTCGAACCGGAGACCTGAACC--CGTAGTGAACCTGGAGATCTTGT 576
QY 518 CTCCTCAAAG--CGGTTGGCTTTGTGAGTGAAGACGAATATCTTGAATTTCA--GGGCATCA 574
DB 577 CCCCTAAGCACCG--GGTTTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 633
QY 575 CCCGGGAGCAGTCAAGGGA--CTACGAGTGCAGTGCCTCCAATGACGTGGCGGCCCGCT 632
DB 634 CTAGGGAGCAGTC--TGGAAATATATGAATGAGTGCCTTGAAGTGAAGTGAAGTGAAGTGA 691
QY 633 GTACGAGAGTAAAGTCAACCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 691
DB 692 TGTCGGAAGGGTTAAATTAACAGTTAATTATCCACCAACCATACATCTCTGGATGACACA--GAA 748

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QY 692 CA---GGTG-TCCCGTGGGACAAAAG-GGACACTCAGTGTGAAGCCTCAGCAGTCCCC 747
Db 749 CATCGGGGCTCCCCCTTGG--CCATCAGAGTATTTTCAGTGTGAAGCCTCTGCTGACCT 806
QY 748 TCAG-CAGAAATTC--CAGTGGTACAGGATGACAAAAGACTGATTCG---A-GGAAGAA 800
Db 807 GCAGCCGACTTCTTC--TGTACAGGAGACAAAAGGCTGAGTGATTCATGAGGG-- 862
QY 801 AGGGGTGAAAGT---GGAA---AACAGAC 823
Db 863 -GGGGTCAAAGTAGAGGAAACCCGAGAGAC 890

RESULT 25
BM556708
LOCUS
DEFINITION
AGENCOURT.6578223 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5467479
5', mRNA sequence.
ACCESSION
BM556708
VERSION
EST.
BM556708.1 GI:18798153
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 1138)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTP/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: LLCM1969 row: i column: 16
High quality sequence start: 8
High quality sequence stop: 517.
Location/Qualifiers
1..1138
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5467479"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NTH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Query Match 47.7%; Score 494.1; DB 12; Length 1138;
Best Local Similarity 86.1%; Pred. No. 1.5;
Matches 520; Conservative 0; Mismatches 11; Indels 73; Gaps 12;

QY 467 CTTGCATAGCACTGGTAGACGAGCCTACGGTACTTGGAGACACATCTCTCCAAAG 526
Db 3 CCTG-----GGT-----G-GC-----GTT-CTCGG-----CAC-----GAG 26
QY 527 CGGTTGGCTTTGTGAGTGAAGACGAACTTGGAAATTCAGGGCATCACCCGGAGCAGT 586
Db 27 -GGTTGGCTTTGTGAGTGAAGACGAACTTGGAAATTCAGGGCATCACCCGGAGCAGT 85

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QY 587 CAGGGGACTACAGTGCAGTGCCTCCAATGACGTGGCGCGCGCGTGTACGGAGATAA 646
Db 86 CAGGGGACTACAGTGCAGTGCCTCCAATGACGTGGCGCGCGCGTGTACGGAGATAA 145
QY 647 AGGTCAACCGTGAACCTATCCACCATACTTCAAGAGCAAGGGTACAGGTGCCCCGTGG 706
Db 146 AGGTCAACCGTGAACCTATCCACCATACTTCAAGAGCAAGGGTACAGGTGCCCCGTGG 205
QY 707 GACAAAGGGGACACTGCAGTGTGAAGCCTCAGAGTCCCTCAGCAGAAATTCAGTGT 766
Db 205 GACAAAGGGGACACTGCAGTGTGAAGCCTCAGAGTCCCTCAGCAGAAATTCAGTGT 265
QY 767 ACAAGGATGACAAAAGACTGATTGAAGGAAAGAGGGGTGAAGTGAAGAAACACACTT 826
Db 265 ACAAGGATGACAAAAGACTGATTGAAGGAAAGAGGGGTGAAGTGAAGAAACACACTT 325
QY 827 TCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTACCTCG 886
Db 326 TCCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTACCTCG 385
QY 887 TGGCCTCCAAAGCTGGGCCACACCACTATGCAGCATCATGCTATTT----- 933
Db 386 TGGCCTCCAAAGCTGGGCCACACCACTATGCAGCATCATGCTATTTGAAGTGAAGAACTA 445
QY 934 -----GGTCCAGGCGCGCTCAGCGAGTGTGAGCAACGCGACGTCGA 973
Db 446 CAGCCCTGACCCCTTGGAAAGGTCCAGGCGCGCTCAGCGAGTGTGAGCAACGCGACGTCGA 505
QY 974 GGAGGCGAGGCTGGCTGTGGCTGTGGC-TCT-TCTGGTCTTGACCTGCT-TCTCAAAT 1030
Db 506 GGAGGCGAGGCTGTGATCTGGCTGTGGCTTCTCCCTGGGCTGGCAGCATGCTGCTCCCACT 565
QY 1031 TTTG 1034
Db 566 CTTG 569

RESULT 26
AK030681
LOCUS
DEFINITION
Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
library, clone:5430428I19 product:LTMBIC SYSTEM-ASSOCIATED MEMBRANE
PROTEIN PRECURSOR (LSAMP) homolog [Rattus norvegicus], full insert
sequence.
ACCESSION
AK030681
VERSION
AK030681.1 GI:26081944
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
10349636
REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED
11042159
REFERENCE
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

```



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Db      1277 AGGAATCAAGG-ATCCGT-----CAGTCTGCCGTACACATGTGGTGTGGCAG 1326
Qy      1000 CTTCTTCTGCTGTGGCACTGCTTCT---CAAATTTT-----GA 1035
Db      1327 CGTC-CTGTTC-TGC-----CTTCTCAGCAAAATGTTAATAGA 1362

RESULT 27
LOCUS   BU320256
DEFINITION 603851118F1 CSEQCHN62 Gallus gallus cDNA clone ChEST847d5 5', mRNA
ACCESSION BU320256
VERSION   BU320256.1 GI:25828257
KEYWORDS EST.
SOURCE   Gallus gallus (chicken)
ORGANISM Gallus gallus

REFERENCE
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE   A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. 840
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST847d5"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEQCHN62"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN
Query Match 46.5%; Score 481.3; DB 13; Length 840;
Best Local Similarity 71.7%; Pred. No. 1.1;
Matches 600; Conservative 0; Mismatches 132; Indels 105; Gaps 29;

Qy      291 GTACAGATCGATCCAGAACGTGGATGTGTATGACG-AGGCCCTTACACCTGTCCG 349
Db      1 GTACAGATCCAGATCCAGAACGTGGATGTGTATGACG-AGGCCCTTACACCTGTCCG 59

Qy      350 TGCAGACAGACACACCCAAAGACCTCTAGGCTCCACCTCATTTGGCAAGTATCTCCCA 409
Db      60 TGCAGACAGACATACCCCAAGACATCTCGCGTGACCTCATTTGGCAAGTGTCCCGA 119

```

```

Qy      410 AAATTTGA--GAGATTTCTTCAGATATCTCCATTAATGAAG--GGAACAATATTAGCTTC 465
Db      120 AAAT--TACCAGAGATCTCTTCTGACATCTCCATCAATGAAGGTGG--CAAGTCAGCTTC 175
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Db      236 GCTGTGGCTTTCACTCAGCGAGCAGAGTACCTGGAGA--TCACAGGCATCACAGGAGCA 294
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Db      295 GTCGGCGAGTACGAGTGCAGTGCCTCCAAAGAGTGGCGCGCTTCTGTGTCAGCGAGT 354
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VERSION   AY406973.1 GI:39762944
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SOURCE   Mus musculus (house mouse)
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C-ark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBMED 14671302
REFERENCE 2 (bases 1 to 1017)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

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Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
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 Matches 709; Conservative 0; Mismatches 173; Indels 267; Gaps 101;

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 - (bases 1 to 740)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 12445392

CONTACT: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 28, 2004, 12:59:14 ; Search time 4693 Seconds
(without alignments)
3177.073 Million cell updates/sec

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Perfect score: 2408

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Searched: 3470272 seqs, 21671516995 residues

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Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2408	100.0	1679	6	AX358872	AX358872 Sequence
2	2408	100.0	1679	6	AX362365	AX362365 Sequence
3	2408	100.0	1679	6	AX403748	AX403748 Sequence
4	2408	100.0	1679	6	AX454470	AX454470 Sequence
5	2408	100.0	1679	6	AX464242	AX464242 Sequence
6	2408	100.0	1679	6	AX490948	AX490948 Sequence
7	2408	100.0	1679	9	AX58331	AX58331 Homo sapi
8	2316.6	96.2	1839	6	AX665342	AX665342 Sequence
9	2316.6	96.2	1839	9	AF126426	AF126426 Homo sapi
10	2303.7	95.7	2040	10	BNH8845	BNH8845 Rattus norv
11	2274.5	94.5	1068	6	AX665344	AX665344 Sequence
12	2273.3	94.4	1104	6	AX665346	AX665346 Sequence
13	2272.1	94.4	1140	6	AX665348	AX665348 Sequence
14	2262.1	93.9	1615	10	BC023307	BC023307 Mus muscu
15	2214.6	92.0	1410	10	AF282980	AF282980 Mus muscu
16	2167.7	90.0	1325	9	BC050716	BC050716 Homo sapi
17	2066.7	85.8	3216	5	GCCEPUI	GCCEPUI Gallus ga
18	2057.1	85.4	1257	5	GGCEPUI	GGCEPUI Gallus ga
19	2049.4	84.9	2935	12	AF271233	AF271233 Synthetic
20	2045	84.9	2935	12	AF271618	AF271618 Synthetic
21	1997.6	83.0	1035	5	AB011810	AB011810 Gallus ga
22	1969	81.8	1058	5	AF292935	AF292935 Gallus ga
23	1914.3	79.5	1013	5	AF292936	AF292936 Gallus ga
24	1902.1	79.0	3069	10	RATCALMA	RATCALMA Rattus norv
25	1901.6	79.0	2593	4	BTBOCAM	BTBOCAM Rattus norv
26	1897.2	78.8	2337	10	RATCALMB	RATCALMB Rattus norv
27	1888.7	78.4	2179	10	RATCALMB	RATCALMB Rattus norv
28	1879.4	78.0	6380	9	HSM805672	HSM805672 Homo sapi
29	1867.8	77.5	1533	5	PFNINH55A	PFNINH55A Homo sapi
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33	1846.8	76.7	20731	9	AP004721	AP004721 Homo sapi
34	1846.8	76.7	43087	9	AP005155	AP005155 Homo sapi
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38	1780.6	73.9	123320	9	AP000863	AP000863 Homo sapi
39	1780.2	73.9	242565	2	AC094728	AC094728 Rattus no
40	1777.8	73.8	93801	6	BD186121	BD186121 Preventio
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45	1772	73.6	171102	2	AP002808	AP002808 Homo sapi
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47	1765.6	73.3	23887	9	HSTITIAN2	HSTITIAN2 Homo sapi
48	1764.3	73.3	15597	3	AF074901	AF074901 Caenorhab
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ALIGNMENTS

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VERSION	AX358872.1				
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL	Patent: WO 0193983-A 125 13-DEC-2001; Genentech Inc. (US)				

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 VERSION AX454470.1 GI:21713859
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 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

TITTLE

Compositions and methods for the diagnosis and treatment of

JOURNAL

Cisorders involving angiogenesis

Patent: WO 0208284-A 55 31-JAN-2002;

Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

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source

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Pred. No.: 8.9e-102 Length: 1679
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ACCESSION AX464242
VERSION AX464242.1 GI:21899137
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1
Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0140466-A 375 07-JUN-2001;
Genentech Inc. (US)
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Pred. No.: 8-9e-102 Length: 1679
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 Sequence 55 from Patent WO0200690.
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 AX490948.1 GI:22323811
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 REFERENCE
 AUTHORS
 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
 Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
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 and Ye, W.
 TITILE
 Compositions and methods for the diagnosis and treatment of
 disorders involving angiogenesis
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 Patent: WO 0200690-A 55 03-JAN-2002;
 Genentech, Inc. (US)
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 AX358331.1 GI:37181786
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
 Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
 Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E.,
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 Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C.,

Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V.,
Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K.,
Xie, M.H., Yansua, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, W.I., and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL PUBMED 12975309

REFERENCE 2 (bases 1 to 1679)

AUTHORS Clark, H.F.

TITLE Direct Submission

JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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Alignment Scores:

Pred. No.: 8..9e-102 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-10-017-084A-523 (1-344) x AY358331 (1-1679)

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Db 1034 CTGGGCCACACCAATGCCAGCATCATGTATTGGTCCAGGGCGCTCAGCAGGTGAGC 1093
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValHisLeu 340
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RESULT 8

AX665342

LOCUS

DEFINITION

AX665342

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

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AUTHORS

TITLE

JOURNAL

FEATURES

source

1..1839

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Matches:

1839

329

Percent Similarity: 79.72%
 Best Local Similarity: 77.59%
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US-10-017-084A-523 (1-344) x AK665342 (1-1839)

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Db 217 CGTGTGCGGTGGCTGCGGAGTTCGGGGAAGTTGTGG-----CTGTGCAAGATGGGG 270
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QY 19 -----GlyLeuAlaLeu-----Cys-----24
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ACCESSION AF126426
VERSION AF126426.1 GI:7158997
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
REFERENCE
AUTHORS Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
TITLE Cloning and identification of human neurotrophin full length cDNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1839)
AUTHORS Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
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Best Local Similarity: 77.59% Mismatches: 2
Query Match: 96.20% Indels: 84
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US-10-017-084A-523 (1-344) x AFL26426 (1-1839)

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 VERSION U16845.1 GI:755184
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 ORGANISM Rattus norvegicus
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Schurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 2040)
 AUTHORS Struyk,A.F., Canoll,P.D., Wolfigang,M.J., Rosen,C.L., D'Eustachio,P.
 and Salzer,J.L.
 TITLE Cloning of neurotrophin defines a new subfamily of differentially
 expressed neural cell adhesion molecules
 JOURNAL J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
 MEDLINE 95198094
 PUBMED 7891157
 REFERENCE 2 (bases 1 to 2040)
 AUTHORS Salzer,J.L.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
 Center, 550 First Avenue, New York, NY 10016, USA
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 US-10-017-084A-523 (1-344) x RNUI6845 (1-2040)

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QY 12 Ile-----SerTrp----- 14
Db 271 GTTCTCAGAGCTGCGAGCTGAGCTGGATTTAGGGAGGAAATATTAGACTTTGGAGAGT 330
QY 15 -----AlaIlePhe----- 19
Db 331 CTGCGCGCT---TTTCTCTCCAGTGCATCGCGGTGCGCGGTAGTTCATCGCTGGGT 387
QY 20 -----LeuAla----- 22
Db 388 CCGCGGCTCACTCCCAACCCACCCACTTCTGTGCTCGCGCGGGCGGTGCGTGC 447
QY 23 -----Leu-----Cys----- 26
Db 448 CACTACCGAGTCTCGGAGTGTGGCTGTGCGAGATGGGGGTGTGGGTACCTGTTC 507
QY 27 -----Gln----- 28
Db 508 CTGCGCTGGAAGTCTGTGTGCTGTCTCTCAGGCTGCTTCTTGTACCCACAGA 567
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Db 1108 GCACCACTGTCAGAGAGTGAAGCTCAGCGTGAACCTATCCACATACATCTCAGAAGCT 1167
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Query Match: 94.46% Indels: 26
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Db 106 GCCACCTTCCCAAGCTATGGACACGTGACGTCCGCGAGGGGAGAGCCACCTTC 165
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QY	56	ArgCysThrIleAspAsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeu	75	
DB	166	AGGTGCACATATGCAACACCGGGTCAACCGGGTGGCTTGCTAAACCGCAGCACCATCCTC	225	
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DB	286	ACGAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGC	345	
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DB	766	TACAAGGATGACAAAAGACTGATTGAGGAAGAAGAAGGGGTGAAAGTGGAAACACAGACT	825	
QY	276	PheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCys	295	

RESULT	12
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LOCUS	linear
DEFINITION	Sequence 104 from Patent WO03002765.
ACCESSION	AX665346
VERSION	AX665346.1 GI:29290466
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1
AUTHORS	Sellar,G.C. and Gabra.H.
TITLE	Cancer
JOURNAL	Patent: WO 03002765-A 104 09-JAN-2003;
FEATURES	Cancer Research Technology Limited (GB) Location/Qualifiers 1..1104
source	

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Db      886  GTGGCTCCAAACAAGCTGGGCCACACCAATGCCAGCATCATGCTATTTGAACATAAATGAG 945
QY      312  -----Gly 312
Db      946  CCTACGAGCTCAACTTTGTTGCAAGAGTGAATACTACAGCCTGACCCCTTGGAAAGT 1005
QY      313  ProGlyValaValSerGluValSerAsnGlyThrSerArgAlaGlyCysValTrpLeu 332
Db      1006  CAGGCGCGGTGACGCGAGTGAGCAACGACGCTGCGAGGAGGCGAGCTGCGTCTGGCTG 1065
QY      333  LeuProLeuLeuValLeuHisLeuLeuLysPhe 344
Db      1066  CTGCTCTTCTGGTCTTGCACCTGCTTCTCAAAATTT 1101

RESULT 13
AX665348 1140 bp DNA linear PAT 26-MAR-2003
LOCUS
DEFINITION Sequence 106 from Patent WO03002765.
ACCESSION AX665348
VERSION AX665348.1 GI:29290467
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 106 09-JAN-2003;
Cancer Research Technology Limited (GB)
FEATURES
Location/Qualifiers
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Alignment Scores:
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Score: 2272.10 Matches: 324
Percent Similarity: 85.68% Conservative: 5
Best Local Similarity: 94.36% Mismatches: 6
Query Match: 50
DB: 6 Gaps: 6

US-10-017-084A-523 (1-344) x AX665348 (1-1140)
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QY 19 GlyLeuAlaAlaLeuCysLeuPhe-----GlnGlyValProValArgSerGlyAsp 35
Db 59 GGC-----TGCTG-TTCCTTGTAACACAGAGTGCCCGTGCAGCGAGAT 105
QY 36 AlaThrPheProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeu 55
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QY 56 ArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeu 75
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QY      196  SerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgVal 215
Db      586  TCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCCGCTGTGTCGAGAGTA 645
QY      216  LysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProVal 235
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QY      236  GlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrp 255
Db      706  GGACAAAGGGGACACTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGG 765
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QY      296  ValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPhe----- 311
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QY      311  ----- 311
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RESULT 14
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LOCUS
DEFINITION Mus musculus neurotrophin, mRNA (cDNA clone MGC:30504
IMAGE:4480983), complete cds.
ACCESSION BC023307
VERSION BC023307.1 GI:23958300
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 1615)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

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Alteschul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaby,S.J., Boeak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. 2002. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22389257
12477932
2 (bases 1 to 1615)
Strausberg,R.
Direct Submission
Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegue, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanaevati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IPAK Plate: 41 Row: h Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 26986610.

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CDS

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Percent Similarity: 90.16% Conservative: 10
Best Local Similarity: 87.43% Mismatches: 6
Query Match: 93.94% Indels: 30
DB: 10 Gaps: 9

US-10-017-084A-523 (1-344) x BC023307 (1-1615)

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QY 39 oLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrII 59
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QY 79 nAspLysTrpCysLeuAspProArgValLeuLeuSerAsnThrGlnThrGlnTyrSe 99
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Db 640 CGAGTGCAGCGCTTCAACAGCAGTGGCGGACCATGTGTGTACGAGGTGAGGTACCGGT 699
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Db      1060  CCTGCTCCTCAAAATTT 1075

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LOCUS Mus musculus neurotrophin mRNA, complete cds.
DEFINITION AF282980
ACCESSION AF282980.1 GI:12642539
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1410)
AUTHORS Kim.T.H., Choi.S.C., Kim.J., Jeon.J.W., Kim.K.D. and Lee.S.H.
TITLE Cloning and expression of mouse neurotrophin gene in the developing nervous system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1410)
AUTHORS Kim.T.H., Choi.S.C., Kim.J., Jeon.J.W., Kim.K.D. and Lee.S.H.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2000) Graduate School of Biotechnology, Korea University, 1,5-ka Anam-dong Sungbuk-ku, Seoul 136-701, Korea

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ORIGIN
Alignment Scores: 5.98e-92 Length: 1410
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Percent Similarity: 92.26% Conservative: 10
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RESULT 16
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ACCESSION BC050716
VERSION   BC050716.1 GI:30047134
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SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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REFERENCE 1 (bases 1 to 1325)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Gerge,J.G.,
          Klauener,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
          Altschul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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          Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
          Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
          Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
          Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
          Generation and initial analysis of more than 15,000 full-length
          human and mouse cDNA sequences
          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
          22388257
JOURNAL  MEDLINE
PUBMED  12477932
REFERENCE 2 (bases 1 to 1325)
AUTHORS   Strausberg,R.
TITLE     Submitted (08-APR-2003) National Institutes of Health, Mammalian
          Gene Collection (MGC), Cancer Genomics Office, National Cancer
          Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
          USA
REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
          Contact: MGC help desk
          Email: gcapbe-remail.nih.gov
          Tissue Procurement: ATCC/DCTD/DTDP
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Sequencing Group at the Stanford Human Genome
          Center, Stanford University School of Medicine, Stanford, CA 94305
          Web site: http://www-shgc.stanford.edu
          Contact: (Dickson, Mark) mcd@paxil.stanford.edu
          Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
          R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAP Plate: 110 Row: m Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7705412.
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 KEYWORDS CEPU gene; neural secreted glycoprotein.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1
 Kim,D.S., Rhew,T.H., Moss,D.J. and Kim,J.Y.
 cDNA cloning of the CEPU, a secreted type of neural glycoprotein
 belonging to the immunoglobulin-like oploid binding cell adhesion

molecule (OBCAM) subfamily
 Mol. Cells 9 (3), 270-276 (1999)
 93347334
 PUBMED 10420985
 2 (bases 1 to 3216)
 Kim,D.
 Direct Submission
 Submitted (16-FEB-1998) Pukyong National University, Microbiology,
 599-1 Daeyeon-3dong, Nam-gu, Pusan 608-737, KOREA (ROK)
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ACCESSION 272437
VERSION 272437.1 GI:1325950
KEYWORDS Brain; CPU-1; glycoprotein; GPI-anchor protein.
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ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1257)
AUTHORS Spaltmann, F. and Brummendorf, T.
TITLE CPU-1, a novel immunoglobulin superfamily molecule, is expressed
by developing cerebellar Purkinje cells
J. Neurosci. 16 (5), 1770-1779 (1996)
JOURNAL 96370549
MEDLINE 8774445
PUBMED 8774445
REFERENCE 2 (bases 1 to 1257)
AUTHORS Brummendorf, T.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-1996) Brummendorf T., Max-Planck-Institute for
Developmental Biology, Molecular Biology, Spemannstrasse 35,
Tuebingen, Germany, 72076
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Query Match: 85.43% Indels: 79
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(IgCEPUS-GFP) gene, complete cds.
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1. (bases 1 to 1638)
Kim, D.-S. and Moss, D.J.
Direct Submission
Submitted (24-MAY-2000) College of Natural Resources and Life
Science, Division of Biological Resources R-6517, Dong-A
University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of
Korea

FEATURES
source
gene
CDS

Location/Qualifiers
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1. .1638
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ORIGIN

Alignment Scores:
Pred. No.: 4,43e-82 Length: 1638
Score: 2049.40 Matches: 286
Percent Similarity: 65.28% Conservative: 28
Best Local Similarity: 59.46% Mismatches: 21
Indels: 146
Query Match: 85.11% Gaps: 31
Db: 12

US-10-017-084A-523 (1-344) x AF271233 (1-1638)

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Db 1 ATG-----GCCAGCGGAAATAATGCAGCAC---CCGCTCATGGGTGATCTTCGCCGGG 51
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Qy 40 LysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIle 59
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Qy 60 AspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsn 79
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Db 592 GAGTGCAGTGCCTCCACACAGACGTGGCGCGCTGTGTGTCAGCGAGTCAAGTCAACCGTC 651
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Qy 240 ThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAsp 259
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Qy 260 LysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLys 279
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Qy 280 LeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsn 299
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QY 312---Gly-----Pro-----GlyAlaVal-----Ser 317
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QY 318 GluValSerAsn-----Gly-----ThrSerArgArgAlaGly----- 328
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QY 341-----Leu-----LeuLys----- 343
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QY 344 Phe 344
Db 1414 TTC 1416

RESULT 20
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LOCUS Synthetic construct secretory IgCEPUS-GFP fusion protein
DEFINITION (IgCEPUS-GFP) gene, complete cds.
ACCESSION AF271618
VERSION AF271618.1 GI:14161270
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 2935)
AUTHORS Kim,D.-S. and Moss,D.J.
TITLE Neuronal-specific secretory IgCEPUS-GFP fusion protein expression
in transfected cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2935)
AUTHORS Kim,D.-S. and Moss,D.J.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2000) College of Natural Resources and Life
Science, Division of Biological Resources R-6517, Dong-A
University, 840 Hadan-2 Dong Saha-Gu, Pusan 604-714, Republic of
Korea
FEATURES
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CDS

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ORIGIN

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Alignment Scores:
Pred. No.: 5,87e-79 Length: 2935
Score: 2045.00 Matches: 290
Percent Similarity: 41.28% Conservative: 31
Best local Similarity: 37.28% Mismatches: 17
Query Match: 84.93% Indels: 440
DB: 12 Gaps: 46

US-10-017-084A-523 (1-344) x AF271618 (1-2935)
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QY 3-----Gln----- 5
Db 459 ACCACTCTCTGTCGGGGTCTCTCTGGGCAGACGGAGGGGTCTGGACCAACAGGAAGGCC 517
QY 5-----ProLys----- 7
Db 519 TTGGCCCATCCCATGTTGACCGAGCTGTATATAAGGAGGGCGCATCCGCCAAGTCCGC 577
QY 7----- 7
Db 578 TACCGGACTCAGATCTCGAGCTCAAGCTTCGAATTTCTGCAGTCGACGGTACCGGGGCC 637
QY 8 Met-----His-----Asn-----Ser----- 11
Db 638 CTGGCAGTCAGTGGGGGAGGAGGGGAGGACGACGAGCTCCGAATATGCCCCAGCGGAA 697
QY 12-----IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPheGln 27
Db 698 ATGCAGCACCCCGTCTCATGGGTGATCTTCGGCGGGATGGCGGCACCTCTCTCTCTCA 757
QY 28 GlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrVal 47
Db 758 GGAGTGCCCGTCGCGCAGCGAGATGCCACCTTCCCAAGCTATGACACACGACTGTG 817
QY 48 ArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAla 67
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QY 68 TrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArg 87
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QY 88 ValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspVal 107
Db 938 GTGGTCTCTTGGCCAAACACCAACCCAGTACAGATCCAGATCCAGATCCAGCGTGGAC 997
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Db      1058  GTGCACCTCATGTGCAAGTGTGCGGAAATATACCGAGATCTCTTGACATCTCCATC 1117
QY      148  AsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrVal 167
Db      1118  AATGAAGTGGCAACGTACGCTCAGCTCAGCTCATAGCCACGGCGAGCCAGACCCCAATC 1177
QY      168  ThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTrpLeuGlu 187
Db      1178  ACCTGAGACACATCTCGGCCCAAGCTGTGGCTTCATCAGCGAGACAGTACCTGGAG 1237
QY      188  IleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspVal 207
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QY      208  AlaAlaProValValArgArgValLysValThrValAsn-----Tyr----- 221
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QY      223  ----- 223
Db      1418  TCCACACCCAGCCTGGCAGCAGCAGGTTTCCAGCAGGTGGTGTCTTGGCCCTTTATT 1477
QY      224  -----Tyr----- 224
Db      1478  CCCCTTTTGTGTGTTTCAAGTCTAGTGTGTTTTCACCTCCTCCTCAGCTGTCTCTAT 1537
QY      224  ----- 224
Db      1538  CAACCTGAGTTTTCTGCTGTGTGAGATGCTGTGTGATAAAGTCAAGGAGAGAGGG 1597
QY      224  ----- 224
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QY      228  -----AlaLys----- 229
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QY      230  ----- 230
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QY      231  -----ThrGlyValProValGlyGlnLysGlyThrLeuGln 242
Db      1958  CCGTACATCTCGGATCGCAAGAGCACCGTGTGCGGTGGGGCAGAGAGGCGATCTGATG 2017
QY      243  CysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLysArgLeu 262
Db      2018  TGTGAAGCCTCGCTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2077
QY      263  IleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeuIlePhe 282

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Db      2138  TTCACGCTCTCCGAGCAGGACTACGCAACTACACTGCTGGCTGCCAACCAG---GGG 2194
QY      303  ---His-----ThrAsnAlaSerIleMet-----LeuPhe---Gly--- 312
Db      2195  ATCCACCGCGCGGTGCGCCACCATGTGTGAGC---AAGGCGGAGGAGCTGTTCAACGGGGTG 2251
QY      313  ---Pro-----GlyAlaVal-----SerGluValSer 320
Db      2252  GTGCCCATCTGTCGAGCTGGAGCGGCGAGCTAAACGGCCACCAAGTTCAGC---GTGTCC 2308
QY      321  Asn-----Gly-----ThrSerArgArgAlaGly----- 328
Db      2309  GCGGAGGCGAGGGCGATGCCACC-----TAC-----GGCAAGCTGACCTGAAGTTCATC 2359
QY      323  Cys-----Val---Trp-----Leu----- 333
Db      2360  TGCACACACGGCAAGCTGCCCTGTCCTGGCCACCTCGTGACCACTGACCTACGGC 2419
QY      333  ----- 333
Db      2420  GTGCAGTGTCTTCAGCGGCTACCCCGACACACATGAAGCAGCAGCACTTCTTCAAGTCCGCG 2479
QY      334  ---Pro----- 334
Db      2480  ATGCCCGAAGGCTACGTCCAGGAGCGACCATCTTCTTCAAGGAGCAGCGCAACTACAG 2539
QY      335  -----Leu----- 336
Db      2540  ACCCGCGCGAGTGAAGTTCGAGGGCGACACCTCGTGAACCGCATCGAGCTGAAGGC 2599
QY      337  -----ValLeu---His---Leu----- 340
Db      2600  ATCGACTTCAAGGAGGAGCGCAACATCTCTGGGCGACAAGCTGGAGTACAACTACACAGC 2659
QY      341  -----Leu-----LeuLys-----Phe 344
Db      2660  CACAACGTCTATATCATGCGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2713

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RESULT 21

AB011810 LOCUS 1035 bp mRNA linear VRT 09-JUL-1998
Gallus gallus mRNA for CEPU-1, complete cds.

AB011810 DEFINITION

AB011810 VERSION

AB011810.1 GI:3298455

alternative splicing; CEPU-1.

Gallus gallus (chicken)

Gallus gallus

ORGANISM

REFERENCE

1 (sites)

Kimura, Y., Shirabe, K., Fukushima, M., Takeshita, M. and Tanaka, H.

CEPU-1: an immunoglobulin Superfamily Molecule, Has Cell Adhesion

Activity and Shows Dynamic Expression Patterns in Chick Embryonic

Spinal Cord

Unpublished

2 (bases 1 to 1035)

Kimura, Y., Shirabe, K. and Tanaka, H.

Direct Submission

Submitted (03-MAR-1998) Yoshihide Kimura, Kumamoto University

Graduate School of Medical Sciences, Division of Developmental

Neurobiology; 4-24-1 Kihonji, Kumamoto, Kumamoto 862-0976, Japan

(E-mail: ykimura@gpo.kumamoto-u.ac.jp, Tel: 81-96-373-5294,

Fax: 81-96-373-5292)

Location/Qualifiers

1. 1035

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FEATURES

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CDS

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ORIGIN

Alignment Scores:
 Pred. No.: 1,75e-81 Length: 1035
 Score: 1997.60 Matches: 274
 Percent Similarity: 83.33% Conservative: 31
 Best Local Similarity: 74.86% Mismatches: 17
 Query Match: 82.96% Indels: 44
 DB: 5 Gaps: 19

US-10-017-084A-523 (1-344) x AB011810 (1-1035)

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 QY 28 GlyValProValArgSerGlyAspAlaThrPheProIlyAlaMetAspAsnValThrVal 47
 Db 82 GGAGTCCCGTGGCGAGGAGATGCCCTCCCAAGCTATGACACACGAGCTGTG 141
 QY 48 ArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAla 67
 Db 142 CGCAAGGGAGAGTGGCAGCTCAGTGTCTCGTGGACACCGCGTCAACCGCGTGGCC 201
 QY 68 TrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArg 87
 Db 202 TGGCTGAACCGCAGCATCTCTATCGCGCAATGACAAGTGTGTCTTGGACCGCAGG 261
 QY 88 ValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspVal 107
 Db 262 GTGGTGTCTCTGGCCAAACCAACCCAGTACAGCATCCAGATCCACGAGTGTGACGTG 321
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 Db 322 TACGATGAAGGCCCTTACCTGCTCGTCGACAGACACATCACCCCAAGACATCTCGC 381
 QY 128 ValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIle 147
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 QY 168 ThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGlu 187
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 QY 288 HisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSer 307
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 QY 308 ---IleMetLeuPheGlyProGlyAlaValSerGluValSerAsn---GlyThrSer--- 324
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 QY 325 ArgArgAlaGly---CysValTrpLeu-----LeuProLeu-----LeuValLeuHis 339
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 QY 340 LeuLeuLeuLys---phe 344
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RESULT 22
 AF292935 1058 bp mRNA linear VMT 24-AUG-2000
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 DEFINITION
 ACCESSION AF292935
 VERSION AF292935.1 GI:9887384
 KEYWORDS Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1058)
 REFERENCE
 AUTHORS Lodge, A.P., McNamee, C.J., Howard, M.R., Reed, J.E. and Moss, D.J.
 TITLE Characterisation of CEPU-Se, a secreted isoform of the IGLN family
 JOURNAL protein CEPU-1
 REFERENCE 2 (bases 1 to 1058)
 AUTHORS Lodge, A.P. and Moss, D.J.
 TITLE Direct Submission
 JOURNAL Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The
 University of Liverpool, Ashton Street, Liverpool, Merseyside L69
 3GE, UK

FEATURES
 Location/Qualifiers
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gene
 CDS

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ORIGIN

Alignment Scores:
Pred. No.: 8.56e-80 Length: 1058
Score: 1969.00 Matches: 273
Percent Similarity: 83.57% Conservative: 27
Best Local Similarity: 76.04% Mismatches: 19
Query Match: 81.77% Indels: 41
DB: 5 Gaps: 12

US-10-017-084A-523 (1-344) x AF292935 (1-1058)

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QY 27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAenValThr 45
Db 124 CAAGGAGTGGCGGTGGCGAGGAGATGCCACCTTCCCAAAGCTATGGACAACGTGACT 183
QY 47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAenArgValThrArgVal 66
Db 184 GTGGCGGAGAGGAGAGTGCACCGTCACTGAGTGCTCCGTGGACCAACCGGTGAC 243
QY 67 AlaTrpLeuAenArgSerThrIleLeuTyAlaGlyAenAspLysTrpCysLeuAspPro 86
Db 244 GCCTGGCTGAACCGCAGCAGCATCTCTATGCCGCAATGACAAAGTGGTGTGGACCCG 303
QY 87 ArgValValLeuLeuSerAenThrGlnThrClnTrpSerIleGluIleGlnAenValAsp 106
Db 304 AGGCTGTGTCTCTGGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 363
QY 107 ValTrpAspGluGlyProTyThrCysSerValGlnThrAspAenHisProLysThrSer 126
Db 364 GTGATGATGAGGGCCCTACCTGTCTCGTGAGACAGACATCACCACACATCT 423
QY 127 ArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer 146
Db 424 CGCGTGACCTCATTTGTCAAGTGTGCGGCAAAATTAACGAGATCTCTCTGACATCTCC 483
QY 147 IleAenGluGlyAenAenIleSerLeuThrCysIleAlaThrGlyArgProGluProThr 166
Db 484 ATCAATGAAGTGGCAACGTCAAGCTCACTGTGATAGTACGAGTCCAGACGTGGAC 543
QY 167 ValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyIleu 186
Db 544 ATCACTGGAGACACATCTGCCCAAGCTGTGGCTTCATCAGGAGGAGGAGTACTG 603
QY 187 GluIleGlnGlyIleThrArgGluClnSerGlyAspTyGluCysSerAlaSerAenAsp 206
Db 604 GAGATACAGGCATCACAGGAGGAGTGGCGGAGTACGAGTGCAGTGCCTCCAAACGAC 663
QY 207 ValAlaProValValArgValLysValThrValAenTyTrpProTyTrpIleSer 226
Db 664 GTGGCCGCGCTGTCTGTCAGGAGTCAAGTCAACCTCACTCCACCCACCTGATCTCG 723
QY 227 GluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSer 246
Db 724 GATGCGAGAGACACCGGTGTGCGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 783
QY 247 AlaValProSerAlaGluPheClnTrpTyTrpIleAspLysArgLeuIleGluGlyLys 266
Db 784 GCTGTGCGCTCTGCTGACTTCCAGTGTGTACAAAGACGACAAAGCGGCTGGCTGAAGGACAG 843
QY 267 LysGlyValLysValGluAenArgProPheLeuSerLysLeuIlePheAenValSer 286
Db 844 AAAGGGCTGAAGGTGAAACAAAGCCCTTCTCTCCGACTGACTTTCTTCTCAACGCTCTCC 903
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QY 287 GluHisAspTyGlyAenTyThrCysValAlaSerAenLysLeuGlyHisThrAenAla 306
Db 904 GAGCAGGACTACGGCAACTTACACCTTCGCTGGCTCCACACGACTAGAAACACCAACGCC 963
QY 307 Ser---IleMetLeuPheGlyPro-----GlyAlaValSerGluValSerAenGly 322
Db 964 AGCATGATC---CTTATGTGAGCAGCAGCTGAGGG---TCT-----GGGATGGGG 1008
QY 323 ThrSerArg-----ArgAlaGlyCysValTrp 331
Db 1009 ACC---CGCACAGCTTAACGGAGTGACCACTGTGCAAGACG---TGCAG-TGG 1058

RESULT 23

AF292936 1013 bp mRNA linear VRT 24-AUG-2000
LOCUS
DEFINITION
Gallus gallus CEPU-Se alpha 1 isoform (CEPU-Se) mRNA, complete cds.

AF292936
VERSION
AF292936.1 GI:9887386

KEYWORDS
Gallus gallus (chicken)
ORGANISM
Gallus gallus

REFERENCE
1 (bases 1 to 1013)
Lodge, A.P., McNamee, C.J., Howard, M.R., Reed, J.E. and Moss, D.J.
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

TITLE
Characterisation of CEPU-Se, a secreted isoform of the Iglon family
protein CEPU-1

JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1013)
Lodge, A.P. and Moss, D.J.
Direct Submission

TITLE
Submitted (04-AUG-2000) Human Anatomy and Cell Biology, The
University of Liverpool, Ashton Street, Liverpool, Merseyside L69
3GE, UK

FEATURES
source
1. .1013
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/tissue_type="brain"
/dev_stage="E18"
/gene="CEPU-Se"
/gene="CEPU-Se"
/gene="CEPU-Se"
/notes="Iglon family protein; secreted isoform of CEPU-1"

gene
CDS
1. .948
/codon_start=1
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/protein_id="AAG01879.1"
/db_xref="GI:9887387"

ORIGIN
Alignment Scores:
Pred. No.: 5.51e-77 Length: 1013
Score: 1944.30 Matches: 264
Percent Similarity: 81.84% Conservative: 29
Best Local Similarity: 73.74% Mismatches: 18
Query Match: 79.50% Indels: 48
DB: 5 Gaps: 15

US-10-017-084A-523 (1-344) x AF292936 (1-1013)

QY 1 MetLysThr-----IleGln---ProLysMethisAenSerIleSerTrp----- 14
Db 1 ATGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 39

QY 15 ---AlaIlePheThrGlyLeuAlaLeuCys-----LeuPhe-----Gln 27
 Db 40 CTAGTCGTC-----CTCTGCTCAGGCTCTCTTCTTGTCGCCGCA 81
 QY 28 GlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrVal 47
 Db 82 GGAGTGCCCGTGGCAGCGGAGATGCCCTTCCCAAGCTATGACAACTGACTGTG 141
 QY 48 ArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAla 67
 Db 142 CGCAAGGGGAGAGTCCACGCTCAGGTCTCCGTGGCAACCGGTACCCGCGTGGCC 201
 QY 68 TrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTyrCysLeuAspProArg 87
 Db 202 TGCTGACCGCAGCAGATCTCTATGCGCAATGACAGTGTGTCTTGACCGGAG 261
 QY 88 ValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspVal 107
 Db 262 GTGGTGTCTCTGGCCCAACCAACCAACCCAGTACAGCATCCAGATCCAGCGTGGACGTG 321
 QY 108 TyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArg 127
 Db 322 TACGATGAAGGGCCCTACACCTCTCCGTGCACAGACAAATCACCACCAATCTCGC 381
 QY 128 ValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIle 147
 Db 382 GTGCACCTCATTTGTGCAGTGTGCGCGAAATACCGAGATCTCTTCTGACATCTCAATC 441
 QY 148 AsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrArgProGluProThrVal 167
 Db 442 AATGAAGGTGGCAACGTCACCTCCATGTCATGCCAGCGAGGAGCAGCCCAATC 501
 QY 168 ThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGlu 187
 Db 502 ACTGGAGACACATCTCGCCCAAGCTGTGGCTTATCAGCAGGACGAGTACCTGGAG 561
 QY 188 IleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAspVal 207
 Db 562 ATCAGAGCATCAGAGGAGCAGTGGGGCAGTACGAGTGCAGTGCCTCCACAGCAGTG 621
 QY 208 AlaAlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGlu 227
 Db 622 GCGCGCCTCTGTCAGCAGGTCAAAGTCAACGCTCACTACCCACGCTACATCTCGAT 681
 QY 228 AlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAla 247
 Db 682 GCGAGAGCACCCTGTGCGGTGGGGCAGAGGGCATCTGATGTGTGAAGCTCCGCT 741
 QY 248 ValProSerAlaGluPheGlnTyrTyrLysAspAspLysArgLeuIleGluGlyLysLys 267
 Db 742 GTGCGCTCTGCTGACTTCCAGTGTGTACAAAGACGACAAAGCGGTGGCTGAAGGACAGAA 801
 QY 268 GlyValLysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGlu 287
 Db 802 GGGCTGAAGGTGGAACAAAGCCCTTCTTCCGACTGACTTCTTCAAGCTCTCCAG 861
 QY 288 HisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSer 307
 Db 862 CAGCACTACGGCACTACACCTGGTGGCTCCCAACGAGCTAGGAACACCAACCGCAGC 921
 QY 308 ---IleMetLeuPheGlyPro-----GlyAlaValSerGluValSerAsnGlyThr 323
 Db 922 ATGATC---CTTTATGGTGGACGACACTGAGGG-----TCT-----GGGATGGGACC 966
 QY 324 SerArg-----ArgAlaGlyCysValTyr 331
 Db 967 ---CGGCACGCTTAACGGAGTGACCACTGTGCAAGACG---TGCAG-TGG 1013

RESULT 24
 LOCUS RATCALMA 3069 bp mRNA linear ROD 08-MAY-1993
 DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete CDS.

M88709
 M88709.1 GI:203245
 cell adhesion-like molecule; opioid binding protein.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 (bases 1 to 3069)
 Lippman, D.A., Lee, N.M. and Loh, H.H.
 Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
 rat brain cDNA library
 Gene 117 (2), 249-254 (1992)
 92347701
 1339369
 PUBMED
 COMMENT source text: Rattus norvegicus (strain Simonsen ICR)
 (library: UZ) brain cDNA to mRNA.
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 556..603
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 TWRHLSVGGGFGVEDEVLFTSDIKRQSGVECSALNDVAAPDVRVKVITVNPYPY
 ISKAKNTGVSGQKGLSCASAVPWAEFOMFKEDRLATGLDGVRIENKGRISTLT
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ORIGIN

Alignment Scores:
 Pred. No.: 7,7e-71 Length: 3069
 Score: 1902.10 Matches: 276
 Percent Similarity: 41.79% Conservative: 27
 Best Local Similarity: 38.07% Mismatches: 32
 Query Match: 78.99% Indels: 390
 DB: 10 Gaps: 43

US-10-017-084A-523 (1-344) x RATCALMA (1-3069)

QY 1 Met---Lys-----ThrIle-----GlnPro----- 6
 Db 47 ATGATAAGGCTTTGGCATGGGTATTAGTTAATTCCTGCCAGGAAGCAGCTTTCTCTGTT 106
 QY 6 ----- 6
 Db 107 CTTGTGTCTGAGACCTGCTAGGTTAGATTAGGGAAGGGCATTAGACCCCTCCCGCT 166
 QY 7 -----LysMet-----His----- 9
 Db 167 GCCACCCAGGACGGGTGTGCCATCGAGTCACACTGGCATACTACACAAATCCAG 226
 QY 9 ----- 9
 Db 227 CAGTACTGTGCGGTGAGGGGTGCGCAAGGACGAGCTTCAACTCCCTTCGGAGTG 286
 QY 10 -----Asn-----Ser-----IleSer 13
 Db 287 AGCCTTCCCAACAGGAAGTCTCCCGGTGTCAGGAGAGTGGAGCCCAATGTGTGGCT 346
 QY 14 Trp-----Ala-----Ile-----Phe----- 17

EMBO J. 8 (2), 489-495 (1989)
 MEDLINE 89251576
 PUBMED 2721489
 REFERENCE 2 (bases 1 to 2593)
 AUTHORS Schofield,P.R.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-1988) Schofield P.R
 COMMENT Data kindly reviewed (19-may-1989) by Schofield P.R.
 FEATURES
 Location/Qualifiers
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 /organism="Bos taurus"
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 /clone="lambda BOM159, lambda BOM106"
 /tissue_type="brain"
 /clone_lib="lambda gt10."
 785..1822
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 /protein_id="CAA31192.1"
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 /db_xref="GOA:P11834"
 /db_xref="SWISS-PROT:P11834"
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 QTVRDEGPTCTSVOTDHPKTSRVHLIVQVFPQIMNISSDVTVNEGSSVTLICLA
 GREPTVWRHLGKQGVSVSEYLEISDIKRQDGSVECSALNDVAAPDVRVKTKI
 TUNYPVISAKNTGVSQVKGILSCSASAVPMAEFQWPKEDTRLATGLDGMRIENKG
 HISLTFPNVSEKDYNTCVATNKLGITNASITLYGPGAVIDGVNSASRALACLMS
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 785..865
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 866..1819
 /product="put. OPCAM (AA 1 - 318)"
 2593
 /note="polyA site"
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 Alignment Scores:
 Pred. No.: 1,21e-71 Length: 2593
 Score: 1901.60 Matches: 270
 Percent Similarity: 42.58% Conservative: 34
 Best Local Similarity: 37.82% Mismatches: 35
 Query Match: 78.97% Indels: 375
 DB: 4 Gaps: 43
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 QY 1 MetLysThr-----Ile--Gln-----5
 Db 337 ATG---ACATCTCTTATGTGCAGACACTTGCTGGCTCTTTGGGTATAAACITTT 393
 QY 6 -----ProLys-----Met-----His-----9
 Db 394 GATGCCAGACCTCGCAGGACGTGCCCAACTGAATGTAAAGTAGCATCTCGAAGAGAGG 453
 QY 10 -----Asn-Ser-----Ile-----12
 Db 454 CAGAGAAGAACAACCGTGACCTTCATCCCGCACCTTCCTCTCTCTCTCTCCCTTCCCGG 513
 QY 13 -----Ser-----Tyr-----14
 Db 514 CGCCTCCCTCTTCCCGAGGGAGCATCGAAGAGCGCTTTTIGATGCAGGAGGGGCG 573
 QY 15 -----Ala-----Ile-----16
 Db 574 ATCTGTTGTGCCAGCTGGAAGCTGAGCAGGATCTCAGGAGAACAGTAGACTCCGG 633
 QY 17 -----PheThr-----Gly-----19
 Db 634 AGAGCCTGACTCCGCTTCTCTTACCCCCCTCTCGGTTCTGGTGGTTCAGCCCTCG 693
 QY 20 -----LeuAla-----21

Db 1762 AGCGTGGCTGCTGGCTATCAGGACCCCTCTTGCCCACTTCTCATCAAGTTTG 1821
Qy 318 ----Glu---Val-----SerAsnGly-----Thr-----Se 324
Db 1822 ATAGAAACCATAGGTCTCTGAGCAACGCTGCTTCTCCATATACAGACTTACCTGC 1881
Qy 324 r---Argarg----- 326
Db 1882 ACTCGGAGGGCCAGTTTGGGCTCTCTTCTGTTCTGTTCTCTCTCAGTATTTTTT 1941
Qy 326 ----- 326
Db 1942 TTTTITTTGGACTTTTCTTTGTTGATTGATTTTCTTCTAGTTCACACGAGTGGT 2001
Qy 327 -----AlaGly-----CysVal----- 330
Db 2002 TTGGGAGGGTGGGCGGTCTACATGATGATATCTCATATGATGATGTCCAAAC 2061
Qy 330 ----- 330
Db 2062 TGAACCCATTCTCCACCCTTCCCTCCCTGCTGCTCCCTGGGCAATGTCACCAC 2121
Qy 330 ----- 330
Db 2122 CAACCAACCTCCCTCCACACCAACATAGTTCCATTTGGGCAAAACGTGCTGTGA 2181
Qy 330 ----- 330
Db 2182 TAAACACCTGAAGACACAACTTGATATATGATGATGATGATGATATATATCCAA 2241
Qy 331 -----Trp-----Leu----- 332
Db 2242 GTGCTCTATCTGCTGCTTTTAAAGCTGTGACCAATTTCTGACTATATGATGATGATC 2301
Qy 333 -Leu---Pro---LeuLeu-----Val-----LeuHis----- 339
Db 2302 CCTCTCTCCATGTTTATTATGATGATGATGATGATGATGATGATGATGATGATGATG 2361
Qy 340 -----Leu-----Leu----- 341
Db 2362 AGTCT 2421
Qy 341 uLeuLys-----Phe 344
Db 2422 CTACAAATATGAAACATGCGCATCTCTCTAGTCAATC 2461

RESULT 26
RATCALMC 2337 bp mRNA linear ROD 08-MAY-1993
LOCUS Rattus norvegicus cell adhesion-like molecule mRNA, complete cds.
ACCESSION M89711
VERSION M89711.1 GI:203249
KEYWORDS cell adhesion-like molecule; opioid binding protein.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1. (bases 1 to 2337)
Lippman,D.A., Lee,N.M. and Loh,H.H.
TITLE Opioid-binding cell adhesion molecule (OBCAM)-related clones from a
rat brain cDNA library
JOURNAL Gene 117 (2), 249-254 (1992)
MEDLINE 92347701
PUBMED 1339369
COMMENT source text: Rattus norvegicus brain cDNA to mRNA.
FEATURES
Location/Qualifiers
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/map="chromosome 9"
/tissue_type="brain"

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/db_xref="GI:203250"
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GTFFAHFFIK"

ORIGIN
Alignment Scores:
Pred. No.: 2337
Score: 1897.20 Matches: 275
Percent Similarity: 45.48% Conservative: 27
Best Local Similarity: 41.42% Mismatches: 33
Query Match: 78.79% Indels: 329
DB: 10 Gaps: 44
US-10-017-084a-523 (1-344) x RATCALMC (1-2337)
Qy 1 MetLys---Thr-----Ile---Gln-----Pro---LysMet 8
Db 80 ATGCCAGACCTCTGCAGAAATGCCCACTGAATCTTAAAGTAGCTTCCCGAGAGGCA 139
Qy 9 HisAsn-----SerIle----- 12
Db 140 GAGAACGACATCTGACCTCTGCTCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 199
Qy 13 -----Ser-----Tip----- 14
Db 200 GCTCCCTCCGCCCGGAGCGTTGAGAAAGCTCTTTTGGATGAGAGGGGGCATCT 259
Qy 15 -----Ala-----Ile----- 16
Db 260 GGTTCGCCAGGCTGGAAGAGCTGAGCTGGAGCAGAGGAAGACTTATTAGACTCCGAGA 319
Qy 17 -----Phe 17
Db 320 GCCTGGACTCAGCTTGCCTTCTCCCGCTCCAGCTCTCTGCTCTCTCTCTCTCTCTCT 379
Qy 18 -----Thr-----Gly----- 19
Db 380 CGTCCCTCAACATTCGCGCTATTCTGAGAGGCGAGGGAACAGACCGTCAGCTGCAAG 439
Qy 20 -----LeuAla-----Ala-----Leu----- 23
Db 440 AGTTCTAGGAAGTTGGCTGTGAGAGATGGGGTCTGTGGGTACCTGTTCTCTGCCCTGG 499
Qy 24 ---Cys-----LeuPhe-----GlnGlyValProVal 31
Db 500 AAGTGCCTCTGCTGCTGCTCTCTGAGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 559
Qy 32 ArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGlyGlu 51
Db 560 CGCAGCGGAGATGCCACCTTTCCCAAGCTATGACCAACGAGACGTCGCGCAGGAGAG 619
Qy 52 SerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaThrLeuAsnArg 71
Db 620 AGCGCCACCTCAGTGTACATAGATGACCGGTCCACAGAGTAGCTGGCTGGCTAAACCGC 679
Qy 72 SerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeu 91
Db 680 AGCAATCTCTACGCTGGGATGACAAAGTGGTCCCATAGACCTCCAGTATCATCTGT 739
Qy 92 SerAsnThrGlnThrGlnTySerIleGlnIleGlnAsnValAspValTyrAspGluGly 111
Db 740 GTCAACACGCTACCCAGTACAGTATCATGATCATGATGATGATGATGATGATGATGAT 799
Qy 112 ProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeuLeu 131

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Db      800  CCGTACACCTGCTCTGTGCAGACAGACATACCCCAAAACCTCCCGGCTCCACCTCAT 859
QY      132  ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
Db      860  GTGCAAGTTCTCTCCAGATAATGACATCTCTCTGACATTAATCTGTAATGAG----- 913
QY      152  AsnIle-----SerLeuThr-----CysIleAlaThrGlyArgProGluProThrValThr 168
Db      914  ---ATAAGCAGTGTGACCTTGTATGTCCTGCAATTTGGCAGACCAACACAGTGACA 970
QY      169  TrpArgHisIleSerProLysAlaVal-----GlyPheValSerGluAspGlu 184
Db      971  TGGCGACACCTGTCA-----GTCAAGGAAGCGCAGGGCTTTTGTGAGTGAAGATGAA 1021
QY      185  TyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlnCysSerAlaSer 204
Db      1022  TACCTGGAATCTCAGACATCAAAACGCGACCAATCTGGAGAGTATGAGTGCAGCGCTTG 1081
QY      205  AsnAspValAlaAlaProValValArgArgValIleValThrValAsnTyrProTyr 224
Db      1082  AATGATGTCTGCTGCACCTGATGTTTCGGAAGTAATAATCACTGTAACCTATCTCTCTAT 1141
QY      225  IleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGlu 244
Db      1142  ATCTCAAAAGCGAAGAACACCTGGCTTTTCAGTAGGCGCAGAAAGGCGATCTCTGAGCTG 1201
QY      245  AlaSerAlaValProSerAlaGluPheGlnTyrTyrIleAspAspLysArgLeuIleGlu 264
Db      1202  GCCTCTGCTGTCCCATATGCTGCTGAATTCAGTGTTCAGGAAGTAAATCACTGTAACCT 1261
QY      265  GlyLysLysGlyValLysValGluAsn-----ArgProPheLeuSerTyrLeuIlePhe 282
Db      1262  GGCTGTGATGCGGTGAGATTGAGAACAAAGCGCG-----ATATCCACTTTGACTTTC 1315
QY      283  PheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGly 302
Db      1316  TTCAATGTCTCAGAGAAGGATTATGGAACTATACCTGTGTGGCCCAAAACAAGCTTGGG 1375
QY      303  HisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaVal----- 316
Db      1376  AACACCAATCCAGCATCACCTGTATGGGCTGTGGAGCAGTCAATGTGTGTAACACTCG 1435
QY      317  ---Ser-Glu-----ValSerAsn-----Gly-----ThrSer----- 324
Db      1436  GCCTCTAGACACTGGCTGTCTCTGCTCTCAGGACCTTCTTTGGCCACTTCTTCATC 1495
QY      324  ----- 324
Db      1496  AAGTTTTGATAAGAAACCTTAGGTCCTCTGAGCATCGCTTCTCCATACAGACT 1555
QY      325  -----ArgArgAlaGly----- 329
Db      1556  TTAATCTACACTGGGAGG---GGCAACACAGTTTGGCTTCTTTGGTTATTTTITG 1612
QY      329  s----- 329
Db      1613  TTCTCTCTGACTGTTAGTTTGTGTTTGTGTTTCTGGGATTTTCAATTTGTTT 1672
QY      330  -----Val----- 330
Db      1673  TCCTTTTTCGTTGATGAGACCGGGGTTGGGGTTGGGATGGGCGAGGTTCTACCACGAG 1732
QY      331  -----Tip-----LeuLeuPro----- 334
Db      1733  TAGGATATACAGTATTGTTGGGCCCCCAATGAATATATATCTCTGCTACCTTGGCCTTC 1792
QY      335  -----LeuLeu----- 336
Db      1793  CTTTCTCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1852
QY      337  -----Val-----Leu----- 338

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Db      1853  AGATGGCCTAAAAAATGTCCATGACACGACCCCTGAAGGTACAACTTGGCCCAAGTGC 1912
QY      339  ---His-----Leu-----Leu----- 341
Db      1913  AGTACACAATAAGAGTTCATCTACATTTCTCTGTTCTTTCTTTTAAAGTTTCAATA 1972
QY      342  -----LeuLys----- 343
Db      1973  AGACAGTTTAAAAAGAGACACATCTTATCCCTATGTTGTATACCTATCCATTAAGCT 2032
QY      344  -----Phe 344
Db      2033  GCACACCTTT 2042

RESULT 27
RATCALMB
LOCUS      RATCALMB      2179 bp      mRNA      linear      ROD 27-APR-1993
DEFINITION Rattus norvegicus cell adhesion-like molecule mRNA, complete cds.
ACCESSION M88710
VERSION    M88710.1 GI:203247
KEYWORDS   cell adhesion-like molecule; opiod binding protein.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 2179)
AUTHORS   Lipman,D.A., Lee,N.M. and Loh,H.H.
TITLE      Opiod-binding cell adhesion molecule (OBCAM)-related clones from a
            rat brain cDNA library (1992)
JOURNAL    Gene 117 (2), 249-254 (1992)
MEDLINE    92347701
PUBMED     1339369
COMMENT    Original source text: Rattus norvegicus (strain Simonsen ICR) brain
            cDNA to mRNA.
FEATURES   Location/Qualifiers
            1..2179
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CDS
Alignment Scores:
Pred. No.:      8,64e-72      Length:      2179
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Percent Similarity: 47.69%      Conservative: 29
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Query Match:    78.43%      Indels:     294
DB:             10          Gaps:       41

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QY 16 ----Ile----Phe-----Thr-----Gly 19
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QY 20 -----LeuAla-----Ala-----22
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DEFINITION complete cds.
ACCESSION BX537377
VERSION BX537377.1 GI:31873255
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 6380)
AUTHORS Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobo, G., Han, M. and Wiemann, S.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Resequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp686H1949) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
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information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.

FEATURES

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ACCESSION Y08170
VERSION Y08170.2 GI:4688845
KEYWORDS OBAM protein.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE 1 Wilson,D.J., Kim,D.S., Clarke,G.A., Marshall-Clarke,S. and Moss,D.J.
AUTHORS A family of glycoproteins (GP55), which inhibit neurite outgrowth,
TITLE are members of the Ig superfamily and are related to OBAM,
neurotrophin, LAMP and CEPU-1
JOURNAL J. Cell. Sci. 109 (Pt 13), 3129-3138 (1996)

97157768 MEDLINE
9004047 PUBMED
2 REFERENCE
Lodge, A.P., Kim, D.S., Howard, M.R., McNamee, C.J., Smith, N. and Moss, D.J.
TITLE Cloning of CEPU-s, a secreted isoform of CEPU-1, and OBCAM cDNAs from chick: structural diversity of IgLON family proteins
JOURNAL Unpublished
3 Wilson, D.J.A.
REFERENCE Direct Submission
AUTHORS Submitted (21-MAR-1996) D.J.A. Wilson, Liverpool University, Human Anatomy and Cell Biology, Liverpool, L69 3BX, UK
REMARK Revised by (3) 4 (bases 1 to 1533)
Moss, D.J.
JOURNAL Direct Submission
AUTHORS Submitted (20-APR-1999) D.J. Moss, Liverpool University, Human Anatomy and Cell Biology, Liverpool, L69 3BX, UK
COMMENT On Apr 26, 1999 this sequence version replaced gi:1617043.
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Best Local Similarity: 51.85% Mismatches: 33
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QY 315 aValSerGluValSer---Asn-----Gly----- 322
Db 938 GGTGCGACGAC---AGTGGCAATGACGCTCCCGGCGAGCGGTGGCTTGTGCTTGTGGC 994
QY 323 -Thr-----SerArg----- 325
Db 995 CACCTCTCTCGCTCGCTCTCTCTCGACTTTTGAAGGAGTGGAGGTCCCGGAGCGG 1054
QY 325 ----- 325
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QY 328 ----- 328
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QY 329 -----Cys-----Val-----Trr-----LeuLeu---Pro----- 334
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QY 338 -Leu-----His-----Leu----- 340
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QY 341 -----Leu-----Phe 344
Db 1475 TGAAGCCCTGCTGCTGCTGCACCGTCTCCGCTCG 1511

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LOCUS AX665340 Sequence 98 from Patent WO03002765.
DEFINITION AX665340
ACCESSION AX665340
VERSION AX665340.1 GI:29290463
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sellar, G.C. and Gabra, H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 98 09-JAN-2003;
Cancer Research Technology Limited (GB)
FEATURES
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1. 3110
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Score: 1866.00 Matches: 261
Percent Similarity: 56.87% Conservative: 37
Best Local Similarity: 49.81% Mismatches: 35
Query Match: 77.49% Indels: 191
DB: 6 Gaps: 31

US-10-017-084A-523 (1-344) x AX665340 (1-3110)
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QY 19 -----GlyLeu-----Ala---AlaLeu-----Cys----- 24
Db 50 AATGGGGTCTGTGGGTACTCTTCTGCTGCTGGAAGTGCCTCGTGTGCTCTCTCAG 109
QY 25 -----LeuPhe-----GlnGlyValProValArgSerGlyAspAlaThrPheProly 40
Db 110 GCTGTGTCTTGTGTACCCAGGAGTGCCTGCGCAGCGGAGAGCCACCTCAGGTACCATAGA 169
QY 40 sAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAs 60
Db 170 ACTATGACAACAGTGACCGTCCGACAGGGGAGAGGCCACCTCAGGTACCATAGA 229
QY 60 pAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAs 80
Db 230 TGACCGGGTAAACCGGGTGGCTGGTAAACCGCAGCAGCATCTCTACGCTGGGAATGA 289
QY 80 pLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle 100
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QY 100 eGluIleGlnAsnValAspValTyArgGluGlyProTyThrCysSerValGlnThrAs 120
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Db 470 TATCTCTCAGACATCATCTGTGTGANTGAGGAGCAGTGTGACCTGTCTGTCTGTCTAT 529
QY 160 rGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaVal----- 177
Db 530 TGGCAGCAGAGCCAACTGTGACATGGAGACACCTGTCA-----GTCAAGGAAGG 580
QY 178 -----GlyPheValSerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSe 196
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Db 881 C-----ATGCTCACTCTGACTTCTTCAATGTCTTCTGAAAGAGATTATGGGAACATAC 934
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QY 337 -----Val-----LeuHisLeu----- 340
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QY 341 -----Leu-----Lys----- 343
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Job time : 4745 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 28, 2004, 12:59:14 ; Search time 530 Seconds
(without alignments)

2757.321 Million cell updates/sec

Title: US-10-017-084a-523

Perfect score: 2408

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Ygapop 1.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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 96 2408 100.0 1679 8 ADB23630 Human PRO
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 99 2408 100.0 1679 8 ADB83615 Novel hum
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ALIGNMENTS

RESULT 1
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 ID AAZ47892 standard; cDNA; 1032 BP.
 XX AC AAZ47892;
 XX
 DT 10-MAR-2000 (first entry)
 XX Human protein encoding cDNA SEQ ID NO:2.

XX Human; haematopoietic cell regulation; tissue generation; reparation;
 KW activin; inhibin; taxis; chemotaxis; blood coagulation; thrombus;
 KW receptor; ligand; autoimmune; infection-related immunodeficiency;
 KW inflammatory disorder; neurological disease; ss.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH 1..1032
 FT /*tag= a
 FT /note= "no stop codon given"
 XX

XX W09958668-A1.

XX 18-NOV-1999.

XX 13-MAY-1999; 99WO-JP002485.

XX 14-MAY-1998; 98JP-00131815.

XX (ONCY) ONO PHARM CO LTD.

XX Fukushima D, Shibayama S, Tada H;

XX WPI; 2000-062298/05.

XX P-PSDB; AAY57601.

XX New polypeptides of human origin having cell regulatory, tissue
 PT generation, coagulant and other activities.
 XX Claim 4; Page 41; 84pp; Japanese.

XX The present sequence encodes a specifically claimed novel human protein.
 CC The novel human protein can be used in therapeutic drugs for the
 CC prevention and treatment of a broad range of disorders including
 CC autoimmune and infection-related immunodeficiency, inflammatory
 CC disorders, and neurological diseases. The novel protein is expected of
 CC having haematopoietic cell regulatory activity, tissue generation/
 CC reparation activity, activin/inhibin activity, taxis/chemotaxis activity,
 CC blood coagulation and thrombus activity, and receptor/ligand activity

XX Sequence 1032 BP; 267 A; 281 C; 270 G; 214 T; 0 U; 0 Other;
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 Score: 2408.00 Matches: 344
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 DB 61 GCTGCTCTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAA 120
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 121 GCTATGGACACGTGACGTCCGGGAGGGAGAGGGCCACCTCAGGTGCACTATTGAC 180
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
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 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrClnTyrSerIle 100
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 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 421 ATTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCTTACCTGCACTAGCACT 480
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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 QY 181 SerGluAspGluTyrLeuGlnIleGlnGlyIleThrArgGlnSerGlyAspTyrGlu 200
 DB 541 AGTGAAGACGAATACTTGGAAATTCAGGGCATCCCGGAGCAGTCAGGGGACTACGAG 600
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
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 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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PR	07-MAY-1998;	98US-0084643P.	
PR	13-MAY-1998;	98US-0085323P.	
PR	13-MAY-1998;	98US-0085338P.	
PR	13-MAY-1998;	98US-0085339P.	
PR	15-MAY-1998;	98US-0085573P.	
PR	15-MAY-1998;	98US-0085579P.	
PR	15-MAY-1998;	98US-0085580P.	
PR	15-MAY-1998;	98US-0085582P.	
PR	15-MAY-1998;	98US-0085689P.	
PR	15-MAY-1998;	98US-0085697P.	
PR	15-MAY-1998;	98US-0085700P.	
PR	15-MAY-1998;	98US-0085704P.	
PR	18-MAY-1998;	98US-0086023P.	
PR	22-MAY-1998;	98US-0086392P.	
PR	22-MAY-1998;	98US-0086414P.	
PR	22-MAY-1998;	98US-0086430P.	
PR	22-MAY-1998;	98US-0086486P.	
PR	28-MAY-1998;	98US-0087098P.	
PR	28-MAY-1998;	98US-0087106P.	
PR	28-MAY-1998;	98US-0087208P.	
PR	30-JUL-1998;	98US-0094651P.	
PR	11-SEP-1998;	98US-0100038P.	
XX	(GETH) GENENTECH INC.		
XX	Wood Wf, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;		
XX	WPI; 1999-551358/46.		
XX	P-PSDB; AAY41773.		
XX	New secreted and transmembrane polypeptides and their polynucleotides,		
PT	useful for treating blood coagulation disorders, cancers and cellular		
PT	adhesion disorders.		
XX	Claim 2; Fig 221; 530pp; English.		
XX	The present invention describes secreted and transmembrane polypeptides		
CC	and their polynucleotides. The nucleotide sequences are useful as sources		
CC	of probes, primers, for chromosome mapping, and for generation of		
CC	antisense sequences. They can also be used to create transgenic animals.		
CC	The proteins can be used to treat a variety of diseases and disorders,		
CC	depending on their function. Diseases that may be treated include blood		
CC	coagulation disorders, cancers and cellular adhesion disorders. They may		
CC	also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to		
CC	AAY41774 represent polynucleotide and polypeptide sequence given in the		
CC	exemplification of the present invention		

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,72e-36 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-017-084A-523 (1-344) x AA234324 (1-1679)

```
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAATAACCATCCAGCCAAATAATGCAATTTCTATCTTTGGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAGAGAGTGCCGTCGCGCAGCGGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrIleuArgCysThrIleAsp 60
DB 254 GCTATGCAACACGTGACGGTCCGCGAGGGGAGAGCCACCCCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGTACACCGGGTGGCTGGCTGTAAACCGCAGCACCCATCTCTATGCTGGGATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTGCTGGATCCTCGCTGGTCTCTTCTGAGCAACACCCAAACGCGAGTACGACATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTTGATGTATGAGCAGGGGCTTTACACCTGCTCGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACACCCAAAGACCTTAGGTCCACTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATAATTAGCCTCACCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACGAGAGCCTACGGTTACTTTGAGACACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGCAGGAATACTTGGAAATTCAGGGCATCCCGGAGCAGTCCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
DB 734 TGCAGTGTCTCCATGACGTGCGCGCGCGCTGTGAGAGAGTAAGGTACCCTGTAAC 793
QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATATCTTCAAGACCCAGGAGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
DB 854 CTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTTGAGGAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCAATGCTCTTGACATGACATGATGGAATCTACATCTGCGTGGCTCCCAACAG 1033
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```
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCCACACCAATGCGCAGCATCATGCTATTGGTCCAGGCGCGTCAAGGAGTGAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
DB 1094 AACGGCAGTCGAGAGGAGGAGGCTGCTGGCTGTGCTCTTCTTGGTCTTGACCTG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTTCTCAAAATTT 1165
```

RESULT 3

AACT78590
ID AACT78590 standard; cDNA; 1679 BP.

XX AC AACT78590;

XX DT 08-FEB-2001 (first entry)

DE Human PRO337 nucleotide sequence SEQ ID NO:522.

KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
KW expressed sequence tag; detection; cancer; ss.

XX OS Homo sapiens.

XX PN WO200053756-A2.

XX PD 14-SEP-2000.

PF 18-FEB-2000; 2000WO-US004341.

XX 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.

PR 29-MAR-1999; 99US-0126773P.

PR 21-APR-1999; 99US-0130232P.

PR 28-APR-1999; 99US-0131445P.

PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.

PR 26-JUL-1999; 99US-0145698P.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 30-DEC-1999; 99WO-US031243.

PR 05-JAN-2000; 99WO-US031274.

PR 06-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen MB;
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI: 2000-611443/58.

P-PSDB: AAB44329.

XX Novel PRO polypeptides and polynucleotides used in detection methods, to
XX target bioactive molecules to specific cells, and to modulate cellular
XX activities.

XX Claim 2; Fig 221; 636pp; English.

XX AACT78458 to AACT78599 represent polynucleotide and EST (expressed sequence
XX tag) sequences which encode secreted or transmembrane PRO polypeptides.
XX The PRO polynucleotides and polypeptides have cytosstatic activity. The
XX polynucleotides and polypeptides can be used for detecting the presence

CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores: 6.72e-36 Length: 1679
Pred. No.: 2408.00 Matches: 344
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 3 Gaps: 0
DB:

US-10-017-084A-523 (1-344) x AAC78590 (1-1679)

QY 1 MetIysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAATATCTATCTCTTGGGCAATCTTTCACGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTGTCTCTTCCAGAGAGTGCCGTGCGCAGCGGAGATGCCACCTTCCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGACAAACGTGACGGTCCGCGAGGGGAGAGCGCCACCTTCAGGTGCATTTATGAC 313
QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGGTCAACCGGGTGGCTGTGCTAAACGCGAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrInTyrSerile 100
DB 374 AAGTGGTGGCTGGATCTCGGTGGTCTCTGAGCAACACCCAAACGACGATCAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCACACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCAITTTGCAAGTATCTCCAAATTTGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTCTTTCAGATATCTCCATTAAAGAGGGAACATATATTAGCCTCACCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACAGAGCCTTACCGTTACTTTGGAGACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGACGAAATCTTGGAAATTCAGGGCATCACCGGGAGCAGTCAAGGGGACTTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValArgValIleValThrValAsn 220
DB 734 TGCAGTGGCTCCAAATGACGTGCGCGCGCGGTGGTACGGAGAGTAAAGGTCAACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTTTCAAGACCAAGGTTACAGGTGTCCCGTGGGCAAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
DB 854 CTGCACTGTGAAGCCTTACAGATGCCCTTCCGCGAATTTCCAGTGTGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGlnAsnArgProPheLeuSerIleLeu 280

DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACAGACCTTTCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCAATGCTCTTGAACATGACTATGGAACTACACTTGGTGGCTTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu 340
DB 1094 AACGGCACATCGAGAGGGGAGGCTGCGTCTGCTGCTCTTCTGCTTCTGCTTGCACCTG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTCTCAAAATTT 1165
RESULT 4
AAC87037
ID AAC87037 standard; cDNA; 1679 BP.
XX
AC AAC87037;
XX
DT 20-APR-2001 (first entry)
XX
DE Nucleotide sequence of human polypeptide PRO337.
XX
KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO365; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW ss.
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 134..1168
FT sig_peptide 134..216
FT /*tag= a
FT /*tag= b
XX WO200077037-A2.
XX PD 21-DEC-2000.
XX PF 22-MAY-2000; 2000WO-US014042.
XX PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.

XX (GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;

PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;

PI Wood WI, Zhang Z;

XX WPI; 2001-050091/06.

DR P-PSDB; AAB31204.

XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a

PT transmembrane polypeptide is useful for gene therapy and identification

PT of related polypeptides.

XX Claim 2; Fig 51; 244pp; English.

XX The present sequence encodes a human secreted and transmembrane

CC polypeptide. The specification describes human polypeptides, designated

CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,

CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,

CC PRO248, PRO353, PRO1318, PRO1600, PRO940, PRO533, PRO301, PRO187,

CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,

CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells

CC can be modulated with agents that bind to these polypeptides, resulting

CC in the death of the cells. The polynucleotides encoding the

CC polypeptides are useful in the recombinant production of the

CC polypeptides, as a hybridisation probe to screen libraries to isolate

CC homologous sequences, or to map the gene. They may also be used for

CC analysing genetic disorders, and to produce transgenic animals which are

CC useful for the development and screening of therapeutically useful

CC reagents. The polynucleotides can also be used in gene therapy e.g. to

CC replace a defective gene

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.72e-36	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-017-084A-523 (1-344) x AAC87037 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20

Db 134 ATGAAACCCATCCAGCCAAATATGCAATTTCTTGGGCAATCTTCACGGGGCTG 193

Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40

Db 194 GCTGCTCTGTGTCTCTTCCAGAGAGTCCGCGCAGCGGAGATGCCACCTTCCCAAA 253

Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60

Db 254 GCTATGACACAGTGACGGTCCGCGAGGGGAGAGCGCCACCTTCAGGTGCATTATGAC 313

Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80

Db 314 AACCGGGTCACCCCGGGTGGCTGGCTAAACGCGAGCACCATCTCTATGCTGGGATGAC 373

Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100

Db 374 AAGTGGTGCCTGGATCTCTCGGTGGTCTCTGAGCAACACCCAAACGACGATCAGCATC 433

Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120

Db 434 GAGATCCAGAACGTGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy 121 AsnHisProLysThrSerArgValHisLeuValGlnValSerProLysIleValGlu 140

Db 494 AACACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTTGTAGAG 553

Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160

Db 554 ATTTCCTCAGATATCTCAATTAATAGGGAACAATATTAGCCTCACCCTGCATAGCAACT 613

Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180

Db 614 GGTAGACCAGACCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673

Qy 191 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200

Db 674 AGTGAAGACGAAATCTTGGAAATTCAGGCGATCACCCGGGAGCAGTCAAGGAGCTACAG 733

Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220

Db 734 TGCAGTGCCTCAATGACGTGGCGCGCGCTGGTACGAGAGTAAAGGTCAACGTGAAC 793

Qy 221 TyrProProTyrIleSerGluAlaIleGlyThrGlyValProValGlyGlnIleGlyThr 240

Db 794 TATCCACCATATCTTCAGAACCCCAAGGGTACAGGTGCCCCGTGGGACAAAAGGGGACA 853

Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260

Db 854 CTGCAAGTGTGAAGCTCAGCAGTCCCTCAGCAGATTCAGTGGTACAGGATGACAAA 913

Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280

Db 914 AGACTGATTGAAGAAAGAAAGGGTGAAGTGAAGTGAAGAAACAGACCTTTCCTCTCAAACTC 973

Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300

Db 974 ATCTCTTCAATGTCTCGAACATGACATGATGGAACTACACTTGGTGGCTCCCAACAG 1033

Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320

Db 1034 CTGGGCCACCAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGGTGAGC 1093

Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340

Db 1094 AACGGCAGCTCAGGAGGGGAGGCTCGCTCTGGCTGCTGCTCTTCTGTGCTTGTGACCTG 1153

Qy 341 LeuLeuLysPhe 344

Db 1154 CTCTCAAAATTT 1165

RESULT 5

AAS21431

ID AAS21431 standard; cDNA; 1679 BP.

XX AAS21431;

AC AAS21431;

XX 24-OCT-2001 (first entry)

DT Human cDNA sequence encoding for PRO337 polypeptide.

DE Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;

XX prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;

KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;

KM A-peptide; factor VIIA; gene therapy; ss.

XX Homo sapiens.

OS WO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US032678.

XX 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.

(GETH) GENENTECH INC.

Baker KP, Bereini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI: 2001-408281/43.

P-PSDB; RAU12359.

Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung, breast, prostate, cervical.

Claim 3; Fig 375; 813pp; English.

AA521244-AA521518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6, 72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 4

US-10-017-084A-523 (1-344) x AAS21431 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCATCCAGCAAAATGACAAATCTATCTCTTGGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCCAGGAGTGCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGACAAAGTGACGCTCCGGCAGGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGGTCACCGGGTGCGCTGCTTAAACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGTGCTTGGATCCTCGGCGGTCCTTCTGAGCAACACCCAAACGAGTACAGCAATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTCGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGACAGACAG 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTCTTTCAGATATCTCCATTAATGAAGGAGCAATATAGCTCCTCAGTCATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAGAGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAGACGCAATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGAGCTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
 DB 734 TGCAGTGCCTCCATGACGTGGCGCGCCGCGGTGTGTCGAGAGTAAAGGTCCACCGTGAAC 793
 QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTTCAGAAAGCCAGGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys 260
 DB 854 CTGCAGTGTGAAGCTCAGCAGTCCCTTCAGCAAGATTCAGAGTTCAGAGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGATCTATTGAAGAGAAAGAGGGGTGAAAGTGGAAACACAGACCTTCTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTCAATGTCTCTGAAACATGACTATGGGAACACTACCTTGGTGGCCCTCCAAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320

Db 734 TGCAAGTGCCTCCAAATGACGTGGCCGCGCCGCTGGTACGAGAGATAAGGTCACCGTGAAC 793

QY 221 TTTProProTyrTrpTrpSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240

Db 794 TATCCACCATACATTTTCAAGCAAGGTTACAGGTGTCCCGTGGGACAAAGGGGACA 853

QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260

Db 854 CTCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA 913

QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280

Db 914 AGACTGATTCAAGGAAGAAAGGGTGAAAGTGGAAACAGACCTTCTCTCAAAATC 973

QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300

Db 974 ATCTTCTCAATGCTCTGAACATGACTATGGGAACATACACTTGGCGGCTTCAACAG 1033

QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320

Db 1034 CTGGGCCACCAATGCGAGCATCATCTATTGTTCCAGGCGCGTCAGGAGTGAGC 1093

QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340

Db 1094 AACGGCAGTCGAGGAGGAGGCTGGTCTGGCTGCTGCTCTCTCTGTCTTGTGCTG 1153

QY 341 LeuLeuLysPhe 344

Db 1154 CTTCTCAAAATT 1165

RESULT 7

ABL88099

ID ABL88099 standard; cDNA; 1679 BP.

XX

AC ABL88099;

DT 16-MAY-2002 (first entry)

XX

DE Human PRO337 cDNA sequence SEQ ID NO:55.

XX

KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;

KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;

KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;

KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;

KW age-related macular degeneration; arterial restenosis; angina;

KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;

KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;

KW wound healing; chromosome mapping; gene mapping; gene; ss.

XX

OS Homo sapiens.

XX

FN WO200200690-A2.

XX

PD 03-JAN-2002.

XX

PF 20-JUN-2001; 2001WO-US019692.

XX

PR 23-JUN-2000; 2000US-0213637P.

PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR 25-JUL-2000; 2000US-0220664P.

PR 28-JUL-2000; 2000WO-US020710.

PR 02-AUG-2000; 2000US-0222695P.

PR 17-AUG-2000; 2000US-00643657.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.

PR 18-SEP-2000; 2000US-00665350.

PR 24-OCT-2000; 2000US-0242922P.

PR 08-NOV-2000; 2000US-00709238.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 22-JAN-2001; 2001US-00767609.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 25-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX

WPI; 2002-090516/12.

DR P-PSDB; ABB84844.

DR

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal.

XX

PS Claim 2; Fig 55; 565pp; English.

XX

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to

CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,

CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic

CC activities, and can be used in gene therapy. The PRO polynucleotides,

CC proteins, agonists and antagonists are useful for treating or diagnosing

CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.

CC a cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The PRO polynucleotides have applications in molecular biology,

CC including use as hybridisation probes, and in chromosome and gene

CC mapping. ABL88259 to ABL88267 represent primers and probes used in the

CC exemplification of the present invention

XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.72e-36	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-017-084A-523 (1-344) x ABL88099 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20

Db 134 ATGAAACCATCCAGCAAAATGCAATTTCTATCTCTGGGCAATTTTTCACGGGGGTG 193

QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40

Db 194 GCTGCTGTGTCTCTTCCAGGAGTGCCGTCGCGCAGGAGATGCCACCTTCCCCAAA 253

QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60

Db 254 GCTATGGACAACGTGACGTCGTCGGCAGGGGAGAGCGCACCTCAGGTGCATTATGAC 313

us-10-017-084a-523.p2n.rng

Tue Jun 1 09:37:51 2004

cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
antiarteriosclerotic; gene; ss.

Homo sapiens.

WO200208284-A2.

31-JAN-2002.

09-JUL-2001; 2001WO-US021735.

20-JUL-2000; 2000US-0219556P.

25-JUL-2000; 2000US-0220624P.

25-JUL-2000; 2000US-0220664P.

28-JUL-2000; 2000WO-US020710.

02-AUG-2000; 2000US-0222695P.

17-AUG-2000; 2000US-00643657.

23-AUG-2000; 2000WO-US023522.

24-AUG-2000; 2000WO-US023328.

07-SEP-2000; 2000US-0230978P.

18-SEP-2000; 2000US-00664610.

18-SEP-2000; 2000US-00665350.

24-OCT-2000; 2000US-0242922P.

08-NOV-2000; 2000US-00709238.

08-NOV-2000; 2000WO-US030952.

10-NOV-2000; 2000WO-US030873.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.

20-DEC-2000; 2000WO-US034956.

22-JAN-2001; 2001US-00767609.

28-FEB-2001; 2001US-00796498.

28-FEB-2001; 2001WO-US006520.

01-MAR-2001; 2001WO-US006666.

09-MAR-2001; 2001US-00802706.

14-MAR-2001; 2001US-00808689.

22-MAR-2001; 2001US-00816744.

05-APR-2001; 2001US-00828366.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854280.

25-MAY-2001; 2001US-00866028.

25-MAY-2001; 2001US-00866034.

30-MAY-2001; 2001WO-US017092.

30-MAY-2001; 2001US-00870574.

30-MAY-2001; 2001WO-US017443.

01-JUN-2001; 2001WO-US017800.

20-JUN-2001; 2001WO-US019692.

(GETH) GENENTECH INC.

(BAKE/) BAKER K P.

(FERR/) FERRARA N.

(GERB/) GERBER H.

(GERB/) GERRITSEN M E.

(GODD/) GODDARD A.

(GODO/) GODOWSKI P J.

(GURN/) GURNEY A L.

(HILL/) HILLAN K J.

(MARS/) MARSTERS S A.

(PANJ/) PAN J.

(PAON/) PAONI N F.

(STEP/) STEPHAN J F.

(WATA/) WATANABE C K.

(WILL/) WILLIAMS P M.

(WOOD/) WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-171999/22.

P-PSDB; ABB95450.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial

61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
314 AACCGGGTCAACCGGGTGGCTGCTAAACCGGACGACCATCTCTATGCTGGGAATGAC 373
81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
374 AAGTGTGCTGGATCCCTCGCGTGGTCTCTTGAGAACACCCCAACGCGAGTACAGCATC 433
101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
434 GAGATCCAGAACGTCGATGTCATGACGAGCGCCCTTACACCTGCTCGGTGCAGACAGAC 493
121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
494 AACCAACCAACGACCTAGGGTCCACCTCATTTGCAAGTATCTCCCAAAATTTGAGAG 553
141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
554 ATTCTCTCAGATATCTCCATTAATGAGGAACAATATTAGCTTCACCTGCATAGCAACT 613
161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
614 GGTAGACACGACCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGTG 673
181 SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
674 AGTGAAGACGAAATCTTGGAATTCAGGGCATCACCCTGGAGCAGTCCAGGGACCTACGAG 733
201 CysSerAsnAspValAlaAlaProValValArgArgValLysValThrValLys 220
734 TGCAGTGCCTCCATGACGTGGCGCGCGCGGTACGAGAGAGTAAGGTCCACCGTGAAC 793
221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
794 TATCCACCATACATTTTCAAGCAAGGAGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrLysAspAspLys 260
854 CTGAGTGTGAACCTTCAGCAGTCCCTCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
914 AGACTGATTGAGAAAGAAAGAGGGGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 973
281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaLysAsnLys 300
974 ATCTTCTCAATGTCTGAACATGACTATGGGAGTACACTTGGGTGGGCTCCACAGAG 1033
301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
1034 CTGGGCGACACCAATGCGACATCATCTATTGGTCCAGCGCGCTCAGCGAGGTGAGC 1093
321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
1094 AACGGCAGCTCGAGGAGCGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1153
341 LeuLeuLysPhe 344
1154 CTTCTCAAAATTT 1165
RESULT 8
ABL95588
ID ABL95588 standard; cDNA; 1679 BP.
XX
AC ABL95588;
XX
DT 19-JUL-2002 (first entry)
XX Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.
DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW

PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 23-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005501.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 15-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-341980/32.
XX P-PSDB; ABO17803.
XX New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 2; Fig 375; 660pp; English.
XX The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome (AIDS),
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This sequence encodes a novel human secreted and transmembrane PRO
CC polypeptide
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.72e-36 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACD24040 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAATAACCATCCAGCCAAATGCAATCTATCTCTTGGGCAATCTTCAAGGGCTG 193

Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTCCCGTGGCAGCGAGATGCCACCTTCCCCAA 253

Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGACAACTGACGGTCCGCGAGGGGAGAGCCACCTCAGTGCACATTATGAC 313

Qy 61 AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
Db 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTTATGTGGGAATGAC 373

PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021086.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JF, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;
 PI Wood WI, Zhang Z;
 XX WPI; 2003-503396/47.
 DR P-PSDB; ABO25175.
 XX
 PT New secreted and transmembrane PRO polypeptides, useful for treating
 PT diabetes, retinal disorders and stimulating an immune response.
 XX
 PS Claim 2; Fig 51; 254pp; English.
 XX
 CC The invention describes an isolated polypeptide (I) having at least 80 %
 CC amino acid sequence identity to 30 secreted and transmembrane
 CC polypeptides. PRO polypeptides are also useful for stimulating
 CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
 CC factor stimulated proliferation of endothelial cells, stimulating
 CC proliferation of stimulated T-lymphocytes and for inducing proliferation
 CC of PB12 pancreatic ductal cells and are thus useful in the treatment of
 CC disorders which involve protein secretion by the pancreas, including
 CC diabetes. PRO polypeptides are useful for inducing vascular permeability
 CC and in enhancing survival of retinal neurons cells and are thus useful
 CC for the treatment of retinal disorders. PRO polypeptides are also useful
 CC for stimulating an immune response and inducing inflammation by inducing
 CC mononuclear cell and eosinophil infiltration at the site of infection of
 CC an animal. The PRO polypeptides are further useful for inducing apoptosis
 CC in endothelial cells for inhibiting neoplastic growth. This sequence
 CC encodes a novel human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACD42387 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 Db 134 ATGAACACCTCCAGCCAAATGACAAATCTATCTCTGGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTGTGTCTCTTCCAGGAGTGGCCGTCGCGCAGCGAGATGCCACCTCTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGGACAACGTCACGCTCGCGAGGGGAGAGCGCCACCTCAGGTGACATATTGAC 313
 QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaIleAsnAsp 80
 Db 314 AACCGGTGTCACCGGGTGGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 Db 374 AAGTGGTGGCTGGATCCTCGCGTGTCTCTTCTGAGCAACACCAACCGCAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGACAGAC 493

QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 Db 494 AACCAACCCAAAGAGCCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluClyAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAAATATTAGCCTCACCCTGATGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGACCAAGAGCCTACGGTACTTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAspAspValAlaAlaProValValArgValValValValValAsn 220
 Db 734 TGCAGTGGCTCCATGACGTGGCCGCGCCGCTGAGTACGGAGAGTAAAGTCAACGTTGAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCCACCATACATTTCAAGCCAAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260
 Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA 913
 QY 261 ArgLeuIleGluClyLysLysGlyValLysValLysValGluAsnArgProPheLeuSerLysLeu 280
 Db 914 AGACTGATTGAAGGAAAGAAAGGGTGAAGTGAAGTGAAGAAACAGACCTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 Db 974 ATCTTCTTCAATGCTCTCTGAACATGACTATGGAACTACACTTGCCTGGGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCCACACCAATGCCAGCATCTATGCTATTTGGTCCAGGCGCGCTCAGCGAGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 Db 1094 AACGGCAGCTCGAGAGGGGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153
 QY 341 LeuLeuLysPhe 344
 Db 1154 CTTCTCAAAATTT 1165

RESULT 12
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 ID ACD42857 standard; cDNA; 1679 BP.
 XX AC
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 DI 09-SEP-2003 (first entry)
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 DE Novel human secreted and transmembrane protein PRO337 cDNA.
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 KW Human; secreted and transmembrane protein; PRO; virucide; gene therapy;
 KW cell death; growth induction cascade; blood coagulation cascade;
 KW viral infection; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003050239-A1.
 XX
 XX 13-MAR-2003.
 PD
 XX 15-OCT-2001; 2001US-00978191.
 PF
 XX 17-OCT-1997; 97US-0062250P.
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PR 13-NOV-1997; 97US-0065311P.
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PR 22-DEC-1998; 98US-00202054.
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PR 06-JAN-2000; 2000US000277.
PR 06-JAN-2000; 2000US000376.
PR 11-FEB-2000; 2000US003565.
PR 18-FEB-2000; 2000US004341.
PR 24-FEB-2000; 2000US005004.
PR 02-MAR-2000; 2000US005841.
PR 10-MAR-2000; 2000US006319.
PR 21-MAR-2000; 2000US007532.
PR 30-MAR-2000; 2000US008439.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WL;
 XX P-PSDB; ABO33767.
 DR WPI; 2003-512315/48.
 DR P-PSDB; ABO33767.
 XX New genes, and its encoded secreted and transmembrane polypeptides,
 PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
 PT pericyte proliferation, especially for treating lung tumors, arthritis or
 PT wounds in a mammal.
 XX Claim 2; Fig 125; 314pp; English.
 XX The invention describes an isolated nucleic acid molecule comprising a
 CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
 CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
 CC fully defined in the specification; or (b) any of 122 nucleotide
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
 CC specification; or the full length coding sequence of any of these 122
 CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
 CC particularly useful for detecting tumours (e.g. lung tumour, colon
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
 CC in a mammal, for stimulating the release of TNF-alpha from human blood,
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells, for stimulating proliferation of pericyte cells, or for modulating
 CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
 CC polypeptide is also useful for treating tumours or various bone and/or
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
 CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome
 CC identification. The PRO genes are useful as hybridisation probes, or for
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 CC also be used in gene therapy, particularly for replacing a defective
 CC gene. This sequence encodes a novel human secreted and transmembrane PRO
 CC polypeptide
 XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACD68655 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
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 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleasp 60
 Db 254 GCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCCTCAGGTGCATTTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
 Db 314 AACCGGGTCCACCGGGTGGCTGGTAAACCGCAGCACCATCTTATGCTGGGATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle 100
 Db 374 AAGTGGTGGCTGATCTCTCGGTGCTCTCTGAGCAACACCCAAACGACGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyArgGluGlyProTyThrCysSerValGlnThrAsp 120

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 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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 Db 554 ATTTCTTCAGATATCTCAATTAATGAAGGGAAACAATATTAGCCTCCTCCTGATCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGACCAAGACCTTACGTTTACTTTGGAGACATCTCTCCCAAGCGTTGGCTTTGTG 673
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 Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTTACGAG 733
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 Db 734 TGCAGTGGCTCCCAATGACGTGGCGCGCCGCGTGGTACGGAGAGTAAGGTACCCGTGAAC 793
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 Db 794 TATCCACCATACATTTCAAGGCCAAGGGTACAGGTGTCCTCGTGGACAAAGGGGACA 853
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 Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCCAGCAGAAATCCAGTGGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValIleValGluAsnArgProPheLeuSerLysLeu 280
 Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGTGAAGAACAGACCTTCTCTCAAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyTrpGlyAsnTyThrCysValAlaSerAsnLys 300
 Db 974 ATCTTCTTCAATGTCTCTGAACATGATGATGGAACATACACTTGGTGGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCGCACCAATGCGCAGCATCATGTATTGGTCCAGGGCGCGTCCAGCGAGGTGAGC 1093
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 QY 341 LeuLeuLysPhe 344
 Db 1154 CTCTCTCAAAATTT 1165
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 ID ACA67181 standard; cDNA; 1679 BP.
 XX AC
 AC ACA67181;
 XX XX
 DT 23-JUN-2003 (first entry)
 XX DE cDNA encoding human PRO polypeptide #188.
 XX KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
 KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
 KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
 KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
 KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;
 KW antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.
 XX OS Homo sapiens.
 XX PN US2003004311-A1.
 XX XX

PD 02-JAN-2003.
 XX 19-DEC-2001; 2001US-00028072.
 XX 18-JUN-1997; 97US-0049911P.
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059113P.
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 PR 20-MAR-1998; 98US-0077919P.
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PR 02-JUN-1999; 99WO-US012252.
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 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
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 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
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 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Deenoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI: 2003-352836/33.
 P-PSDB; ABU81057.

New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or heart attack.

Claim 2: Fig 3/5; 643pp; English.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ACA68994-ACA67268 represent cDNA sequences encoding the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:			
Pred. No.:	6.72e-36	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-017-084A-523 (1-344) x ACA67181 (1-1679)

RESULT 15			ACA63892	
ID	ACA63892	standard; cDNA; 1679 BP.		
XX	XX			
AC	ACA63892;			
XX	XX	16-JUN-2003 (first entry)		
DT	DT			
XX	XX			
DE	DE	Novel human secreted and transmembrane protein PRO337 cDNA.		
XX	XX	Human; secreted and transmembrane protein; PRO; antiinflammatory;		
KW	KW	antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;		
KW	KW	antidiabetic; gene therapy; inflammatory disease; organ failure;		
KW	KW	atherosclerosis; cardiac injury; infertility; birth defect;		
KW	KW	premature aging; AIDS; cancer; diabetic complication; chromosome mapping;		
KW	KW	gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;		
XX	XX	tissue typing; gene; ss.		
OS	OS	Homo sapiens.		
XX	XX	US2002192706-A1.		
PN	PN			
XX	XX	19-DEC-2002.		
PD	PD			
XX	XX	24-OCT-2001; 2001US-00999832.		
PF	PF			
XX	XX	17-OCT-1997; 97US-0062250P.		
PR	PR	03-NOV-1997; 97US-0064249P.		
PR	PR	13-NOV-1997; 97US-0065311P.		
PR	PR	21-NOV-1997; 97US-0066364P.		
PR	PR	10-MAR-1998; 98US-0077450P.		
PR	PR	11-MAR-1998; 98US-0077632P.		
PR	PR	11-MAR-1998; 98US-0077641P.		
PR	PR	11-MAR-1998; 98US-0077649P.		
PR	PR	12-MAR-1998; 98US-0077791P.		
PR	PR	13-MAR-1998; 98US-0078004P.		
PR	PR	17-MAR-1998; 98US-0004020.		
PR	PR	20-MAR-1998; 98US-0078886P.		
PR	PR	20-MAR-1998; 98US-0078910P.		
PR	PR	20-MAR-1998; 98US-0078936P.		
PR	PR	20-MAR-1998; 98US-0078939P.		
PR	PR	25-MAR-1998; 98US-0079294P.		
PR	PR	26-MAR-1998; 98US-0079656P.		
PR	PR	27-MAR-1998; 98US-0079663P.		
PR	PR	27-MAR-1998; 98US-0079664P.		
PR	PR	27-MAR-1998; 98US-0079689P.		
PR	PR	27-MAR-1998; 98US-0079728P.		
PR	PR	27-MAR-1998; 98US-0079786P.		
PR	PR	30-MAR-1998; 98US-0079920P.		
PR	PR	30-MAR-1998; 98US-0079923P.		
PR	PR	31-MAR-1998; 98US-0080105P.		
PR	PR	31-MAR-1998; 98US-0080107P.		
PR	PR	31-MAR-1998; 98US-0080165P.		
PR	PR	31-MAR-1998; 98US-0080194P.		
PR	PR	01-APR-1998; 98US-0080327P.		
PR	PR	01-APR-1998; 98US-0080328P.		
PR	PR	01-APR-1998; 98US-0080333P.		
PR	PR	01-APR-1998; 98US-0080334P.		
PR	PR	01-APR-1998; 98US-0080344P.		
PR	PR	08-APR-1998; 98US-0081049P.		
PR	PR	08-APR-1998; 98US-0081070P.		
PR	PR	08-APR-1998; 98US-0081071P.		
PR	PR	09-APR-1998; 98US-0081195P.		
PR	PR	09-APR-1998; 98US-0081203P.		
PR	PR	09-APR-1998; 98US-0081229P.		
PR	PR	15-APR-1998; 98US-0081817P.		
PR	PR	15-APR-1998; 98US-0081819P.		
PR	PR	15-APR-1998; 98US-0081838P.		
PR	PR	15-APR-1998; 98US-0081952P.		
PR	PR	15-APR-1998; 98US-0081955P.		
PR	PR	15-APR-1998; 98US-0082568P.		
PR	PR	21-APR-1998; 98US-0082569P.		
PR	PR	21-APR-1998; 98US-0082700P.		
PR	PR	22-APR-1998; 98US-0082704P.		
PR	PR	22-APR-1998; 98US-0082704P.		

QY	1	MetLysThrIleGlnProLysMethHisAsnSerIleSerTyrAlaIlePheThrGlyLeu	20
DB	134	ATGAAACCATTCAGCCAAATATGCAATTTCTTCTTGGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTCTCTTCCAAGAGGTGCGGTGCGCAGCGGAGATGCCACCTTCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATATTGAC	313
QY	61	AsnArgValThrArgValAlaTyrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
DB	314	AACGGGTACCCGGGTGGCTGGCTAACCAGCGAGCACCATCTCTTATGCTGGGAATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
DB	374	AAGTGGTCCCTGGATCCTCGGTGCTTCTGAGCAACACCCAAACGGCAGTACAGCATC	433
QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGAACGTGGATGTATGAGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AACCAACCAAGACCTCTAGGTCACCTCATTTGTGCAAGTAICTCCCAAAATTGTAGAG	553
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTCTTTCAGATATCTCCATTATGAAGGGAACAATATTAGCCCTACCTGCATAGCAACT	613
QY	161	GlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGlyPheVal	180
DB	614	GGTAGACAGAGCTCAGGTACTTCTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG	673
QY	181	SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200
DB	674	AGTGAAGACCAATACTTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTAGAG	733
QY	201	CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn	220
DB	734	TGCAGTGCCTCCAATGACGTGCGCGCCGCTGTGAGAGAGTAAAGGTACCCGTGAAC	793
QY	221	TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
DB	794	TATCCACCATACATTTCAAGCCCAAGGGTACAGTGTCCCGTGGGACAAAAGGGGACA	853
QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnThrTyrLysAspAspLys	260
DB	854	CTGCAGTGTGAAGCCTCAGCAGTCCCTCCACAGAAATTCAGTGTGTATCAAGGATGACAAA	913
QY	261	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
DB	914	AGACTGATTGAAGGAAGAAGGGGTGAAGTGGAAACAGACCTTTCCTCTCAAACTC	973
QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
DB	974	ATCTTCTTCAATGCTCTGAAACATGACTATGGGAACCTACATCTGCTGGCCCTCCAAAG	1033
QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
DB	1034	CTGGGCCACCAATATGCCAGCATCATGTATTGGTCCAGCGCGCGTCAGCGAGGTGAGC	1093
QY	321	AsnGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu	340
DB	1094	AACGGCAGCTCAGAGAGGCGAGGCTGCGTCTGGCTGCTCTTCTGCTTGTGCACTGT	1153
QY	341	LeuLeuLysPhe	344
DB	1154	CTTCTCAATTT	1165

22-APR-1998; 98US-0082797P.
 23-APR-1998; 98US-0082804P.
 23-APR-1998; 98US-0082796P.
 07-OCT-1998; 98WO-US021141.
 20-NOV-1998; 98WO-US024855.
 05-JAN-1999; 99WO-US000106.
 08-MAR-1999; 99WO-US005028.
 10-MAR-1999; 99WO-US005190.
 14-MAY-1999; 99WO-US010733.
 02-JUN-1999; 99WO-US012252.
 02-NOV-1999; 99WO-US028313.
 02-DEC-1999; 99WO-US028551.
 02-DEC-1999; 99WO-US028565.
 16-DEC-1999; 99WO-US030095.
 30-DEC-1999; 99WO-US031243.
 30-DEC-1999; 99WO-US031274.
 05-JAN-2000; 2000WO-US000219.
 06-JAN-2000; 2000WO-US000277.
 06-JAN-2000; 2000WO-US000376.
 11-FEB-2000; 2000WO-US003565.
 18-FEB-2000; 2000WO-US004341.
 24-FEB-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005841.
 10-MAR-2000; 2000WO-US006319.
 21-MAR-2000; 2000WO-US007532.
 30-MAR-2000; 2000WO-US008439.
 17-MAY-2000; 2000WO-US013705.
 22-MAY-2000; 2000WO-US014042.
 30-MAY-2000; 2000WO-US014941.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 24-AUG-2000; 2000WO-US023328.
 01-DEC-2000; 2000WO-US032678.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001WO-US006520.
 22-MAR-2001; 2001WO-US009552.
 25-MAY-2001; 2001WO-US017092.
 01-JUN-2001; 2001WO-US017800.
 20-JUN-2001; 2001WO-US019692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 (GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrara N, Filyaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 Goddard A, Godowski PU, Grimaldi JC, Gurney AL, Hillan KJ;
 Kijavini Iu, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 Stewart TA, Tumas D, Williams PM, Wood WI;
 WPI: 2003-328860/31.
 P-PSDB; ABU72281.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

Claim 2; Fig 221; 453pp; English.

The invention describes an isolated nucleic acid (I) comprising, or which is at least 80 % sequence identity to, or the full-length coding sequence of, any of 118 300-2100 nucleotide sequences, which encodes its corresponding PRO polypeptide selected from 118 100-700 amino acid sequences, all given in the specification. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6,72e-36	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-017-084A-523 (1-344) x ACA63892 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCATCCAGCCAAAATGCAATTCATCTCTGGGCAATCTTACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTGTCCTTCCAGAGTGCCTGCGGAGAGTGCCTGCGGAGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGACACGTCAGCGTCCGCGAGGGGAGAGCGCCACCTCAGGTCGACTATTGAC 313
 QY 61 AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGAGCACCATCTCTATGCTGGGATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGTGCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTCGATGTATGACGAGGGGCCCTTACCTGCTCGGTGCGAGAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTCTAGGTCACCTCATTTGTCAGATATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCACCTCAGTACGAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACACAGGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACCAATACCTTGGAAATTCAGGGCATCACCGGGAGAGTACAGGAGTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
 DB 734 TGCAATGCTCCCAATGACGTCGCGCGCGTGGTACGAGAGTAAAGGTCAACGCTGAAC 793
 QY 221 TyrProTyrIleSerGluAlaLeuGlyThrGlyValProValGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTCCAGAGCCCAAGGGTACAGGTGTCCCGTGGGACCAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 DB 854 CTGACGTTGAGGCTCAGCAGTCCCTTCAGAGAAATTCAGTGGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysIleu 280
 DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGGAAACAGACCTTTCTCTCAAACTC 973
 QY 291 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTTCAATGTCTCTGAACATGACTATGGGAATACACTTGGTGGCTTCCAAACAG 1033

PT typing, and in chromosome identification.

PS Claim 2; Fig 375; 660pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsiDEntry.html

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6,72e-36 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACA03790 (1-1679)

QY 1 MetLysThrLeuGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCACTCCAGCCAAATAATGCAAAATCTATCTCTGGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAAAGGAGTGGCCGCGAGGAGATGACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGAACAGTACGCTCCGCGAGGGGAGAGCGCCACCTCAGTGCTACATTGAC 313
QY 61 AsnArgValThrArgValAlaTrpIleuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGAGCACCATCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTCCCTGGATCTCTCGGTGGTCTCTTGAGCAACACCCAAACGCGATCAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisIleuLeuValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGAGACCTCTAGGGTCCACCTCATTTGGCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTTCAGATATCTCCATTATGAGGGAACATATATTAGCTCCTCAGTGCATCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACAGAGCCTACGGTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200

DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCAGGACAGTACGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValValVal 220
DB 734 TGCATGTGCTCAATGACGTGGCCGCCCGTGGTACGAGAGTAAAGGTCAACCGTGAAC 793
QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACTTTCAGAACCAAGGGTACAGGTGCCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrIleTyrIleAspAspLys 260
DB 854 CTGCGAGTGAAGACCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGAAAGAGGGGTGAAGTGAAGAAACAGACCTTTCCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCTGGCTCCAAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCGACACCAATGCCAGCATCATCTATTGTTCCAGGCGCGCTCAGCGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
DB 1054 AACGGCAGCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTTCTCAAAATTT 1165

RESULT 17
ACA04996
ID ACA04996 standard; cDNA; 1679 BP.
XX
AC ACA04996;
XX
XX
DT 28-MAY-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO337 cDNA.
XX
KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW obesity; diabetes; insulinemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
XX US2003032063-A1.
XX
XX 13-FEB-2003.
XX
XX 01-FEB-2002; 2002US-00066494.
XX
XX 26-AUG-1997; 97US-0056974P.
XX 17-SEP-1997; 97US-0059115P.
XX 18-SEP-1997; 97US-0059263P.
XX 19-SEP-1997; 97US-0059588P.
XX 17-OCT-1997; 97US-0062285P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063082P.
XX 27-OCT-1997; 97US-0063329P.
XX 29-OCT-1997; 97US-0063733P.
XX 21-NOV-1997; 97US-0066364P.
XX 25-NOV-1997; 97US-0066840P.

PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019330.
 PR 24-SEP-1998; 98WO-US019330.
 PR 28-OCT-1998; 98US-0101922P.
 PR 20-NOV-1998; 98US-0106032P.
 PR 20-NOV-1998; 98WO-US019304P.
 PR 25-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025190.
 PR 08-MAR-1999; 98WO-US025108.
 PR 23-MAR-1999; 98WO-US005028.
 PR 02-JUN-1999; 98WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145638P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030399.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski FJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX WPI; 2003-341964/32.
 DR P-PSDB; ABU67293.

XX PT Thirty seven nucleic acids encoding novel secreted and transmembrane PRO
 PT polypeptides, useful for modulating biological activity of cell
 PT expressing the polypeptide, and in chromosome and gene mapping.
 XX Claim 2; Fig 51; 255pp; English.
 XX The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO533, PRO301, PRO187, PRO337, PRO10096, PRO246, PRO6307,
 CC PRO6003, PRO6004, PRO4356, PRO2630, PRO2941, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (II) is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (I) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
 CC or hyper- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This sequence encodes a
 CC novel human secreted and transmembrane polypeptide associated
 CC oligonucleotide

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACA04996 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCATCCAGCCAAATATGCAATCTATCTCTTGGCAATCTTCACGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTCTCCAGGAGTCCCGTGGCAGGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGGACAACTGACGGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
 QY 61 AsnArgValThrArgValAlaTyrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGTACCCGGTGGCTGGCTTAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGGTCTGGATCTCTCGGTGGTCTCTCTGAGCAACACCCCAACGAGCAGTACGATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTTGATGTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 493
 QY 121 AsnHisProLysThrSerArgValHisLeuValGlnValSerProLysIleValGlu 140
 DB 494 AACACCCAAAGACCTCTAGGGTCCACCTCTTGTGCAAGTATCTCCCAATTTGAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160

Db 554 ATTCTTCAGATATCTCCATTAAATGAAGGCAACATATTAGCCTCACCTGCATAGCAACT 613
Qy 161 GlyArgProGluProThrValThrTTPArGHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAGAGCTACGGTTACTTGGAGACATCTCTCCCAAGCGGTGGCTTTGIG 673
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGACGATCTTGGAAATTCAGGGCATCACCGGAGCAGTCAGGGACTACGAG 733
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValIArgArgValLysValThrValAsn 220
Db 734 TGCAGTGCCTCCAATGACGTGGCGCGCGTGTGTACGAGAGTAAGGTCACCGTGAAC 793
Qy 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATACATTTTCAGAACCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrIleAspAspLys 260
Db 854 CTGCAGTGTGAAGCTTCAGCAGTCCCTTCAGCAGATTCAGTGTGTACAAAGGATGACAAA 913
Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerIleLeu 280
Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 973
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTTCAATGTCTTGAACATGACTATGGGAACCTACCTTCGGTGGCTCCCAACAG 1033
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGTAITTTGGTCCAGCGCGCTCAGCAGGTGAGC 1093
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGGCAGCTGAGGAGGCGAGGTGCGTCTGGCTGCTCTTCTGTGTCTTGCACCTG 1153
Qy 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165
RESULT 18
ID ACA72056 standard; cDNA; 1679 BP.
XX
AC ACA72056;
XX
DT 11-AUG-2003 (first entry)
XX
XX Human secreted and transmembrane PRO polypeptide #37 cDNA.
XX
XX Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine;
KW erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;
KW apoptosis related condition; AIDS; amyotrophic lateral sclerosis;
KW inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;
KW gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;
KW hypertension; myocardial ischaemia; kidney disease; carcinogenesis;
KW glomerulonephritis; lung disease; pulmonary hypertension; pre-eclampsia;
KW bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;
KW inflammatory bowel disease; reproductive disorder; premature labour.
XX
OS Homo sapiens.
XX
XX US2002177553-A1.
PN
XX
XX 28-NOV-2002.
XX
XX 15-OCT-2001; 2001US-00978192.
XX
XX 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028113.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.

PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 30-JUL-2001; 2001US-00918585.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
 XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2003-328499/31.
 DR P-PSDB; AB084961.
 DR
 XX New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
 XX pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
 PT modulators of receptor-ligand interactions.
 PT
 XX Claim 2; SEQ ID NO 522; 55pp; English.
 PS
 XX The invention relates to an isolated secreted and transmembrane
 CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
 CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
 CC linking a bioactive molecule to a cell. The PRO polypeptide or an
 CC antibody against it is useful for modulating a biological activity of a
 CC cell. The PRO polypeptide is useful in industrial applications including
 CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
 CC polypeptide is also useful as a thrombolytic agent, interferon,
 CC interleukin, erythropoietin, colony stimulating factor and other
 CC cytokines. The PRO polypeptide is useful for treating disease such as
 CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
 CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
 CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
 CC Parkinson's disease; cardiovascular disease e.g. hypertension and
 CC myocardial ischaemia; kidney disease e.g. renal failure and
 CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
 CC asthma; gastrointestinal disorders e.g. premature labour and inflammatory
 CC bowel disease; reproductive disorders e.g. gastritis ulcer and cataract
 CC precociousness; carcinogenesis. The present sequence represents a cDNA
 CC encoding a PRO polypeptide of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20020177553
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACA72056 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 Db 134 ATGAACCATCTCCAGCAAAATGACAAATCTATCTCTTGGCAATCTTCCAGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTGTGTCTCTTCAAGGAGTGCCCGTGGCGAGAGATGCCACCTTCCCAAA 253

QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGGACACAGTGGACGGTCCGCGAGGGGAGAGCGCCACCTCAGGTGACATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
 Db 314 AACGGGGTCAACCGGGTGGCTTAAACCGCAGCAGCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle 100
 Db 374 AAGTGGTCCCTGGATCTCCGGTGGTCTCTTGAGCAACACCCAAACGAGTACAGATC 433
 QY 101 GluIleGlnAsnValAspValTyAspGluGlyProTyThrCysSerValGlnThrAsp 120
 Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGTCGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisIleuIleValGlnValSerProLysIleValGlu 140
 Db 494 AACCAACCCAAAGACCTTAGGGTCCACTTGTGCAAGTATCTCCCAAAATTGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTCTTCAATATCTCCATTAATGAAGGAAACATATATTAGCCTCACCTGCATCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGACACAGACCTTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTTGGCTTGTG 673
 QY 181 SerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyGlu 200
 Db 674 ACTGAAGACGAATCTTGGAAATTCAGGCATCACCCGGAGCAGTCAAGGACCTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220
 Db 734 TGCAGTGCCTCAATGACGTGSCCGGCCCGTGTACGGAGAGTAAAGGTCAACCGTGAAC 793
 QY 221 TyrProTyThrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCCACCATACATTTCAAGAACCAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyLysAspAspLys 260
 Db 854 CTGCAGTGAAGCCTCAGCAGTCCCTCCGAGAAATTCAGTGGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 Db 914 AGACTGATTGAAGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyGlyAsnTyThrCysValAlaSerAsnLys 300
 Db 974 ATCTTCTCAATGTCTCTGAACATGACTATGGGAACATACACTTGGCGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCCACACCAATGCCAGCATCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 Db 1094 AACGGCACGTGAGGAGGGCAGGCTGCGTCTGCTGCTGCTCTTCTGCTTGTGCACCTG 1153
 QY 341 LeuLeuLysPhe 344
 Db 1154 CTTCTCAAAATTT 1165

RESULT 19
 ABX89328
 ID ABX89328 standard; cDNA; 1679 BP.
 XX
 AC ABX89328;
 XX
 DT 13-MAY-2003 (first entry)
 XX

DE	DNA encoding novel secreted and transmembrane protein PRO337.	
XX	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;	
KW	cardiac insufficiency disorder; cancer; tumour; immune response;	
KW	adrenal cortical capillary endothelial growth; c-fos induction;	
KW	vascular endothelial growth factor inhibition; VEGF inhibition;	
KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;	
KW	retinal neurons cell survival; rod photoreceptor cell survival;	
KW	retinal disorder; retinitis pigmentosa; kidney disorder;	
KW	mammalian kidney mesangial cell proliferation; Berger disease;	
KW	chondrocyte; herpeticiformis; Crohn's disease; chondrocyte proliferation;	
KW	chondrocyte redifferentiation; sports injury; arthritis; gene; ss.	
OS	Homo sapiens.	
XX	US2003017563-A1.	
XX	23-JAN-2003.	
XX	07-MAY-2002; 2002US-00140808.	
XX	31-MAR-1997; 97WO-US005230.	
PR	12-JUN-1998; 98WO-US012456.	
PR	14-JUL-1998; 98WO-US014552.	
PR	28-AUG-1998; 98WO-US017888.	
PR	10-SEP-1998; 98WO-US018824.	
PR	14-SEP-1998; 98WO-US019093.	
PR	14-SEP-1998; 98WO-US019094.	
PR	14-SEP-1998; 98WO-US019177.	
PR	16-SEP-1998; 98WO-US019330.	
PR	17-SEP-1998; 98WO-US019437.	
PR	07-OCT-1998; 98WO-US021141.	
PR	29-OCT-1998; 98WO-US022991.	
PR	29-OCT-1998; 98WO-US022992.	
PR	20-NOV-1998; 98WO-US024855.	
ER	01-DEC-1998; 98WO-US025108.	
PR	05-JAN-1999; 99WO-US000106.	
PR	08-MAR-1999; 99WO-US005028.	
PR	10-MAR-1999; 99WO-US005190.	
PR	20-APR-1999; 99WO-US008615.	
PR	14-MAY-1999; 99WO-US010733.	
PR	02-JUN-1999; 99WO-US012252.	
PR	01-SEP-1999; 99WO-US020111.	
PR	08-SEP-1999; 99WO-US020594.	
PR	13-SEP-1999; 99WO-US020944.	
PR	15-SEP-1999; 99WO-US021090.	
PR	15-SEP-1999; 99WO-US021547.	
PR	05-OCT-1999; 99WO-US023089.	
PR	29-NOV-1999; 99WO-US028214.	
PR	30-NOV-1999; 99WO-US028313.	
PR	30-NOV-1999; 99WO-US028409.	
PR	01-DEC-1999; 99WO-US028301.	
PR	01-DEC-1999; 99WO-US028634.	
PR	02-DEC-1999; 99WO-US028551.	
PR	02-DEC-1999; 99WO-US028564.	
PR	02-DEC-1999; 99WO-US028565.	
PR	16-DEC-1999; 99WO-US030095.	
PR	20-DEC-1999; 99WO-US030911.	
PR	20-DEC-1999; 99WO-US030999.	
PR	22-DEC-1999; 99WO-US030720.	
PR	30-DEC-1999; 99WO-US031243.	
PR	30-DEC-1999; 99WO-US031274.	
PR	05-JAN-2000; 2000WO-US000219.	
PR	06-JAN-2000; 2000WO-US000277.	
PR	11-FEB-2000; 2000WO-US000376.	
PR	18-FEB-2000; 2000WO-US004361.	
PR	18-FEB-2000; 2000WO-US004342.	
PR	22-FEB-2000; 2000WO-US004414.	
PR	24-FEB-2000; 2000WO-US004914.	
PR	24-FEB-2000; 2000WO-US005004.	
PR	01-MAR-2000; 2000WO-US005601.	
PR	02-MAR-2000; 2000WO-US005746.	
PR	10-MAR-2000; 2000WO-US005841.	
PR	10-MAR-2000; 2000WO-US006319.	
PR	15-MAR-2000; 2000WO-US006884.	
PR	20-MAR-2000; 2000WO-US007377.	
PR	21-MAR-2000; 2000WO-US007532.	
PR	20-MAR-2000; 2000WO-US008439.	
PR	17-MAY-2000; 2000WO-US013705.	
PR	20-MAY-2000; 2000WO-US014042.	
PR	30-MAY-2000; 2000WO-US014941.	
PR	02-JUN-2000; 2000WO-US015264.	
PR	28-JUL-2000; 2000WO-US020710.	
PR	11-AUG-2000; 2000WO-US022031.	
PR	23-AUG-2000; 2000WO-US023522.	
PR	24-AUG-2000; 2000WO-US023328.	
PR	08-NOV-2000; 2000WO-US030952.	
PR	10-NOV-2000; 2000WO-US030873.	
PR	01-DEC-2000; 2000WO-US032678.	
PR	20-DEC-2000; 2000US-00747259.	
PR	20-DEC-2000; 2000WO-US034956.	
PR	28-FEB-2001; 2001US-00796498.	
PR	28-FEB-2001; 2001WO-US006520.	
PR	01-MAR-2001; 2001WO-US006666.	
PR	09-MAR-2001; 2001US-00802706.	
PR	14-MAR-2001; 2001US-00808689.	
PR	22-MAR-2001; 2001US-00816744.	
PR	05-APR-2001; 2001US-00828366.	
PR	10-MAY-2001; 2001US-00854208.	
PR	10-MAY-2001; 2001US-00854280.	
PR	18-MAY-2001; 2001US-00860216.	
PR	25-MAY-2001; 2001US-00866028.	
PR	25-MAY-2001; 2001US-00866034.	
PR	25-MAY-2001; 2001WO-US017092.	
PR	01-JUN-2001; 2001US-00872035.	
PR	01-JUN-2001; 2001WO-US017800.	
PR	05-JUN-2001; 2001US-00874503.	
PR	14-JUN-2001; 2001US-00882636.	
PR	19-JUN-2001; 2001US-00886342.	
PR	20-JUN-2001; 2001WO-US019692.	
PR	21-JUN-2001; 2001US-00887879.	
PR	22-JUN-2001; 2001WO-US020116.	
PR	29-JUN-2001; 2001WO-US021066.	
PR	09-JUL-2001; 2001WO-US021735.	
PR	18-JUL-2001; 2001US-00908827.	
PR	06-AUG-2001; 2001US-00924419.	
PR	09-AUG-2001; 2001US-00927796.	
PR	16-AUG-2001; 2001US-00931836.	
PR	19-DEC-2001; 2001US-00028072.	
XX	(GETH) GENENTECH INC.	
PA	Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;	
XX	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;	
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	
XX	WPI; 2003-148238/14.	
DR	P-PSDB; ABUS9838.	
XX	Two hundred and seventy five nucleic acids encoding PRO polypeptides,	
PT	useful for treating pericyte-associated tumors, diabetes and various bone	
PT	and/or cartilage disorders, e.g. arthritis.	
XX	Claim 2; Fig 375; 659pp; English.	
PS	The invention describes an isolated human PRO polypeptide. The PRO	
XX	polypeptides are useful in detecting PRO polypeptides in a sample, in	
CC	linking a bioactive molecule to a cell expressing a PRO polypeptide, and	
CC	in modulating at least one biological activity of a cell expressing a PRO	
CC	polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus	
CC	useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186	
CC	stimulate adrenal cortical capillary endothelial growth, and PRO536,	
CC	PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,	
CC	PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus	
CC	useful for treating conditions or disorders where angiogenesis would be	

CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and are
 CC thus useful for treating sports injuries, and arthritis. This sequence
 CC encodes a novel human PRO protein
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ABX89328 (1-1679)

QY 1 MetIysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCACTCCAGCCAAATGACAAATCTATCTCTGGGCATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaIlePheProLys 40
 DB 194 GCTGCTCTGTCTCTTCCAGAGGTGCTCCGCGAGGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGACACGTCAGCGTCCGCGAGGGGAGAGCCACCTCAGTGACATATGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp 80
 DB 314 AACGGGTCTACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100
 DB 374 AAGTGGTGGCTGGATCCTCGCGTGGTCTCTGAGCAACACCCCAACGCAGTACAGATC 433
 QY 101 GluIleGlnAsnValAspValTrpAspGluGlyProTrpCysSerValGlnThrAsp 120
 DB 434 GAGATCAGAACGCTGGATGTGTATGACAGAGGCCCTTACACCTGCTGGTGCAGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTTAGGGTCCACCTCATTTGCAAGTATCTCCCAAAATGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCAGCTGATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACAGAGCCTTACCGTTACTTGGAGACACATCTCTCCCAAGCGGTGGTGGTGTG 673
 QY 181 SerGluAspGluTrpLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCCCGGGAGCAGTCCAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValArgValLysValThrValAsn 220

DB 734 TGCAAGTGCCTCAATGACGTGGCGCGCCCGTGGTACGGAGTAAAGGTCAACGTGAAC 793
 QY 221 TyrProProTrpIleSerGluAlaIleGlyThrGlyValProValGlyGlyLeuGlyThr 240
 DB 794 TATCCACCATACATTTTCAAGACCAAGGTACAGTGTCCCGTGGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTrpLysAspLys 260
 DB 854 CTGCAAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyGlyGlyValIleValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAAGAGGGGTGAAGCTGGAAAAACACACCTTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTrpGlyAsnTrpCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGCTCTGAACATGACTATGGAACTACACTTGGTGGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTGTTGGTCCAGCGCGCTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpIleLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCACGTCGAGGAGGGGCGAGCTGCGTCTGGCTGCTGCTCTTCTTGGTCTTGGACCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCAAAATTT 1165
 RESULT 20
 ABX92696
 ID ABX92696 standard; cDNA; 1679 BP.
 XX
 AC ABX92696;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE cDNA encoding human PRO337 polypeptide.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
 KW cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
 KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;
 KW cardiant; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002169284-A1.
 XX
 PD 14-NOV-2002.
 XX
 PF 16-OCT-2001; 2001US-00978697.
 XX
 PR 26-MAY-1981; 81US-00267213.
 PR 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-0004022O.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.

PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079668P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-00168978.
PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98US-0024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99US-0000106.
PR 05-JAN-1999; 99US-00254465.
PR 08-MAR-1999; 99US-00050528.
PR 10-MAR-1999; 99US-00265686.
PR 10-MAR-1999; 99US-000505190.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-00311832.
PR 02-JUN-1999; 99US-00107733.
PR 28-AUG-1999; 99US-00380137.
PR 28-AUG-1999; 99US-00380137.
PR 28-AUG-1999; 99US-00380138.
PR 28-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99US-0028313.
PR 02-DEC-1999; 99US-0028551.
PR 02-DEC-1999; 99US-0028551.
PR 16-DEC-1999; 99US-0030095.
PR 30-DEC-1999; 99US-0031243.
PR 30-DEC-1999; 99US-0031243.
PR 05-JAN-2000; 2000US-0000219.
PR 06-JAN-2000; 2000US-0000277.
PR 06-JAN-2000; 2000US-0000376.
PR 11-FEB-2000; 2000US-0003565.
PR 18-FEB-2000; 2000US-0004341.
PR 24-FEB-2000; 2000US-0005004.
PR 02-MAR-2000; 2000US-0005841.
PR 10-MAR-2000; 2000US-0006319.
PR 21-MAR-2000; 2000US-0007532.
PR 30-MAR-2000; 2000US-0008439.
PR 17-MAY-2000; 2000US-0013705.
PR 22-MAY-2000; 2000US-0014842.
PR 30-MAY-2000; 2000US-0014941.
PR 02-JUN-2000; 2000US-0015264.
PR 28-JUL-2000; 2000US-0020710.
PR 24-AUG-2000; 2000US-0023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000US-00732678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2001US-0006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001US-00816920.
PR 10-MAY-2001; 2001US-00854280.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001US-0021735.
PR 30-JUL-2001; 2001US-00918585.
PR 30-JUL-2001; 2001US-00918585.
XX

PA (GETH) GENENTECH INC.
XX Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KU;
PI Kijavini IU, Kuo SS, Napier WA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-288163/28.
DR P-PSDB; ABU61159.
XX Novel secreted and transmembrane polypeptides and polynucleotides
PT encoding them useful for treating cancer, kidney diseases, bone,
PT cartilage disorders and immune deficiencies.
XX Claim 2; Fig 221; 459pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC polypeptides are useful for detecting other PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The bioactive molecule may be a
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
CC The PRO polypeptides are useful for treating immune disorders, diabetes
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
CC tumours, and wound healing. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and gene
CC mapping, in the generation of antisense RNA and DNA, in the preparation
CC of PRO polypeptides, for generating transgenic animals or knockout
CC animals, for the genetic analysis of individuals with genetic disorders,
CC and in gene therapy. The present sequence encodes a human PRO polypeptide
CC of the invention. Note: The sequence data for this patent was obtained in
CC electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipspdidEntry.html
XX

SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6,72e-36 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-10-017-084A-523 (1-344) X ABX92696 (1-1679)
Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAACCATCCAGCCAAATGCAATCTCTTTGGGCAATCTTTCACGGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTCTTCCAGGAGTCCCGTGGCGAGGAGATGACCTTCCCCAAA 253
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACACGTGACGGTCCGGCAGGGGAGAGCCACCTCAGGTGACATTGAC 313
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCCGGGTGGCTGGCTAAACCGCAGCACCCTCTATGTGGGAATGAC 373
Qy 31 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrSerIle 100
Db 374 AAGTGGTCCCTGGATCTCTCGCGTGTCTCTCTAGCAACACCCAAACGAGTACAGCATC 433
Qy 131 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTGCTGACAGACAGAC 493

QY	121	AenHisProLysThSerArgValHisLeuLeuValGlnValSerProLysIleValGlu	140	PF	10-MAY-2002; 2002US-00142431.	XX
DB	494	AACCAACCAACCTAGGTCACCTCTATTGTGCAAGTATCTCCCAAAATTTGAGAG	553	PR	31-MAR-1997; 97WO-US005230.	XX
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAenIleSerLeuThrCysIleAlaThr	160	PR	12-JUN-1998; 98WO-US012456.	XX
DB	554	ATTCTTCAGATATCTCCATTATGAGGACATATATGCTCACCTGCATAGCACT	613	PR	14-JUL-1998; 98WO-US014552.	XX
QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180	PR	28-AUG-1998; 98WO-US017888.	XX
DB	614	GGTAGACCAAGACCTACGGTTACTTTGGACACATCTCTCCCAAGCGGTTGGCTTTGTG	673	PR	10-SEP-1998; 98WO-US018824.	XX
QY	181	SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200	PR	14-SEP-1998; 98WO-US019093.	XX
DB	674	ACTGAAGACGAATCTTGAAATTCAGGCACTACCCGGGACGTCAGGGGACTACGAG	733	PR	14-SEP-1998; 98WO-US019094.	XX
QY	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn	220	PR	14-SEP-1998; 98WO-US019177.	XX
DB	734	TGCAGTGCTCCATGACGTGCGCGGCCGCGTGTACGGAGAGTAAGGTCAACGTGAAC	793	PR	16-SEP-1998; 98WO-US019330.	XX
QY	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240	PR	17-SEP-1998; 98WO-US019437.	XX
DB	794	TATCCACCATACATTTCAAGACCAAGGTACAGGTGTCCCGTGGGACAAAAGGGGACA	853	PR	07-OCT-1998; 98WO-US021141.	XX
QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys	260	PR	29-OCT-1998; 98WO-US022991.	XX
DB	854	CTGCAGTGTGAGCCCTCAGCAGTCCCTCAGCGAATTCAGTGTGTACAGGATGACAA	913	PR	29-OCT-1998; 98WO-US022992.	XX
QY	261	ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280	PR	20-NOV-1998; 98WO-US024855.	XX
DB	914	AGACTGATTGAGGAAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	973	PR	01-DEC-1998; 98WO-US025108.	XX
QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300	PR	05-JAN-1999; 99WO-US000106.	XX
DB	974	ATCTTCTCAATGCTCTGAACTGATGGAATGGAATGGAATGGAATGGAATGGAATG	1033	PR	08-MAR-1999; 99WO-US005028.	XX
QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320	PR	10-MAR-1999; 99WO-US005190.	XX
DB	1034	CTGGGCAACCAATGCCAGCATATGCTATTTGGTCCAGGCCCGCTCAGCGAGGTGAGC	1093	PR	20-APR-1999; 99WO-US008615.	XX
QY	321	AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuValLeuHisLeu	340	PR	14-MAY-1999; 99WO-US010733.	XX
DB	1094	AACGGCACGTCGAGGAGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1153	PR	02-JUN-1999; 99WO-US012252.	XX
QY	341	LeuLeuLysPhe 344		PR	01-SEP-1999; 99WO-US020111.	XX
DB	1154	CTTCTCAAAATTT 1165		PR	08-SEP-1999; 99WO-US020594.	XX
RESULT 21				PR	13-SEP-1999; 99WO-US020944.	XX
ACD41982				PR	15-SEP-1999; 99WO-US021090.	XX
ID ACD41982 standard; cDNA; 1679 BP.				PR	05-OCT-1999; 99WO-US023089.	XX
XX				PR	29-NOV-1999; 99WO-US028214.	XX
AC ACD41982;				PR	30-NOV-1999; 99WO-US028313.	XX
XX				PR	01-DEC-1999; 99WO-US028401.	XX
DT 05-SEP-2003 (first entry)				PR	01-DEC-1999; 99WO-US028551.	XX
XX				PR	02-DEC-1999; 99WO-US028564.	XX
XX				PR	02-DEC-1999; 99WO-US028565.	XX
DE Human secreted/transmembrane protein (PRO) cDNA #188.				PR	16-DEC-1999; 99WO-US030095.	XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein; tumour;				PR	20-DEC-1999; 99WO-US030911.	XX
KW cytosolic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;				PR	20-DEC-1999; 99WO-US030999.	XX
KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;				PR	22-DEC-1999; 99WO-US030720.	XX
KW PBMC; glucose uptake; PFA; skeletal muscle cell; adipocyte cell;				PR	30-DEC-1999; 99WO-US031274.	XX
KW chondrocyte cell proliferation; chondrocyte cell differentiation;				PR	05-JAN-2000; 2000WO-US000219.	XX
KW peicyte cell; inner ear utricular supporting cell; T-lymphocyte cell;				PR	06-JAN-2000; 2000WO-US000376.	XX
KW endothelial cell; A-peptide; factor VIIa.				PR	11-FEB-2000; 2000WO-US003565.	XX
XX				PR	18-FEB-2000; 2000WO-US004341.	XX
OS Homo sapiens.				PR	22-FEB-2000; 2000WO-US004414.	XX
XX				PR	24-FEB-2000; 2000WO-US004914.	XX
XX				PR	24-FEB-2000; 2000WO-US005004.	XX
XX				PR	01-MAR-2000; 2000WO-US005601.	XX
XX				PR	02-MAR-2000; 2000WO-US005746.	XX
XX				PR	02-MAR-2000; 2000WO-US005841.	XX
XX				PR	10-MAR-2000; 2000WO-US006319.	XX
XX				PR	15-MAR-2000; 2000WO-US006884.	XX
XX				PR	20-MAR-2000; 2000WO-US007377.	XX
XX				PR	21-MAR-2000; 2000WO-US007532.	XX
XX				PR	30-MAR-2000; 2000WO-US008439.	XX
XX				PR	17-MAY-2000; 2000WO-US013705.	XX
XX				PR	22-MAY-2000; 2000WO-US014042.	XX
XX				PR	30-MAY-2000; 2000WO-US014941.	XX
XX				PR	02-JUN-2000; 2000WO-US015264.	XX
XX				PR	28-JUL-2000; 2000WO-US020710.	XX
XX				PR	11-AUG-2000; 2000WO-US022031.	XX
XX				PR	23-AUG-2000; 2000WO-US023522.	XX
XX				PR	24-AUG-2000; 2000WO-US023328.	XX
XX				PR	08-NOV-2000; 2000WO-US030952.	XX
XX				PR	10-NOV-2000; 2000WO-US030873.	XX
XX				PR	01-DEC-2000; 2000WO-US032678.	XX
PD				PR	20-DEC-2000; 2000US-00747259.	XX
XX				PR	20-DEC-2000; 2000WO-US034956.	XX

PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00834208.
PR 18-MAY-2001; 2001US-00854280.
PR 10-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-466355/44.
P-PSDB; ABO25028.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or PRO4978, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2; Fig 375; 659pp; English.

The invention relates to an isolated nucleic acid comprising at least 80% sequence identity to a PRO (secreted and transmembrane protein) cDNA comprising a nucleic acid (a) encoding a PRO polypeptide, or its extracellular domain (with or without its associated signal peptide), which comprises any of the 275 120-850 residue amino acid sequences, given in the specification; (b) comprising any of the 275 300-3500 nucleotide sequences, given in the specification; or (c) comprising the full-length coding sequence of the nucleotide sequences given in the specification, or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification. Also included are a vector comprising the novel nucleic acid, a host cell comprising the vector, producing a PRO polypeptide, the isolated PRO polypeptides detailed above, a chimeric molecule comprising the PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO polypeptide in a sample suspected of containing the PRO polypeptide, linking a bioactive molecule to a cell expressing a PRO polypeptide, modulating at least one biological activity of a cell expressing a PRO polypeptide, stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood mononuclear cells (PBMC)), modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, stimulating the proliferation or differentiation of chondrocyte cells (or proliferation of or gene expression in pericyte cells), stimulating the proliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the binding of A-peptide to factor VIIA, or differentiation of adipocyte cells, detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences given in the specification. The polynucleotide is useful in molecular biology,

CC including uses as hybridisation probes, in chromosome and gene mapping,
CC in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide may also be used in preparing PRO polypeptides by
CC recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptide or the
CC antibody is used in preparing a medicament for treating a condition
CC responsive to the polypeptide or antibody, such as tumours, and in
CC various diagnostic assays. The present sequence encodes a PRO polypeptide
XX
SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores: 6.72e-36 Length: 1679
Pred. No.: 2408.00 Matches: 344
Score: 2408.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACD41982 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTIPAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAATGCAATTCATCTCTTGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAGGAGTGGCGTGGCAGCGAGATGCCATCTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACACCTGAGCGTCCGGCAGGGGAGCGCCACCTCAGGTGACATTTGAC 313
QY 61 AsnArgValThrArgValAlaTTPLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGTCCACCGGGTGGCTGGCTTAAACGAGCACCCTCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTGCCTGGATCCTCGGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACCTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCAACCAAGAGCTCTAGGGTCCACTCATTTGCAAGTATCTCCCAAAATTTGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
QY 151 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACAGAGCTTACGTTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTAGACAGAGTACTTGGAAATTCAGGGCATCCCGGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
DB 734 TGCAGTGCCTCCATGACGTGGCGCGCCCGTGGTGTAGCAGAGTAAGAGTCAACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATCATTTTCAGAACCCAGGGTACAGGTGTCCCCGGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGNAATTCAGTGTGTACAGGATGACAAA 913

QY 261 ArgLeuIleGluGlyGlyGlyValIlyValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTCAATGCTCTGACATGACTATGGGAACACACATGCTGGTGGCTCCACCAAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCACACCAATGCCAGCATCATGTTTGGTCCAGGCGCGTCAGCAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrrLeuLeuProLeuValLeuHisLeu 340
 DB 1094 AACGGCACGTCGAGGAGGAGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTTCCTCAAAATTT 1165
 RESULT 22
 ID ACA60526
 AC ACA60526 standard; cDNA; 1679 BP.
 XX AC ACA60526;
 XX AC ACA60526;
 DT 11-JUN-2003 (first entry)
 DE Novel human secreted and transmembrane protein PRO337 cDNA.
 XX Human; secreted and transmembrane polypeptide; PRO;
 KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
 KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
 KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
 KW toxin; radiolabel; antibody; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tissue typing; gene; ss.
 XX Homo sapiens.
 OS US2002177165-A1.
 PN 28-NOV-2002.
 XX 01-FEB-2002; 2002US-00066500.
 XX 26-AUG-1997; 97US-0056974P.
 XX 17-SEP-1997; 97US-0059115P.
 XX 18-SEP-1997; 97US-0059263P.
 XX 19-SEP-1997; 97US-0059588P.
 XX 17-OCT-1997; 97US-0062285P.
 XX 24-OCT-1997; 97US-0062816P.
 XX 24-OCT-1997; 97US-0063082P.
 XX 27-OCT-1997; 97US-0063339P.
 XX 29-OCT-1997; 97US-0063733P.
 XX 21-NOV-1997; 97US-0066364P.
 XX 25-NOV-1997; 97US-0066840P.
 XX 16-DEC-1997; 97US-0069694P.
 XX 09-FEB-1998; 98US-0074086P.
 XX 09-FEB-1998; 98US-0074092P.
 XX 25-MAR-1998; 98US-0079294P.
 XX 08-APR-1998; 98US-0081049P.
 XX 14-JUL-1998; 98WO-US014552.
 XX 10-AUG-1998; 98US-0085988P.
 XX 18-AUG-1998; 98US-0087000P.
 XX 09-SEP-1998; 98US-009601P.
 XX 10-SEP-1998; 98US-0099803P.
 XX 10-SEP-1998; 98US-0099811P.
 XX 10-SEP-1998; 98US-0099812P.
 XX 10-SEP-1998; 98WO-US018824.
 XX 14-SEP-1998; 98WO-US019093.
 XX 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 98WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 26-JUL-1999; 99US-0145070P.
 PR 17-AUG-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US020231.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 03-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX WPI; 2003-328482/31.
 XX P-PSDB; ABU72061.
 XX Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, for identifying agonists or antagonists of polypeptide, and as molecular weight markers.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
 Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 Godowski PJ, Gurney AL, KJjavin IJ, Mather JP, Napier MA, Pan J,
 Paoletti NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
 Wood WI, Zhang Z;

Claim 2; Fig 51; 254pp; English.

The invention describes an isolated, secreted and transmembrane polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP (1). (1) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a cell

CC expressing the above polypeptides. The bioactive molecule, a toxin,
 CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
 CC identify other proteins or molecules involved in binding interaction. The
 CC polynucleotide (II) encoding (I) is useful in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, for generating
 CC transgenic animals or knockout animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, to
 CC construct hybridisation probes for mapping the gene which encodes the PRO
 CC and for the genetic analysis of individuals with genetic disorders, in
 CC gene therapy, for chromosome identification and as a chromosome marker.
 CC (I) and (II) are useful for tissue typing. This sequence encodes a novel
 CC human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084a-523 (1-344) x ACA60526 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAAACCATCCAGCCAAATATGCATATCTCTCTTGGGCATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCCAAAGAGTCCCGTGGCAGCGAGATGCCACTTCCCCCAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 DB 254 GCTATGACACACGTGACGGTCCCGCAGGGGAGAGCGCCACCTTCAGTGCATTTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuValAlaGlyAsnAsp 80
 DB 314 AACCGGTTCACCCGGTGGCTGCTAAACCGCAGACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGGTGCCTGGATCCTCGCTGCTCTCTGAGCAACACCCAAACGCGATCAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluCysProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTTGGATGTGTATGACAGAGGGCCCTTACACCTGCTCGTGACACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCAACCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACAGAGCCCTACCGTTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGATATCTTGGAAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValArgValLysValThrValAsn 220
 DB 734 TGCAGTGCCTCCAAATGACGTGGCCGCGCGTGGTACGAGAGTAAAGGTACCGGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATATATTTCAAGACCCAAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853

QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrTyrAspAspLys 260
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGTGGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGTATTGTGTCAGGCGCGCTCAGCAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
 DB 1094 AACGGCACGTCGAGGAGGCGAGGCTGGCTTGGCTGCTGGCTTCTTGGTCTTGCACTTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTCTCAAAATTT 1165

RESULT 23
 ACA04516
 ID ACA04516 standard; cDNA; 1679 BP.
 XX
 AC ACA04516;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO337 DNA.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
 KW PRO187; PRO337; PRO1411; PRO10056; PRO246; PRO6307; PRO6003; PRO6004;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
 KW obesity; diabetes; insulinemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX US2003032062-A1.
 PD 13-FEB-2003.
 XX
 XX 01-FEB-2002; 2002US-00066273.
 XX
 XX 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.

25-MAR-1998;	PR	98US-00792294P.
26-MAR-1998;	PR	98US-00796566P.
27-MAR-1998;	PR	98US-00796633P.
27-MAR-1998;	PR	98US-00796649P.
27-MAR-1998;	PR	98US-00796898P.
27-MAR-1998;	PR	98US-00797286P.
27-MAR-1998;	PR	98US-00797866P.
30-MAR-1998;	PR	98US-00799202P.
30-MAR-1998;	PR	98US-00799232P.
26-JUN-1998;	PR	98US-00105413.
07-OCT-1998;	PR	98US-00168978.
02-NOV-1998;	PR	98WO-US021141.
02-NOV-1998;	PR	98US-00184216.
06-NOV-1998;	PR	98US-00187368.
26-NOV-1998;	PR	98WO-US024855.
10-MAR-1999;	PR	99WO-US005190.
12-DEC-1998;	PR	99US-00267213.
27-DEC-1998;	PR	99US-00284291.
27-DEC-1998;	PR	99US-00218517.
05-JAN-1999;	PR	99WO-US000106.
05-MAR-1999;	PR	99WO-00254465.
08-MAR-1999;	PR	99WO-US005028.
10-MAR-1999;	PR	99US-00265686.
10-MAR-1999;	PR	99WO-US005190.
12-MAR-1999;	PR	99US-00267213.
12-APR-1999;	PR	99US-00284291.
14-MAY-1999;	PR	99US-00311832.
02-JUN-1999;	PR	99WO-US010733.
12-JUN-1999;	PR	99WO-US012252.
25-AUG-1999;	PR	99US-00380137.
25-AUG-1999;	PR	99US-00380138.
25-AUG-1999;	PR	99WO-US030142.
30-NOV-1999;	PR	99WO-US028313.
02-DEC-1999;	PR	99WO-US028551.
02-DEC-1999;	PR	99WO-US028565.
16-DEC-1999;	PR	99WO-US030095.
30-DEC-1999;	PR	99WO-US031274.
05-JAN-2000;	PR	200WO-US000219.
06-JAN-2000;	PR	200WO-US000277.
06-JAN-2000;	PR	200WO-US000376.
11-FEB-2000;	PR	200WO-US003565.
18-FEB-2000;	PR	200WO-US004341.
24-FEB-2000;	PR	200WO-US005004.
01-MAR-2000;	PR	200WO-US005601.
01-MAR-2000;	PR	200WO-US005841.
10-MAR-2000;	PR	200WO-US006319.
21-MAR-2000;	PR	200WO-US007532.
30-MAR-2000;	PR	200WO-US008439.
17-MAY-2000;	PR	200WO-US013705.
22-MAY-2000;	PR	200WO-US014042.
30-MAY-2000;	PR	200WO-US014941.
28-JUL-2000;	PR	200WO-US015264.
24-AUG-2000;	PR	200WO-US020710.
24-AUG-2000;	PR	200WO-US023328.
08-NOV-2000;	PR	200US-00709238.
10-NOV-2000;	PR	200WO-US030873.
30-NOV-2000;	PR	200US-00723749.
01-DEC-2000;	PR	200WO-US032678.
20-DEC-2000;	PR	200US-00742759.
20-DEC-2000;	PR	200WO-US034956.
28-FEB-2001;	PR	200WO-US006520.
22-MAR-2001;	PR	200US-00816744.
22-MAR-2001;	PR	200WO-US016920.
22-MAR-2001;	PR	200WO-US009552.
10-MAY-2001;	PR	200US-00854208.
10-MAY-2001;	PR	200US-00854280.
25-MAY-2001;	PR	200WO-US017092.
01-JUN-2001;	PR	200US-00872035.
01-JUN-2001;	PR	200WO-US017800.
05-JUN-2001;	PR	200US-00874503.
14-JUN-2001;	PR	200US-00862636.
19-JUN-2001;	PR	200US-00863492.
29-JUN-2001;	PR	200WO-US011962.
29-JUN-2001;	PR	200WO-US021065.

09-JUL-2001; 2001WO-US021735.
30-JUL-2001; 2001US-00918585.

(GETH) GENENTECH INC.

Ashtken AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Filvaroff E, Pong S, Gao W, Gerber H, Gerritsen ME;
Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Klavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
Stewart TA, Tumas D, Williams PM, Wood WI;

WPI: 2003-341189/32.
P-PSDB; ABUS0428.

New genes and secreted and transmembrane polypeptides (e.g. PRO337 or PRO1559), useful for treating or diagnosing e.g. cancers, atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple sclerosis in mammals.

Claim 2; Fig 221; 460pp; English.

The invention relates to a new isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 PRO polypeptides whose sequences are fully defined in the specification; or (b) any of 94 nucleotide sequences fully defined in the specification; or the full length coding sequence of any these 94 nucleotide sequences. Also included are an isolated PRO polypeptide scoring at least 80% positives when compared to any of the PRO polypeptide sequences cited above (or an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) an amino acid sequence encoded by the nucleotide deposited with ATCC numbers listed in the specification; (b) the PRO polypeptide, lacking its associated signal peptide; or (c) an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide), a vector comprising the nucleic acid molecule, a host cell comprising the vector (and producing a PRO polypeptide), a chimeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence and an anti-PRO antibody. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease, necrosis, atherosclerosis, infertility, premature aging, psoriasis, inflammatory disease, renal disease, arthritis, immune-mediated alopecia, stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence encodes a PRO polypeptide

Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:	6,72e-36	Length:	1679
Pred. No.:	2408.00	Matches:	344
Score:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-10-017-084A-523 (1-344) x ACA66437 (1-1679)

Qy 1 MetlysthrileGlnProLysMetHisAsnSerileSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAAACCATCCAGCCAAAATGCAAAATCTATCTCTGGGCAATCTTCACGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTGTGTCTCTCCAAAGAGTGGCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 253

Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleasp 60
Db 254 GCTATGCACAAAGTGCAGGTCCGGCAGGGGAGAGCGCCCTTCAGGTGCACATTATGAC 313
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp 80
Db 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCAATCTCTATGCTGGGAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerile 100
Db 374 AAGTGTGGCTGGATCTCTCGGTGCTCTCTCTGAGCAACACCCAAACGACGTACAGCATC 433
Qy 101 GluIleGlnAsnValAspValTrpAspGluGlyProTrpThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAAACGTGGATGTGTATGACGAGGCGCCCTTACACCTGCTGGTGCAGACAG 493
Qy 121 AsnHisProLysThrSerArgValHisIleuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCCAAAGACCTCTAGGGTCCACTCATTTGTGCAGATATCTCCCAAAATGTAGAG 553
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCACT 613
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACAGAGCCCTACGGTTACTTGGAGACACATCTCTCCAAAGCCGGTGGCTTTGTG 673
Qy 181 SerGluAspGluTrpLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200
Db 674 AGTGAAGACGATATCTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACAG 733
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValVal 220
Db 734 TGCAGTGGCTCCATATGACGTGGCGCCGCGGTGTACGAGAGTAAAGGTCAACCGTGAC 793
Qy 221 TyrProProTrpIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATATACATTTCAGAGCCAAAGGTACAGGTGCCCGTGGGACAAAGGGGACA 853
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTrpLysAspAspLys 260
Db 854 CAGCAGTGTGAAGCTCAGCAGTCCCTCCAGCAGATTCAGTGGTACAGGATGACACAA 913
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
Qy 281 IlePhePheAsnValSerGluHisAspTrpGlyAsnTrpThrCysValAlaSerAsnLys 300
Db 974 ATCTTCTTCAATGTCTCTGAAATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 1033
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACCAATGCCAGCATCATGTATTGTTGTTCCAGGCGCGGTTCAGCGAGGTGAGC 1093
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGGCACGTCGAGGAGGGGAGGCTCGGTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153
Qy 341 LeuLeuLysPhe 344
Db 1154 CTCTCTCAAAATTT 1165

RESULT 25

ACA68559
ID ACA68559 standard; cDNA; 1679 BP.

XX ACA68559;

AC ACA68559;

DT 25-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO337 cDNA.

XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
 KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
 KW gene therapy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; atherosclerosis; hypertension;
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
 KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping; gene;
 KW ss.
 OS Homo sapiens.
 XX
 PN US2003088063-A1.
 XX
 PD 08-MAY-2003.
 XX
 XX 12-AUG-2002; 2002US-00219003.
 PF
 PR 25-JUL-2000; 2000US-0220664P.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 23-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 FI P-PSDB; ABUS2110.
 XX
 DR WPI; 2003-393229/37.
 DR
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 XX Claim 2; Fig 125; 314pp; English.
 PS
 CC The invention describes one hundred and eighty seven nucleic acids
 CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
 CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating or diagnosing a cardiovascular, endothelial or angiogenic
 CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
 CC related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
 CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
 CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
 CC have applications in molecular biology, including use as hybridisation
 CC probes, and in chromosome and gene mapping. This sequence encodes a novel
 CC human secreted and transmembrane PRO polypeptide
 XX
 SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 6.72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACA68559 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 DB 134 ATGAACACCATCCAGCAAAATGACAAATTCATCTTTGGGCAATCTTACGGGGGTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTCTCTTCCAGAGTGCCTGGCGCAGCGGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyLeuSerAlaThrLeuArgCysThrIleAsp 60

DB 254 GCTATGGACAAACGTCACCGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGGTCTGGATCTCGCTGGTCTCTTCGAGCAACACCCAAACGCGAGTACAGCATC 433
 QY 101 GlnIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTGGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 AACCCACCAAGACCTCTAGGGTCCACCTATTGTGCAAGTATCTCCCAAAATTGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
 DB 734 TGCAGTGCCTCCCAATGACGTGGCGGCGCGGTGTACGGAGAGTAAAGGTCAACCGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 DB 794 TATCCACCATACATTTCCAGAACCAAGGGTACAGGTGTCCCCGTGGACAAAGGGGACA 853
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
 DB 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 DB 914 AGACTGATTGAAGAAAGAAAGGGGTGAAAGTGAAGAACAGACCTTTCTCTCAAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 DB 974 ATCTTCTCAATGTCTCTGAACATGACTATGGGNACTACACTTGGTGGCTCCCAACAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 DB 1034 CTGGGCCACACCAATGCGCAGCATCATGTTTGGTCCAGCGCGCGTCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 DB 1094 AACGGCAGCTGAGGAGGAGCGCTGCGTCTGGCTGCTGCTCTTCTGGTCTTGCACCTG 1153
 QY 341 LeuLeuLysPhe 344
 DB 1154 CTTCTCAAAATTT 1165

RESULT 26
 ACA04211
 ID ACA04211 standard; cDNA; 1679 BP.
 XX
 AC ACA04211;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO;

KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.

XX
 OS Homo sapiens.

XX US2003032155-A1.

XX 13-FEB-2003.

XX 03-MAY-2002; 2002US-00137865.

XX 31-MAR-1997; 97WO-US005230.

XX 12-JUN-1998; 98WO-US012456.

XX 14-JUL-1998; 98WO-US014552.

XX 28-AUG-1998; 98WO-US017888.

XX 10-SEP-1998; 98WO-US018824.

XX 14-SEP-1998; 98WO-US019093.

XX 14-SEP-1998; 98WO-US019177.

XX 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1998; 98WO-US019437.

XX 07-OCT-1998; 98WO-US021141.

XX 29-OCT-1998; 98WO-US022991.

XX 20-NOV-1998; 98WO-US024855.

XX 01-DEC-1998; 98WO-US025108.

XX 08-JAN-1999; 99WO-US000106.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1999; 99WO-US005190.

XX 20-APR-1999; 99WO-US008615.

XX 14-MAY-1999; 99WO-US010733.

XX 02-JUN-1999; 99WO-US012252.

XX 08-SEP-1999; 99WO-US020111.

XX 13-SEP-1999; 99WO-US020594.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 05-OCT-1999; 99WO-US023089.

XX 23-NOV-1999; 99WO-US028214.

XX 30-NOV-1999; 99WO-US028313.

XX 30-NOV-1999; 99WO-US028409.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 02-DEC-1999; 99WO-US028565.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030911.

XX 20-DEC-1999; 99WO-US030999.

XX 22-DEC-1999; 99WO-US030720.

XX 30-DEC-1999; 99WO-US031243.

XX 30-DEC-1999; 99WO-US031274.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00806889.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 18-MAY-2001; 2001US-00860216.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 25-MAY-2001; 2001WO-US017092.

PR 01-JUN-2001; 2001US-00872035.

PR 01-JUN-2001; 2001WO-US017800.

PR 05-JUN-2001; 2001US-00874503.

PR 14-JUN-2001; 2001US-00882636.

PR 19-JUN-2001; 2001US-00886342.

PR 20-JUN-2001; 2001WO-US019692.

PR 21-JUN-2001; 2001US-00887879.

PR 22-JUN-2001; 2001WO-US020116.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.

PR 18-JUL-2001; 2001US-00908827.

PR 06-AUG-2001; 2001US-00924419.

PR 09-AUG-2001; 2001US-00927796.

PR 16-AUG-2001; 2001US-00931836.

PR 19-DEC-2001; 2001US-00028072.

XX

XX (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen WE, Goddard A, Godowski PU, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-331925/31.

XX P-PSDB; ABU67033.

XX New secreted and transmembrane nucleic acids and polypeptides, designated

PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,

PT cardiac injury, infertility, birth defects, premature aging, AIDS, or

PT cancer.

XX Claim 2; Fig 375; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is

CC at least 80% identical to, or the full-length coding sequence of, any of

CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide

CC (one of 275 secreted or transmembrane proteins). The nucleic acid further

CC comprises the full-length coding sequence of the DNA deposited under

CC American Type Culture Collection (ATCC) accession number in a list given

CC in the specification. Also included are vectors and host cells for

CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO

CC extracellular domains and mature sequences, methods of detecting PRO

PR 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022991.

PR 20-NOV-1998; 98WO-US024855.

PR 01-DEC-1998; 98WO-US025108.

PR 08-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.

PR 20-APR-1999; 99WO-US008615.

PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.

PR 08-SEP-1999; 99WO-US020111.

PR 13-SEP-1999; 99WO-US020594.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 23-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 22-DEC-1999; 99WO-US030720.

PR 30-DEC-1999; 99WO-US031243.

PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 11-FEB-2000; 2000WO-US000376.

PR 18-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005746.

PR 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.

PR 21-MAR-2000; 2000WO-US007532.

PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

CC fatty acid (FPA) by skeletal muscle cells, a method for inhibiting the
 CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
 CC cells, a method for detecting the presence of a tumour in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences cited
 CC above. The nucleic acids and polypeptides are useful for treating
 CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
 CC infertility, birth defects, premature aging, AIDS (acquired
 CC immunodeficiency syndrome), cancer, or diabetic complications. The
 CC nucleic acids are useful as hybridisation probes, in chromosomes and gene
 CC mapping, and in generating antisense RNA or DNA. The polypeptides are
 CC useful as pharmaceuticals, diagnostics, biosensors or bioeffectors. Both
 CC are useful in tissue typing. The present sequence encodes a PRO protein
 CC of the invention

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-017-084A-523 (1-344) x ACA04211 (1-1679)

QY 1 MetIysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
 Db 134 ATGAAACACCTCCAGCCAAATATGCAATTCATCTTGGGCAATCTTCACGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 Db 194 GCTGCTCTGTCTCTTCCAGAGAGTCCCGTGGCAGCGAGATGCCACCTTCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
 Db 254 GCTATGACAACTGTCGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACATTATGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
 Db 314 AACCGGTGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 Db 374 AAGTGGTGCCTGGATCCTCGGTGTCTCTTCTGAGCAACACCCAAACGCGAGTGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
 Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 Db 494 AACCAACCAAGACCTCTAGGGTCCACTCAATGTGCAAGTATCTCCCAAAATGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 Db 554 ATTTCTTCAGATACTCCATTAAATGAAGAGCAATATTTAGCCTCACCTGCATAGCACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 614 GGTAGACAGACCTTACGTGTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
 Db 674 AGTGAAGACGAATATCTTGAAATTCAGGCATCACCCGGGACGACTAGGGGACTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValArgArgValIleValThrValAsn 220
 Db 734 TGCAGTGCTTCCATGACGTGGCGCGCGCTGGTACGAGAGTAAAGGTACCCGTGAAC 793
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 794 TATCCACCATACATTTTCAAGACCAAGGGGTACAGGTGTCTCCCGTGGGCAAAAGGGGACA 853

QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIysAspAspLys 260
 Db 854 CTGCAAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyValIysGlyValIysValGluAsnArgProPheLeuSerLysLeu 280
 Db 914 AGACTGATTTGAAGAAAGAAAGGGGTGAAGTGAAGTGAAGAAACAGACCTTTCTCTCAAACTC 973
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
 Db 974 ATCTTCTTCATGTCCTCTGAACATGACTATGGAACTACACTTGGTGGCTCCCAACAAG 1033
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1034 CTGGGCCACCAATGTCAGCATCATGCTATTGTGTCAGGGCGCGTCCAGCGAGGTGAGC 1093
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuValLeuHisLeu 340
 Db 1094 AACGGCACGTCGAGGAGGCGAGGCTCGCTGTGCTGCTCTTCTGGTCTTGGACCTG 1153
 QY 341 LeuLeuLysPhe 344
 Db 1154 CTCTCAAAATTT 1165

RESULT 27
 ACA65657
 ID ACA65657 standard; cDNA; 1679 BP.
 XX ACA65657;
 AC
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Human cDNA encoding secreted/transmembrane protein PRO337.
 XX
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
 KW genetic disorder; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003032057-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 15-NOV-2001; 2001US-00002796.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063329P.
 PR 27-OCT-1997; 97US-0063733P.
 PR 29-OCT-1997; 97US-0066364P.
 PR 21-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074093P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.

PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 98WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99US-012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0143698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 03-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin LJ, Mather JP, Napier MA, Pan J;
 PI Paoi NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX WPI; 2003-341960/32.
 DR P-PSDB; ABU79804.

XX Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying biological
 PT antagonists of polypeptide, and as molecular weight markers.

XX Claim 2; Fig 51; 255pp; English.

XX The invention relates to an isolated, secreted/transmembrane polypeptide,
 CC termed PRO polypeptide, having at least 80% sequence identity to a
 CC sequence selected from any one of the 37 sequences appearing as ABU79779
 CC -ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
 CC under any one of the ATCC numbers given in the specification. Also
 CC included are an isolated nucleic acid molecule having at least 80%
 CC sequence identity to a sequence selected from any one of the 37 cDNA
 CC sequences defined in the specification (or encoding the mature PRO

CC protein or a PRO protein extracellular domain), a PRO expression vector,
 CC a host cell comprising the vector, PRO fusion proteins, anti-PRO
 CC antibodies and a method for linking a bioactive molecule to a cell
 CC expressing the above PRO polypeptides, the bioactive molecule is a toxin,
 CC radiolabel or an antibody and causes the death of the cell. PRO or the
 CC antibody is useful for modulating at least one biological activity of
 CC cell expressing the above polypeptides. PRO is useful for identifying
 CC agonists or antagonists of PRO, for preparing a variant of PRO, as
 CC molecular weight markers for protein electrophoresis purpose and PRO
 CC nucleic acid is useful for recombinantly expressing those markers. PRO is
 CC also useful as therapeutic agent. PRO is useful in assays to identify
 CC other proteins or molecules involved in binding interaction. PRO nucleic
 CC acid is useful as hybridisation probes, in chromosome and gene mapping,
 CC in generation of antisense RNA and DNA, in the preparation of PRO
 CC polypeptide, in gene therapy, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and
 CC screening of therapeutically useful reagents, to construct hybridisation
 CC probes for mapping the gene which encodes the PRO and for the genetic
 CC analysis of individuals with genetic disorders, for chromosome
 CC identification, as a chromosome marker, and for generating probes for
 CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
 CC Western analysis. The antibody is useful in diagnostic assays for PRO,
 CC e.g. detecting its expression in specific cells, tissues or serum, for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. PRO or Ab is useful for the preparation of medicament for
 CC treating conditions which is responsive to the PRO polypeptide or anti-
 CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
 CC present sequence encodes a PRO polypeptide

XX SQ Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6,72e-36	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-017-084A-523 (1-344) x ACA65657 (1-1679)

QY	1	MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	AlGRAAACCTCCAGCCAAATGACAAATCTATCTCTTGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTCTCTTCCAGGAGTGCCGCGCAGCGAGATGCCACCTTCCCCAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlySerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACAACGTCACGTCGCGGAGGAGAGCGCCACCTCAGGTGCATATTGAC	313
QY	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
DB	314	ACCGGGTCACCGGGTGCCCTGGCTTAAACCGCAGCACCATCTCTATCTGGGATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
DB	374	AGTGCTGCTGGATCCTCGCGTGGTCTTCTTGAGCAACACCCAAACGAGTACAGCATC	433
QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAC	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AACACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCAAAATTGTAGAG	553
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTTCCTCAGATATCTCCATTATTAAGGAGGACAAATATTAGCTCCTCAGTGAACACT	613

QY 161 GIVArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
Db 614 GGTAGACAGAGCTACGGTTACTTGGACACACATCTCTCCCAAGCGGTGGCTTTGTG 673
PR 17-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
QY 181 SerGluAspGluTyrLeuGluLeuGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
Db 674 AGTGAAGAGCAATACTTGGAAATTCAGGGCATCCACCGGAGCAGTCAGGGAGCTACGAG 733
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
QY 201 CysSerAlaSerAsnAspValAlaProValValArgArgValLysValThrValAsn 220
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
Db 734 TGCAGTGCCTCCCAATACGTGGCGCGCCGCGTGTACGGAGATAAGGTACCGTGAAC 793
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
Db 794 TATCCACCATACATTCAGAAAGCAAGGGTACAGGTGTCCCGCTGGGACAAAGGGGACA 853
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAA 913
PR 15-SEP-1999; 99WO-US021090.
PR 05-OCT-1999; 99WO-US021547.
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
PR 29-NOV-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028213.
Db 914 AGACTGATTGAGAAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAACTC 973
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
Db 974 ATCTTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGGGTGGCTCCAAAG 1033
PR 02-DEC-1999; 99WO-US028564.
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
PR 16-DEC-1999; 99WO-US028565.
PR 20-DEC-1999; 99WO-US030095.
Db 1034 CTGGGCCACCAATGACCATCATCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGC 1093
PR 20-DEC-1999; 99WO-US030911.
PR 22-DEC-1999; 99WO-US030999.
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
PR 30-DEC-1999; 99WO-US030720.
PR 05-JAN-2000; 2000WO-US000219.
Db 1094 AACGGCAGTCGAGGAGGAGGCTGGCTGGGCTGTGGCTTCTTGGTCTTGCACTG 1153
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US003376.
QY 341 LeuLeuLysPhe 344
PR 18-FEB-2000; 2000WO-US003565.
Db 1154 CTTCCTCAAAATTT 1165
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005061.
PR 10-MAR-2000; 2000WO-US005746.
PR 15-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US007532.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.

RESULT 28

ADA45894

ID ADA45894 standard; cDNA; 1679 BP.

XX AC ADA45894;

XX DE 20-NOV-2003 (first entry)

XX DT Novel human secreted and transmembrane protein PRO337 cDNA.

XX KW Human; secreted and transmembrane protein; PRO; gene; ss;

XX KW Tumour necrosis factor alpha release; TNF-alpha release;

XX KW Glucose uptake modulator; FFA uptake modulator;

XX KW cell proliferation stimulator; cell differentiation stimulator;

XX KW cell differentiation inhibitor; cytokine release stimulator; tumour;

XX KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;

XX KW cervical tumour; liver tumour; chromosome mapping; gene mapping;

XX KW gene therapy; chromosome identification; chromosome marker.

XX OS Homo sapiens.

XX FN US2003022328-A1.

XX PD 30-JAN-2003.

XX PF 16-APR-2002; 2002US-00123904.

XX XX 31-MAR-1997; 97WO-US005230.

XX PR 12-JUN-1998; 98WO-US012456.

XX PR 14-JUL-1998; 98WO-US014552.

XX PR 28-AUG-1998; 98WO-US017888.

XX PR 10-SEP-1998; 98WO-US018824.

XX PR 14-SEP-1998; 98WO-US019093.

PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 23-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 28-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

BAKER KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI: 2003-584997/55.
 DR P-PSDB; ADA45895.

XX Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.

XX Claim 2; Fig 375; 659pp; English.

XX The invention describes 305 nucleic acids encoding PRO (secreted and
 CC transmembrane) polypeptides (I). (I) is useful for stimulating the
 CC release of TNF-alpha from human blood, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating the proliferation or differentiation of chondrocyte cells,
 CC for stimulating the proliferation of or gene expression in pericyte
 CC cells, for stimulating the release of proteoglycans from cartilage, for
 CC stimulating the proliferation of inner ear utricular supporting cells,
 CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
 CC the release of a cytokine from BMC cells, for inhibiting the binding of
 CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
 CC cells, for stimulating proliferation of endothelial cells, for detecting
 CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
 CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
 CC are useful for isolating genomic and cDNA nucleotide sequences or
 CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
 CC in assays to identify other proteins or molecules involved in binding
 CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
 CC and gene mapping, in generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptide, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and
 CC screening of therapeutically useful reagents, in gene therapy, for
 CC chromosome identification, as chromosome marker, and for generating
 CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
 CC detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. (I) and (II) are useful for tissue typing. This sequence encodes
 CC a novel human secreted and transmembrane PRO polypeptide.

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.72e-36	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0

DB:	8	Gaps:	0
US-10-017-084a-523 (1-344) x ADA45894 (1-1679)			
QY	1	MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAAACCATCCAGCCAAAATGCAATTTCTCTTGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACAACTGACGGTCCGGCAGGGGAGAGCGCCCTCAGGTGCTACTATTGAC	313
QY	61	AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
DB	314	AACCGGGTCACCGGGTGGCCCTGGCTAAACCCGACACCATCTCTATGCTGGGAATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
DB	374	AGTGGTGGCTGGATCCTCGCGTGGTCTCTTGAGCAACACCCAAACGCGAGTACAGCATC	433
QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGAGACAGAC	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AACCCACCCAAAGACCTTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG	553
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTCTCTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCCTACCTGCGATAGCACT	613
QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
DB	614	GGTAGACCAAGACCTTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG	673
QY	181	SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200
DB	674	AGTGAAGACGATATCTTGGAAATTCAGGGCATCACC CGGAGCAGTCAGGGAGTACGAG	733
QY	201	CysSerAlaSerAsnAspValAlaProValValArgValLysValThrValAsn	220
DB	734	TGCAGTGGCTCTCAATCACGTCGGCGCGCGTGTGTACGGAGAGTAAAGGTCACCGTGAAC	793
QY	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
DB	794	TATCCACCATACATTTCAAGACCAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA	853
QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys	260
DB	854	CTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAAGGATGACAAA	913
QY	261	ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu	280
DB	914	AGACTGATTGAAGAAAGAAAGGGGTGAAGGTGAAAGAGAGACCTTTCTCTCAAAACTC	973
QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
DB	974	AUCTTTCTCAATGCTCTGACATGACTATGGAACTACACTTGGTGGCTTCAACACAG	1033
QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
DB	1034	CTGGGCCACACCAATGCCAGCATCATTTGGTCCAGGCCCGCTCAGCGAGGTGAGC	1093
QY	321	AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu	340
DB	1094	AACGGCACGTCGAGGAGGGCAGGCTCGCTGGCTCTTCTTGGTCTTGGACCTG	1153
QY	341	LeuLeuLysPhe	344

Db 1154 CTCTCAATT 1165
 RESULT 29
 ADA76325
 ID ADA76325 standard; cDNA; 1679 BP.
 XX
 AC ADA76325;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human PRO polynucleotide #188.
 XX
 KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
 KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
 KW liver; microvascular endothelial cell; glucose; FFA;
 KW skeletal muscle cell; adipocyte cell; pericyte cell;
 KW inner ear utricular supporting cell; T-lymphocyte cell;
 KW endothelial cell tube formation; bone disorder; cartilage disorder;
 KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
 KW immune system cell infiltration.
 XX
 OS Homo sapiens.
 XX
 XX US2003073212-A1.
 XX
 XX 17-APR-2003.
 XX
 XX 16-APR-2002; 2002US-00123303.
 XX
 PR 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUN-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028584.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00818744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.

(GETH : GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-687639/65.

P-PSDB; ADA76326.

New isolated nucleic acid encoding a secreted and transmembrane
 polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
 gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2; Fig 375; 659pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor- α (TNF- α) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating differentiation of adipocyte cells, for stimulating
 CC proliferation of or gene expression in pericyte cells, for stimulating
 CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
 CC cells, for inducing endothelial cell tube formation and for treating
 CC various bone and/or cartilage disorders such as sports injuries and
 CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
 CC from cartilage are useful for treating sports-related joint problems. PRO
 CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
 CC polypeptides are also useful for treating various mammalian haemoglobin-
 CC associated disorders such as various thalassaemias and conditions which
 CC may benefit from enhanced local immune system cell infiltration. This
 CC sequence represents a human PRO polynucleotide of the invention. Note:
 CC The sequence data for this patent is also available in electronic format
 CC from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6,72e-36 Length: 1679
 Score: 2408.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-017-084A-523 (1-344) x ADA76325 (1-1679)

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 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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 DB 254 GCTATGGACAACTGACGCTCGCGAGGGGAGAGCGCCACCTCAGTGCCTATTGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyzAlaGlyAsnAsp 80
 DB 314 AACGGGTCCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyzSerIle 100
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 QY 101 GluIleGlnAsnValAspValTyzAspGluGlyProTyzThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGCTGGATGTGTATGACGAGGGCCCTTACACCTCGCTCGTGCAGACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140

DB 494 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTCTGCAAGTATCTCCCAAAATTGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTTCCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCCTGATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACACGAGGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
 QY 181 SerGluAspGluTyzLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyzGlu 200
 DB 674 AGTGAAGACGAATACTTGAAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTTACGAG 733
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValThrValAsn 220
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 QY 221 TyrProTyzIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyzLysAspAspLys 260
 DB 854 CTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
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 XX
 DT 06-NOV-2003 (first entry)
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 DE Human PRO337 cDNA.
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 KW differentiation; dermal fibroblast; tumour; gene therapy; gene;
 KW cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003050448-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 28-AUG-2002; 2002US-00230414.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.

XX Baker XP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2003-521818/49.
 DR P-PSDB; ABJ72290.
 XX
 XX New nucleic acid encoding for a PRO protein, useful for the manufacture
 PT of a medicament for diagnosing or treating tumors or for measuring or
 PT detecting expression of an associated gene.
 XX
 XX Claim 2; Fig 125; 315pp; English.
 XX
 XX The invention relates to a novel isolated nucleic acid encoding a fully
 CC defined PRO polypeptide. The molecules of the invention may be useful for
 CC stimulating proliferation or gene expression in pericyte cells or the
 CC release of TNF-alpha from human blood. Other possible uses include the
 CC stimulation or inhibition of chondrocyte proliferation or
 CC differentiation, the stimulation of human dermal fibroblast cell
 CC proliferation and the detection of the presence of a tumour within a
 CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
 CC of a medicament for diagnosing or treating a tumour within a mammal or
 CC for measuring or detecting the expression of an associated gene, as well
 CC as during gene therapy. The current sequence is that of the human PRO
 CC cDNA of the invention
 XX
 XX Sequence 1679 BP; 498 A; 432 C; 419 G; 330 T; 0 U; 0 Other;
 SQ

Alignment Scores: 6.72e-36 Length: 1679
 Pred. No.: 2408.00 Matches: 344
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
 DB: 8

US-10-017-084A-523 (1-344) x APT44288 (1-1679)

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 DB 134 ATGAACACCATCCAGCCAAATATGCAATCTATCTCTGGGCAATCTTCACGGGGCTG 193
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
 DB 194 GCTGCTCTGTGTCCTCTCCAAAGAGATGCCCGTGGCGAGCGAGATGCCACCTTCCCCAAA 253
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrIleArgCysThrIleAsp 60
 DB 254 GCTATGGACCAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTTCAGGTGCATTAITGAC 313
 QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuIleuValAlaGlyAsnAsp 80
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 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
 DB 374 AAGTGGTGGCTGGATCCTCGCGTGGTCTCTGAGCAACACCCAAACGCGAGTACAGCATC 433
 QY 101 GluIleGlnAsnValAspValTyrAspGluCysProTyrThrCysSerValGlnThrAsp 120
 DB 434 GAGATCCAGAACGTGGATGTGTATGACAGGGGCCCTTACACCTGCTCGGTGCACAGAC 493
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
 DB 494 ACCACCCAAAGACCTCTAGGGTCACCTCATTTGGCAAGTATCTCCCAAATTTGTAGAG 553
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
 DB 554 ATTTCTTCAGATATCTCCATTAAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 DB 614 GGTAGACAGAGCCTTACCTGGTGTACTTGGAGACACATCTCTCCCAAAGCGGTGGCTTTGTG 673

QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
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Search completed: May 28, 2004, 13:09:00
 Job time : 575 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 28, 2004, 12:59:15 ; Search time 114 Seconds
(without alignments)
1674.589 Million cell updates/sec

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1748.8	72.6	11673	4	US-09-334-220-3
5	1737.1	72.1	11580	4	US-09-334-220-4
6	1727.6	71.7	35100	2	US-08-770-379-17
7	1727.6	71.7	35100	3	US-08-757-669A-17
8	1727.6	71.7	35100	4	US-09-230-371A-17
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US-09-700-397-2

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US-10-017-084a-523 (1-344) x US-09-700-397-2 (1-1693)

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 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
 Db 610 GGTAGACACAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 669
 QY 181 SerGluAspGluTyrlLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrlGlu 200
 Db 670 AGTGAAGACGAATACCTTGGAAATTCAGGGCATCACCCTGGAGCAGTCAGGGACATACGAG 729
 QY 201 CysSerAlaSerAsnAspValAlaProValValArgArgValLysValThrValAsn 220
 Db 730 TGCAGTGCCTCCANTAGCTGGCGCGCGCTGGTACGGAGAGTAAGGTCCCGTGAAC 789
 QY 221 TyrProProTyrlIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
 Db 790 TATCCACCATACATTTCCAGAACCAAGGGTACAGGTGTCCTCCCGTGGGACAAAGGGGACA 849
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrlAspAspLys 260
 Db 850 CTGCAGTGTGAAGCCTCAGCAGTCCCTCCAGCAGAAATTCAGTGGTACAGAGATGACAA 909
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
 Db 910 AGACTGATTGAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAACTC 969

QY 281 IlePhePheAsnValSerGluHisAspTyThrCysValAlaIleSerAsnLys 300
 Db 370 ATCTTCTCAATGTCTTGAACATGACTATGGAACTACACTTGGTGGCTTCAACAG 1029
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
 Db 1030 CTGGGCCACACCAATGCCAGCATCTGCTATTGTTCCAGGCGCGTCAGGAGTGAGC 1089
 QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
 Db 1090 AACGGCAGCTCAGGAGGGCAGCTGCTGGCTGCTGCTCTCTCTGCTTGTGCTTGCACCTG 1149
 QY 341 LeuLeuLysPhe 344
 Db 1150 CTTCTCAATTT 1161

RESULT 3

US-09-700-397-5
 ; Sequence 5, Application US/09700397
 ; Patent No. 6664383
 ; GENERAL INFORMATION:
 ; APPLICANT: Onco Pharmaceutical Co., Ltd.
 ; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
 ; FILE REFERENCE: Q61459
 ; CURRENT APPLICATION NUMBER: US/09700,397
 ; CURRENT FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: JP 10-131815
 ; PRIOR FILING DATE: 1998-05-14
 ; PRIOR APPLICATION NUMBER: PCT/JP99/02485
 ; PRIOR FILING DATE: 1999-05-13
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 939
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-700-397-5

Alignment Scores:

Pred. No.: 2,33e-41 Length: 939
 Score: 2185.00 Matches: 313
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 90.74% Indels: 0
 DB: 4 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-700-397-5 (1-939)

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 QY 52 SerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArg 71
 Db 61 AGCGCCACCTCAGGTGCACATTTACCAACCGGTGTCACCGGGTGGCTGGCTAAACCGC 120
 QY 72 SerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeu 91
 Db 121 AGCACCATCTCTATCTGGGAATGACAGTGGTCTGGATCTCGGTGGTGGTCTCTTCG 180
 QY 92 SerAsnThrGlnThrGlnTySerIleGluIleGlnAsnValAspValTyAspGluGly 111
 Db 181 AGCAACACCAACCGCAGTACAGCATCGAGATCCAGACGTGATGTGTATGACGGGGC 240
 QY 112 ProTyThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIle 131
 Db 241 CTTACACCTGCTCGGTGCAGACACACCAACACCTCTAGGGTCCACCTCAT 300
 QY 132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
 Db 301 GTGCAAGTATCTCCCAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAAC 360

Db 1363 CTGGAGGCAACCTCGACCGGTCGACACGGGCAACTGGCTCTTCTTCCCTGGAGCAAGC 1422
QY 49 -----Gln-----Gly----- 50
Db 1423 GTCAAGCATAGCTGTCAAGTGGGAATCCATTTATTTCCATGGAATGAAGGCAGC 1482
QY 50 -----Gln----- 50
Db 1483 GAGTTCAATTTGGCCACACCGGGATGTAGATCTTCTTACAGAGATATTCAGAGCAG 1542
QY 51 -----GluSer----- 52
Db 1543 TGGTCAGAGAATTTGAGAGCCAGCCACAGGATGGGATATCTTGGGAGCAGTAGTTGGT 1602
QY 53 Ala-----Thr-----Leu-----Arg 56
Db 1603 GCAGACTGTGAACCGTAGAATCAGGACTATCACTGGTGTCTCTCAAGATGGAGAGAGG 1662
QY 57 -----CysThr----- 58
Db 1663 AAGCTTTGCACCCCTACATGGATACAACCTGGTTATGGCAACTGAGGTTCTACTTCGTT 1722
QY 59 -----Ile---Asp-----Asn----- 61
Db 1723 ATGGGAGGAATGTGACCCCTGGAGTCTCTCATGAACAGATATCATCTTATATGCAAG 1782
QY 62 -----Arg----- 62
Db 1783 ATTGAAGGAAGAAAGACACATTCGACTGGACACTTACCTTATTTCTTCTATTAAGTT 1842
QY 63 -----Val-----Thr----- 64
Db 1843 CGGTCTTTGGTTCTGTGTCTCAACCTGAACTTCAGACACCTGCCACCAATTTTGT 1902
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Db 1903 CTCAGGCAAAAGAGCCACCAAGGGTATATCGGAATGTC---TGGGCTGTGGACTTCTTC 1959
QY 68 ----- 68
Db 1960 CATGTGCTGCCGTTCTCCCTTCAACAATGTCTACATGATCCAGTTTCTTATTAATTG 2019
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Db 2020 GGATCGGCACACACACCGCTGGGAACAGCGTCAGCTTGGAGTTTCTTACTAACCATGGA 2079
QY 71 ArgSer-----Thr-----Ile-----Leu 75
Db 2080 CGTCTGTCCCTACTCCACACTGAGTGCTTGGCGGAGATCTGTGCAGGCCGCCACCTC 2139
QY 76 -----TyrAlaGly----- 78
Db 2140 CCCCACAGCACTGTCTACTCTCTCAGAAAACCTACCGGGTGGAAACCGAATCAGATTCT 2199
QY 79 -----Asn-----Asp----- 80
Db 2200 CTCCTAATGACGACTCACCGGACACACAGGATTCTGTGGAGACAAACAGGCCCAATC 2259
QY 81 -----LysTrp-----CysLeu----- 84
Db 2260 CTGGGAATATGTGGGCAATGTATATGTTTATATAGTCTCTGTCTCAAAATTCGT 2319
QY 85 -----AspPro----- 86
Db 2320 TCTGCGAGGACAATGCATCGGCTGCAAGTGTGACCCAGGATTTCTGGCCCA 2379
QY 86 ----- 86
Db 2380 GCTTGTGAGTGGCATCTCAGACATTCCTCAATGTTTATTTGGAAAGCTTTTGGCAGTCC 2439
QY 87 -----Arg-----Val----- 88
Db 2440 AGACTTTCCTCTTACCATAACTTTTACTATACCGTGTGTGAAGTCAGCTTTGGTTGT 2499

QY 89 ---ValLeuLeuSer-----Asn----- 93
Db 2500 GGTGTCTTAGCCAGTGGTAAGGCTCTGGTTTTCACAAAGATGGAGGGCGAGCTAATC 2559
QY 94 Thr-----Gln----- 95
Db 2560 AGCTCCTTTCTGGACAGCTCGCAGTCCAGGTTCTTCTAGTTTACACTGAGGCTGGGAGC 2619
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QY 98 TyrSer-----Ile----- 100
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QY 101 ---Glu-----Ile-----Gln---AsnVal--- 105
Db 2740 CACGAGCCAGAAATATCTCTGTAGAGCTACCGGATGATGCAAGACAGTTTGGAAATCCAG 2799
QY 106 -----AspValTyr-----AspGlu 110
Db 2800 TTCAGATGGTGCAGCCTTACCATTTCTCCCAAGGAGAGACGTGTGGGCCCATTTGATGAG 2859
QY 110 ----- 110
Db 2860 ATTGTCATGACCTCAGTCTCTTCAACAGCATCATCTCTGACATTCGACATTTACCAATCTTGTGGAA 2919
QY 111 -----Gly-----ProTyr----- 113
Db 2920 GTCACTCAATCCCTGGGATTTCTACTTGGCAATGTTCAACCATATCTGTGGCCATGACTGG 2979
QY 114 Thr---Cys----- 115
Db 2980 ACGTTTGTTTTACGGGAGATTCTAAACTTGCTCAAGCATGCGCTATGTGGAACACAG 3039
QY 116 -----Ser---Val-----Gln 118
Db 3040 TCCATGACATGCGAGCATCTATATGATTCACTTCAAGCTAGTTCAGCTAGTGGATGTGGCCAG 3099
QY 119 -----Thr-----AspAsn----- 121
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QY 122 -----His----- 122
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QY 123 Pro---LysThr---Ser-----Arg----- 127
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QY 127 ----- 127
Db 3340 CAGGATGAGTGGGCTTTAGACAACATTTACATTTGGGCGAGCAGTCCGCCAACATGTGAGT 3399
QY 128 -----Val----- 128
Db 3400 GGGCATGGCTCATGTGACCATGGCGTGTGCAGAGTGTGCCAGGGATACCGAGGCACCTGAA 3459
QY 129 ---His-----Leu-----Ile-----Val----- 132
Db 3460 TGCCACCCAGAGAGCTGCACCTTCTTCCACGATATATGTCAGATTTTGAACCCGAGCAGT 3519
QY 133 -----Gln-----ValSerProLys----- 137
Db 3520 TGGGAATCAGATGGCAGGAAGTTATTGGGGGAGAGTTTGTAAAGCTGTAGCAAGGCTGT 3579

4657	CTAAGCCCACTGTGGTACAAATACACCGGGGGTCAGGTTGGCAGCGGCTGTGGCACCCCTC	4717
185	-----Tyr-----Leu-----Glu-----	187
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188	-----IleGln-----	189
4777	CTGGACACCGAATATCAGTCTGTGTTCAGTTTTATATACAAATGGAAGTAAACATCA	4836
190	GlyIleThr-----	192
4837	GGGATTACGTACATCACCCACCGGCTAGATATGAGGGGCTGTGTTCAGTATTCGAAT	4896
192	-----	192
4897	GATAATGGGATACTTTGGCATTTGCTGAGAGAGTGTGGATTTCATGTCTTCCTGGAGCCA	4956
193	-----ArgGlu-----	194
4957	CAGATCATTTCCATGTGACCTGCCCCGGGAAGAACACACCTGSCACAGCTTTCGGTGG	5016
195	-----Gln-----Ser-----GlyAsp-----	198
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198	-----	198
5077	GTGAATGACAGCTCTCAAACTGGATTTCAGATATAAATGTGATGGCTCCATAGACTTGCAA	5136
198	-----	198
5137	GCCAACTGGTATCGAATCCAGGAGGCCAAGTTGATATCGACTGCCTCTCTATGGACACT	5196
199	-----Tyr-----	199
5197	GCCCTTATATTCACTGAAACATAGGAACCCCTGCTATGCTCAGACCTGGGACTTCCAT	5256
200	-----Glu-----CysSer-----	202
5257	GTGTGAGTCAAGCTTCTTTACAGTGGGAAATGAACATGGGCTGCAGCAAGCCTTTCAGT	5316
203	-----Ala-----Ser-----Asp-----Val-----	207
5317	GGTGCCACGGCATACAGCTCCAGTACTCTCTGAACACGGCAAGCACTGGCAGCTTGTC	5376
208	Ala-----AlaPro-----Val-----	212
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213	-----ArgArgValLysVal-----	217
5437	ACATCAGAAAGATTCCAGAACTGGAGCGGGTCACGGTCTACCTGCCACTCGCCACCAAT	5496
218	-----Thr-----Val-----AsnTyr-----	221
5497	TCTCCAGGACTCGGTTCCAGATTCAGACCACTATCTGTGGAGCAGATTCCTGG	5556
221	-----	221
5557	GCTATTGATAATGTATCCTGGCCTCGGGCTGTCTGGATGTCTCAGGACGAGGGATC	5616
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222	-----Pro-----	222
5677	GTTCTCTTCCCTCATCTAAAGATGATTTCATGGGAATTCATCTCGACCTTGG	5736
223	Pro-----Tyr-----Ile-----Ser-----	226

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QY 227 -----Glu----- 227
Db 5797 TGTCTGATCTTTAAAGGGAGGAGCTAAGAAATGCTTATTTCCAGAGATCTAGATTGTACC 5856
QY 228 -----AlaLysGlyThr----- 231
Db 5857 AATACTATGATGCCAGTTCTCTCTCGAATTTATAGGAAAGGTACCCAGAGAGGTCT 5916
QY 232 -----GlyVal----- 233
Db 5917 CACTCCATPCTTTACAGTTCTCTGTCTAGTGGAGAGTCACTGGCACTGATGATGAA 5976
QY 234 -----Pro-----Val-----Gly----- 236
Db 5977 TTCTACTTCCCTCAAAACGACGAGCACTTTTTCATCAATGTTCCCTTACCATACGGTGCC 6036
QY 237 -----Gln----- 237
Db 6037 CAACCAACGCTACAGATTCTGACTCTGGCAAACGTTACATAATGTTAAGAAAGAA 6096
QY 237 -----LysGly----- 237
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QY 242 -----Gln-----Cys----- 243
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QY 244 -----Glu-----Ala----- 245
Db 6397 CCGGTCTAGACTGGAATTTCTCAAGGAGCTTTGGAGCCACTGGCACCTGCTGCTCTC 6456
QY 246 -----SerAla-----Val-----ProSer----- 250
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QY 253 -----Phe----- 254
Db 6577 CACCTTTGTGATCTGTGCTTTCCGTTGTPACGAGGATTTTATCTCTGCTGCTCTCAG 6636
QY 255 -----Tyr----- 255
Db 6637 CCGGTCTACATGGCCATTGACAATGTCTACATGGTCCCGAGTGTGAAGATGTCTAT 6696
QY 256 -----Tyr----- 256
Db 6697 GGGCAGCGGAGCTGATCAATGGAACCAAGTGTATATGTGACCCGGGCTACTCTGGGCCA 6756
QY 257 -----LysAsp----- 259
Db 6757 ACCTGTAAATAAGCACCAAAAATCCTGATTTTCTCAAGAGCAGCTTTGAAGGTCAACTG 6816
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QY 264 -----Glu-----Gly----- 265
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QY 266 -----Lys----- 268
Db 6937 CTGGATTTATCATCATGCAAGTTTGTGCGAGTTCTTTCATGAGACTGGGATGTGTAAGGT 6996
QY 269 Val-----LysVal----- 271
Db 6997 GTTCCAGACCCAGGAGCCAGCCGCTGCTTCTGTCAGTACTCCCTCAATGGGGCTCTCC 7056
QY 272 -----Glu-----Asn----- 273
Db 7057 TGGAGTCTTCTTCAAGAGTTCTCTTCCAGCACTCCAGCAATGGGCAAGTACATTGCC 7116
QY 274 -----Arg-----Pro----- 275
Db 7117 CTGGAATGCCCTGAAAGCCGCTTCTGGTTCGACACGCCCTCCCTGGTGGCAGCATCT 7176
QY 276 -----PheLeuSerLys-----LeuIle----- 281
Db 7177 GAAATGGGCACCTCTATAGCCCTGGGTGATCGACCAGATTCTTATTGGAGGAATATC 7236
QY 282 -----Phe----- 282
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QY 283 -----Phe----- 283
Db 7297 CACCCAGGAGCCACCAAGATGCCGTGTGTGGCTCCACAGCGGATGCCCTGGTCTTATT 7356
QY 284 -----Asn----- 284
Db 7357 GAAAGCCAGCACCCGTTACGTGGTCCAGCAGACATCGCTGTAATGAGACTCATTC 7416
QY 285 -----Val-----Ser----- 286
Db 7417 CTACAGATAGACTTTGTGCTGCTCTCAGTCACAGACTCTCTGTATGTAATGTAAGT 7476
QY 287 Glu-----His-----Asp----- 289
Db 7477 GAGTACTCGGTGGATCTCGGTCTGTCTGGCACCCTGGTGGTGGGACTCCCTGCCCTACC 7536
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QY 294 ----- 294
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Db 7717 GGGGATGGTTGCTTAGACATGTGTCAGTGGCCACGGGAGATGCGTCCAGGGAAGCTGTGTC 7776
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Db 7777 TGTGATGAACAGTGGGAGCCCTGTACTGTGATGAGCTTGAGACCTCCCTTCCACCCAG 7836
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QY 304 -----ThrAsnAla----- 306
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Db 8017 TACTTTATGATGATGCTCATTAACCGGAGCAACCGTAACACGAGGAGTCTGCTGGAG 8076
QY 307 ---Ser---Ile---Met---LeuPhe----- 311
Db 8077 TACTCTGCTCAATGAGGACATCACTGGAACCTGCTGATGGAGATTTTCTATGACCACTAC 8136
QY 312 -----Gly----- 312
Db 8137 AGCAAACTGGATTGTGAATATCTTCTCCCTCCTGATGCTAAAGAGATTGCCACTGCG 8196
QY 313 -----Pro----- 313
Db 8197 TTCGATGTGGCAGCCACGACATGATGGCTTTGACCAAGATGACTGGGCCATTGACAAT 8256
QY 314 -----Gly---Ala-----Val-----Ser--- 317
Db 8257 GTCTCTATCTCGGCTCTGCGGACGACAGACAGTCAATGCTGACACCTTTAGCAGCGCC 8316
QY 318 -----Glu-----Val----- 319
Db 8317 CCAGTACCACAGCATGAGCGCTCCCGCGACAGCGCTGGCCCTGTTGGAAGATTGCTTTT 8376
QY 320 -----Ser-----AsnGly----- 322
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QY 323 Thr---SerArg----- 325
Db 8437 ACAGTGGAAAGATCTGTGACTCGCCAGATGGTGTGATGCTCTGTGGCAGCCAGTAGGA 8496
QY 326 Arg-----Ala----- 327
Db 8497 CGAGAGGTGATGACGTCACTCATGACCTGACGCCCACTGAGAACTGGATCATGCACTTC 8556
QY 328 -----GlyCys----- 329
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QY 330 -----Val---Trp-----Leu----- 332
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QY 332 ----- 332
Db 8677 CCAAAGTGTCTGGAAGCGTTTCTCAACCGTCTGTGTCTTCCCACTGAAGGGTGGA 8736
QY 333 -----LeuProLeu-----Leu----- 336
Db 8737 AGGATCACCTACCCGTTCTGTAAGCTTAAACGGGGAATCCTGTAAGATTTAGTGTCTAC 8796
QY 337 -----Val-----Leu 338
Db 8797 CAAAAGTACTCAGATGTGAGTGGGCAATTGACAAATTTCTACTTGGCCCTGGATGTTTG 8856
QY 339 -----His----- 339
Db 8857 GACAACTGTGGAGGCCACGGAGACTGCTAAAGGAACAGTGTATCTGTGACCCAGGCTAC 8916
QY 340 -----LeuLeu-----LeuLys---Phe 344
Db 8917 TCAGGCCAAAAGTGTACTTAATCACTCAAGCTGAAGACTTTC 8958
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RESULT 5

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US-09-334-220-4
; Sequence 4, Application US/09334220
; Patent No. 6323177
; GENERAL INFORMATION:
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; APPLICANT: St. Jude's Children's Research Hospital
; APPLICANT: Curran, Thomas
; APPLICANT: D'Arcangelo, Gabriella
; TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW
; TITLE OF INVENTION: DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND
; TITLE OF INVENTION: THERAPIES
; FILE REFERENCE: 2427/0F704
; CURRENT APPLICATION NUMBER: US/09/334,220
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11580
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-334-220-4
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Alignment Scores:

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Pred. No.: 1,47e-25 Length: 11580
Score: 1737.10 Matches: 296
Percent Similarity: 11.27% Conservative: 41
Best Local Similarity: 9.90% Mismatches: 4
Query Match: 72.14% Indels: 2649
DB: 4 Gaps: 249
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US-10-017-084a-523 (1-344) x US-09-334-220-4 (1-11580)

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QY 2 -----Lys-----Thr----- 3
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QY 4 -----Ile-----Gln---Pro----- 6
Db 1733 CGGTCTTTGGTTCTGTGTGTCATCAATCCTGAACTTCAGACTCCTGTACCAAAATTTGT 1792
QY 7 -----Lys----- 7
Db 1793 CTCAGGCAAAAGAACCATCAAGGACATAATAGGAATGTCTGGGCTGTAGACTTTTTCAT 1852
QY 8 -----Met----- 8
Db 1853 GTCCTGCTGTCTCCCTTCTACAAATGCTCATATGATATCTCATATCAATCTGGGA 1912
QY 9 -----His-----AsnSer----- 11
Db 1913 TGTGGAACGCATCACCTGGTTACAGTGTCACTTGGAAATTTTCTACCAACCATGGGCGC 1972
QY 12 -----Ile----- 12
Db 1973 TCCTGGTCCCTCTTTCACACTGAATGCTTACCTGAGATCTGTCTGTGGACCCACCTCC 2032
QY 13 -----Ser----- 13
Db 2033 CACAGCACTGTACTCTCTCTGAAAACTACAGTGGGTGGAAACCGAATAACAATCCCTT 2092
QY 13 ----- 13
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QY 14 -----TrpAlaIle-----Phe----- 17
Db 2153 GGAACATGTGGCAATTTGATATTTATATGCGCGTCAATGTCTCAAAATCTGTCTTCT 2212
QY 18 -----Thr-----GlyLeu-----Ala 21
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QY 22 -----Ala----- 22
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Db 2273 TGTGAGATGGCATCCAGACATCCCAATGTTTATTTCTGAAAGCTTTGGCAGTTCACAG 2332
Qy 23 Leu-----Cys--- 24
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Qy 25 -----Leu----- 25
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Db 2393 GTCTTGGCCAGTGTAGGCCCTCGTTTCAACAAAGAGGGCGCGTCAGCTAATTACA 2452
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Qy 31 ----- 31
Db 2573 TCCTTATGATAATGGGATAACTTGGAACTCTCTGGAGCATTATTTCATATCTCAGCTATCAT 2632
Qy 32 ---Arg---Ser---GlyAspAla----- 38
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Qy 74 ----- 74
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Qy 75 -----LeuTyr-----AlaGly----- 78
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Db 3470 GGTGTCTATCTTCTTGGATCATCTCTGTAATTTTCTGAGCAAGGCTGGGAAAAACAGCAGCTGGT 3529
Qy 78 ----- 78
Db 3530 AGTTGGGACCTGGATACTTCTTGGGTGGACTTTTCCAGTTTCTACATCCAGATAGGCGGA 3589
Qy 79 -----Asn---Asp---Lys----- 81
|||
Db 3590 GAGAGTCTTCAATGCAACAAGCCCTGACAGAGAGAGGGGGCTCTCTCTTCTAGTACAGC 3649
Qy 82 -----Trp----- 82
|||
Db 3650 AACAAATGGGGGCATCCAGTGGCACCTGCTAGCAGAGATGTACTTTTTCAGACTTTCAGCAA 3709
Qy 83 -----Cys----- 83
|||
Db 3710 CCCAGATTTGTCTATCTGGAGCTTCCAGCTGTCTGCCAAGACCCCTTGCACCAAGTTCGCG 3769
Qy 83 ----- 83
Db 3770 TGGTGGCAGCCCGTGTCTCAGGGGAGGACTATGACCGAGTGGGAGTCGATGATCATC 3829
Qy 84 -----Leu----- 84
|||
Db 3830 ATTCTGTGCCAGAGAGCAGATCATCCAGTTTATCAATCCAATTTTACCTTTCAGAAC 3889
Qy 85 -----Asp----- 85
|||
Db 3890 TTTTATGAGAACCCAGCTTTTGTATTACCTTATGATCAGATGAGTGTGGTGTGATGTTG 3949
Qy 86 -----Pro----- 86
|||
Db 3950 GCTAATGAAGATGGTTAAATAATGAACCTTCTGTGCTGCCACACCATCAGCAATGATA 4009
Qy 87 -----Arg---Val----- 88
|||
Db 4010 TTTGAAAAATCAGATGAGATCGATTTTGCAGTAACTCGAGATTTGACCCCTGAAACCTGGA 4069
Qy 89 ---ValLeu---LeuSerAsn---ThrGln--- 96
|||
Db 4070 TATGTCTACAGTTCAGCTA---AACATAGGTGTGCGCAATCAATTCAGCAGTACTGCT 4126
Qy 97 -----GlnTyrSer-----Ile----- 100
|||
Db 4127 CCAGTTCTTCTTTCAGTACTCTCATGATGCTGTGTATGTCCTGTTTCTGGTGAAGAAGGC 4186
Qy 100 ----- 100
Db 4187 TGTTACCAGCTTTCAGGCAAGAGATGCGAAGGAACTCCAGAGAACTAAGTGAAGCCC 4246
Qy 101 -----Glu----- 101
|||
Db 4247 ACCATGATACACAGGGGACTTTTGAAGAATGGAAGAATCACCATTGTTTATTCGAAG 4306
Qy 102 -----IleGln---Asn 104
|||
Db 4307 TCTTTCATCCAGCAAGACAGATTCCGATGATCCAGGAGGAGCTCAGAGAAAC 4366
Qy 105 Val-----Asp---ValTyr----- 108
|||
Db 4367 GTGCTTCCATTTGGTTTATAGTGGAGTGTACATATCGAGCCTTGTCCAGTACTGCACT 4426
Qy 109 -----Asp----- 109
|||
Db 4427 GGCATGGGACTGCAATTTCAAGAGTGTGTTTCTGTGACCTGGGATATATCTGTCACAA 4486

QY 110 ----- GluGly--- 111
Db 4487 GGAACCTGTGTCAAATGTCCTCCCAATCACAATGAGATGTTGCGATGTTGGGGGAAG 4546
QY 112 -----Pro-----Tyr-----Thr-----Cys----- 115
Db 4547 CTCAGCCCTCTGTGGTACAAGATAACAGGTGCCAGGTGTGGAACACTGCTGTGGAACACTT 4606
QY 116 -----Ser----- 116
Db 4607 AACGATGGCAATCTCTACTCAATGCGCTGGGAAAAGGAGGCCGAGCGGTCCCT 4666
QY 117 -----ValGln----- 118
Db 4667 CTGACACACAGGAATATCAGACTGTGTTCAATTTTATATACAAATTTGGAAGCAAACTTCA 4726
QY 119 -----Thr----- 119
Db 4727 GGCATTACCTGCATCAAAACCAAGAACTAGAAATGAAGGGCTTATTGTTCAAGTATTCAAAT 4786
QY 120 AspAsn-----His----- 122
Db 4787 GACAAATGGGATCTCTGGCAATTTGCTTCGAGAGTTGAGCTTCATGCTTCCTCGGAACCA 4846
QY 123 -----Pro-----LysThr-----Arg-----Ser----- 127
Db 4847 CAGATCATTTCCATTGACCTGCCACAGCAGCGAAGACACTGCAACGGCATTTCCGATGG 4906
QY 128 -----ValHis----- 131
Db 4907 TGGCAACCGCAACATGGGAAGCAATTCAGCCAGTGGGCTTTGGATGATGTTCTTATAGGA 4966
QY 131 -----ValGln----- 133
Db 4967 ATCAATGACAGCTCTCAAACTGGATTTCAGACAAATTTGATGGCTCTATAGATTTGCAA 5026
QY 132 -----ValGln----- 133
Db 5027 GCCAACTGGTATCGAATCCAAAGGAGGTCAAGTTGATATTGACTGTCTCTATGGATACT 5086
QY 133 ----- 133
Db 5087 GCTCTGATATTCACTGAABACATAGGAABACCTCGTTATGCTGAGACCTGGGATTTTCAT 5146
QY 134 ValSer-----Pro----- 136
Db 5147 GTGTCAGCATCTACCTTTTTCAGTTTGAATGAGCATGGCGTGTAGCAAGCCCTTCAGC 5206
QY 137 -----Lys----- 137
Db 5207 AACTCCACAGTGTA CAGCTCCAGTATTTCTGGAACAATGGCAAGGACTGGCATCTTTGTC 5266
QY 138 -----Ile-----Val----- 139
Db 5267 ACCGAAGAGTGTGTTCTCCCAACCAATTGGCTGTCTGCTGATTCACGAAAGTTCAATTTAC 5326
QY 140 -----Glu----- 141
Db 5327 ACCTCGAAAGATTCCAGAAATTGGAAGCGGATCACTGTCTCCTTCCACTCTCCACCAATT 5386
QY 142 Ser-----Ser----- 143
Db 5387 TCTCCAGGACCGGTTTCAGATGGATTTCAGGCCAACTACACTGTGGGGGCTGATTCCTGG 5446
QY 144 -----Asp----- 145
Db 5447 GCGATTGATAATGTTGTACTGGCTTCAGGTCGCCCTTGGATGTGCTCAGGACGAGGATT 5506
QY 145 ----- 145
Db 5507 TGTGATGCTGGACGTGTGTGTGACCGGGGCTTTGGTGGACCTATTGTGTCTCTGTT 5566
QY 146 -----SerIle-----Asn----- 148

Db 5567 GTTCCTCTGCCCTCGAATTTCTTAAAGACGATTTCAATGGGAATTTATACCTCTGACCTTTGG 5626
QY 149 -----Glu-----GlyAsn-----Asn-----Ile----- 153
Db 5627 CCTGAAGTGTATGTCAGAGAGGGGGAATCTGAATGTTGAAACCATCAAAATCTGGAACA 5686
QY 154 SerLeu-----Thr-----Cys----- 157
Db 5687 TCTCTAAATTTTAAAGGGAAGGACTAGGATGCTTTATTTCAGAGATCTAGATTGTACA 5746
QY 158 -----IleAla-----Thr----- 160
Db 5747 AATACAATGATGTCCAGTTTTCACCTAGATTATAGCAAAAAGTAGTACCCAGAGAGATCT 5806
QY 161 -----Gly----- 161
Db 5807 CACTCTATTCTGTATCAAAATTTCTCCATCAGTGGAGGAATCACTTGGCACCTGATGGATGA 5866
QY 161 ----- 161
Db 5867 TTTTACTTTCCTCAAAACAAGAAATATCTTTTCATCAATGTTTCCTTGCCATACACTGCC 5926
QY 162 -----Arg-----Pro-----Glu 164
Db 5927 CAAACCAATGCTACAAGATTTCAGACTCTGGCAACCTTATAATAACGGTAAAGAAAGAA 5986
QY 165 -----ProThrVal----- 167
Db 5987 ATCTGATGTTGATGACTTTCATTATTCGATGGAATAATGTAAACAACCT---GTGATG 6043
QY 168 -----Thr-----Trp----- 169
Db 5044 CTCCTGGATCAATTTGATTTTGGGCCCGAGAGAACAATTTGTTTCTATCTCGTGTGT 6103
QY 169 ----- 169
Db 5104 AACATCGGCTTTTANTGTCCATATTTCTCAAAGGGGGCACCTGGAAGAGATTCAGCTATG 6163
QY 169 ----- 169
Db 5164 GTGTTGTTTCAAATGAAGTTGGTGAGCATTCATTACCACCGTGACCTAAATGTGAAT 6223
QY 169 ----- 169
Db 6224 GAGAACCATCATACAATTTGAGATCAACGTTGCTGTGTGACTGATAGCTCATCCGG 6283
QY 170 -----Arg----- 170
Db 6284 GATCCAGTGAGACTGGAATTTTCAAGGGACTTCGGGGCGACCTGSCACCTTCTGCTGCC 6343
QY 171 -----HisIleSer-----Pro----- 174
Db 6344 CTCCTGTACCAGCAGCAGCAAGCAAGTCAAGTCTTTTATGCTCCACCGAGCACCCCAAGC 6403
QY 175 -----Lys 175
Db 6404 AGCACCTACTACGCAAGGAACCATGCAAGGCTGGAGGGAGGTGCTGCACCTTTGGGAAG 6463
QY 176 -----AlaVal-----GlyPhe----- 179
Db 6464 CTGCACCTTTGTGGATCTGTCCGTTTTCAGATGTTACAGGAGATTTTACCTTCCGGCTCT 6523
QY 180 -----ValSer-----Glu----- 182
Db 6524 CAGCCAGTGAATGGGCCCATTTGATATGCTACATCGGTCCCGAGTGTGAGGAGATGTGT 6583
QY 183 -----AspGlu-----Tyr----- 185
Db 6584 AATGGACAGGAGCTGTATCAATGGAACCAAAATGTATGTGACCTTGGCTTCTCAGGT 6643
QY 185 ----- 185

Db	6644	CCAACCTGTAAATAAGACACCAAAAAATCCTGATTTTCTCAAAAGATGATTTCTCAAGAGTCAG	6703
Qy	186	LeuGlu-----Ile188	188
Db	6704	CTAGAATCTGATAGATTCTTAAATGAGTGGTGGGAACCATCTCGAAAGTGTGGAATC	6763
Qy	188	-----188	188
Db	6764	CTTTCTAGTGAACAACCTCTTTTCAATGAAGATGGCTTGGCATGTTGATGACACGA	6823
Qy	188	-----188	188
Db	6824	GACCTGGATTATCACATGTAGATTGTGCAATTCTCATGAGACTGGGATGTGTAA	6883
Qy	188	-----188	188
Db	6884	GGCGTTCCTGACCCAGGAGTCAACCCGCTCTCTACAGTATTCTCTCAACGGTGGCCTC	6943
Qy	189	-----Gln-----Gly-----190	190
Db	6944	TCGTGGAGTCTTTCTCAGGAGTTCCTTTTCAGCAATCCAGCAATGGCGCAGGTACATT	7003
Qy	191	-----Ile-----ThrArg-----193	193
Db	7004	GCCCTGGAGATACCCCTTGAAGCCGCTTCGTGTTCTACTCGCTTCGCTGGTGGCAACCG	7063
Qy	194	-----Glu-----Gln-----195	195
Db	7064	TCTGAAATGGCACTTCTACAGCCCTGGGTATCGATCAGATCTTATTGGAGGAAT	7123
Qy	195	-----195	195
Db	7124	ATTTCGTGTAATACGGTCTTGGAAGATGATTTCAACCCCTTGATAGTGAATGSGCTG	7183
Qy	196	-----Ser---GlyAsp-----198	198
Db	7184	CTTCACCCAGAGGCAACAAGATCCCGTGTGTGGCTCTACTGTGATGCCCTGGTCTTC	7243
Qy	199	-----Tyr-----Glu-----200	200
Db	7244	ATTGAAGGCCAGCACCCGTTACGTGTGTCAGCACAGCGTTGCCGTGAATGAGGATTC	7303
Qy	201	-----CysSer-----Ala-----203	203
Db	7304	TTCCTACAGATAGACTTCGTGCTCCTCTGCTCAGTCACAGACTCTTGTATGCGATTGAA	7363
Qy	204	-----Ser-----204	204
Db	7364	TTGAATACTCAGTATGATCTTGGATTTGTCATGGCACCCATTTGTTAAGGAGACTGTCTG	7423
Qy	205	-----Asn-----Asp-----206	206
Db	7424	ACCAATGTGGATGTCAGTCTATCTCTGCAACGGATCTCTGTTGTGAGACTTTTCAAC	7483
Qy	207	-----Val-----Ala-----208	208
Db	7484	AAGTGGACTAGAAATCACTCTGCCTCTCCCTCTTATACAGGTCCCAAGCCACTCGTTTC	7543
Qy	209	-----AlaPro-----Val-----211	211
Db	7544	CGTTGGCATCAACGACTCTCTTTTGACAAGCAGCAGCATGGGCAATAGATAATGTCTAT	7603
Qy	212	-----Val-----Arg-----213	213
Db	7604	ATCGGGATGGCTGCATAGACATGTGTCAGTGGCCATGGGAGATGCATCCAGGAAACTGC	7663
Qy	213	-----213	213
Db	7664	GTCTGTGATGAACAGTGGGTGGCCTGTACTGTGATGACCCCGAGACCTCTCTTCCAAAC	7723
Qy	214	-----Arg-----Val-----215	215
Db	7724	CAACTCAAGACAACTTCAATCGAGTCTCCATCCAGTCAAGACTGGTGTGATGTGAACCGGA	7783

QY	216	--Lys--	211
Db	7784	GGGAAATTGAGTACAGTGTGTGGAGCCGTGGCGTCGGGAATGGCTCTCCAATTTCAGTGGG	7843
QY	217	ValThrVal- 	219
Db	7844	GGTTGTAGTCGATTATTAGTCACTGTGGATCTAAACCTCACTAATGCTAGATTCAATCAA	7903
QY	219	-----	219
Db	7904	TTTTACTTCATGTATGGTGCTGATTACACCAAAACCGTAACCAAGGTTTCTCTCTTG	7963
QY	220	-----Asn-----	220
Db	7964	GAATATCTGTCAATGGAGGCAATTACCTGGGAACCTGCTCATGGAGATTTTCTCATGACAG	8023
QY	221	Tyr-----ProPro-----	223
Db	8024	TACAGTAAGCCCGGATTGTGAATATCTTCTCCCTCTCTGATGCTAAAGAGATTGCCACT	8083
QY	224	-----Tyr-----	224
Db	8084	CGTTCCGCTGGTGGCACCACGACATGACGGCCTGGATCAGAAGCATGGGCCAATTGAC	8143
QY	225	-----IleSer-----	226
Db	8144	AATGTCCTCATCTCAGGCTCTGTGACCAAGGACCGTTATGCTGGACACCTTCAGCAGC	8203
QY	227	-----Glu-----Ala 228	228
Db	8204	GCCCCAGTACCCACGACGAGCGCTCCCTGCAGATGCCGCCCTGTGCGGAGGATGCC	8263
QY	229	-----Lys-----	229
Db	8264	TTTGACATGTTTATGGAAGACAAACTTCAGTGAATGAGCAGCTGGCTATTCCATGATGAT	8323
QY	230	-----GlyThr-----	231
Db	8324	TGTACAGTAGAAGATTCTGTGACTCCCTGATGCTGTGTGATGCTCTGTGGCAGTCATGAT	8383
QY	232	Gly-----Val-----ProVal-----Gln 237	237
Db	8384	GGCGGAGGTGTATGACGTAGCCATGACCTGACTCCCACTGAAGCTCGATTATGCAA	8443
QY	238	-----Lys-----Gly-----	239
Db	8444	TTCAAGATCTCAGTTGGATGTAAGTGTCGAAAAAATTGCCAGATCAAATTCATGTG	8503
QY	240	-----Thr-----Leu-----GlnCys-----GluAla 245	245
Db	8504	CAGTATTCTACTGACTTCGGTGTGAGTTGGAATATCTGTGTCCTCAGTCTGTCCTGCT	8563
QY	246	-----Ser-----AlaVal-----ProSerAla-----	251
Db	8564	GACCCAAAATGCTCTGGAAGTGTTCTCAGCCATCTGTATCTTCCAACTAAAGGGTGG	8623
QY	252	-----Glu-----	253
Db	8524	AAAAGGATCACCTACCCACTTCTGAAAAGCTTAGTGGAAATCCGGTAAGTTTAGTTTC	8683
QY	254	-----GlnTyr-----	256
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QY	257	-----Lys-----Asp-----	259
Db	8744	TTGGACAACTGCAGGGGCCATGGAGATTGCTTAAGGGAACAGTGCATCTGTGATCCGGGA	8803
QY	260	-----Lys-----Arg-----	261
Db	8804	TACTCAGGGCCAACTGCTACTTACGCCCACTCTGAAGACTTTCTCTGAAGAACCGTTT	8863

QY 262 -----Leu----- 262
Db 8864 GACAGTGAAGAAATCAAACTGACTTATGGATGCTTATAGAGGTGGAGTACTTGCACT 8923
QY 263 -----Glu----- 264
Db 8924 GAGTGTGAATTTCTGCGAGGACACTGCACTCTAATTTTGGGGGATCCACTGTGAGACAA 8983
QY 264 ----- 264
Db 8984 GCGTTACAAAGATTGGATCTTCGAGGTGCAAGTTCTGCAATACTGCGGGCGCATC 9043
QY 265 Gly-----LysLysGlyVal--- 269
Db 9044 GGTAGTGAGAACAAATGACCTCTTGCCATGCTGCCATCTGCCGGAAGGAGGCTGCTG 9103
QY 269 ----- 269
Db 9104 TTGACTACTCTACCGATGGAGGAATTAACCTGGACTTTGCTCCATGAGATGGATTACCAG 9163
QY 270 Lys-----Val-----Glu-----Asn--- 273
Db 9164 AATAATATTTCTGTAGACACGACTACATATCTTCTCTGAAGATGCCCTCACCACACA 9223
QY 274 -----Arg-----ProPhe---LeuSer--- 278
Db 9224 ACTGACTTCTGCTGGTGGCAGCCTTTTGTGATCAGCAATGGAATTTGTGTCTCTGGGGTG 9283
QY 279 Lys-----LeuLeu----- 281
Db 9284 GAGGTGCTCAGTGGGCACTGGACACATTTTGAATGGTGGAGACAGAAATCAATCCAGC 9343
QY 282 -----Phe----- 283
Db 9344 CAATTTGTGACACTTTTGTATGATGAAGCACTTCCATGAAGAAACTGAGTTTTTAC 9403
QY 284 ---Asn---Val---Ser---Glu-----His--- 288
Db 9404 CCTAATGCTGTAGGACAGCAGGATTTGTGGCAATCCATCTTTCACCTCTATTGGCCA 9463
QY 289 -----Asp----- 289
Db 9464 AATAAAGAGGACAAAGACTCACAATGCTCTCTCTCCGAGAACTCATATACAGCCA 9523
QY 290 ---Tyr--- 292
Db 9524 GGATACATGATGAGTTAAATTTGGTGGTGTGTGAAGCCACTCTTGTGTGACCTT 9583
QY 293 -----TyrThr----- 294
Db 9584 CATTGGTAATGCTGGATACACTAAGGATGCAAGATCGGATTCCTGGCAGCTCGTACAG 9643
QY 295 ---CysVal---AlaSerAsnLysLeuGly-----His--- 303
Db 9644 ACCAGTGCCTTCTCTCTCTCTTAACAGCATTGGTGTCTCCCTTCCAGTTCCATGAA 9703
QY 304 ---Thr---AsnAlaSer-----IleMetLeu--- 310
Db 9704 GCACCATCTACAACTGTGTCAACAGCTCAAGTGGAAAAAGATCACCATCCAGCTGCCT 9763
QY 311 -----Phe----- 311
Db 9764 GACCATGTCTCTCTAGTCAACACAGTTCCGCTGGATCCAGNAGGAGAGAAACTGAG 9823
QY 312 -----Gly-----Pro----- 313
Db 9824 AAGAAAGCTGGCAATTGACACGCTGTATATTGGAGAGGCTTGCCCCCAAGCTCTGCAC 9883
QY 314 -----GlyAla----- 315
Db 9884 GGCACGGATATGTCACGACCGGTGCCATCTGATCTGCGACGAGAGCTTCCAAGTGAT 9943
QY 316 -----Val-----Ser-----Glu----- 318

Db 9944 GACTGCTCTGTTTTCAGTCAGACCTTCCCGTTATATTAAGATAAATTTTGAGTCGCA 10003
QY 319 ---ValSer---Asn-----GlyThr--- 323
Db 10004 AGAGTCACCGAGGACAAACTGGGAGACCAATTCAGAGTGGAGTCATAGGAGTGGCTGTGG 10063
QY 324 ---Ser-----Arg--- 325
Db 10064 CAGCTGGCCCCCTPACGCCCATGGAGACTCACTGTACTTTAATGGCTGTCTCAGATCAGGCAA 10123
QY 326 ---ArgAla----- 327
Db 10124 GCAGCTACCAAGCCTCTGGATCTCACTCGAGCAAGCAAAATCATGTTTGTGCAAAAT 10183
QY 328 Gly-----Cys----- 329
Db 10184 GGGAGCATGTGCGAGACGGACAGCTGCAACAGTGAACCTGAGTGGCCCCCAGCTGTGGAC 10243
QY 330 ---Val-----Tyr----- 331
Db 10244 AAGCGGTGCTGCTGCAATACAGCGTCAACAGCGGATCACCTGGCATGTCTATCGCCAG 10303
QY 331 ----- 331
Db 10304 CACCAGCAAAGGACTTTCACAAAGCTCAGAGTGTCTTACAAATGTCCTCCCTGGAGGCA 10363
QY 332 ---LeuLeu-----Pro----- 334
Db 10364 CGATGAAAGAGTCTTACTGGCTGTGGCAACACAGCCCAATGGAACAGTCTATGAT 10423
QY 335 ---Leu-----LeuVal----- 337
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QY 338 ---Leu---HisLeuLeu--- 342
Db 10484 ATGAATTTTCAGCAACAATGGCTCGACATTTCTACACAGAGAGCAAGTCACTT 10543
QY 343 -----LysPhe 344
Db 10544 AGCGATACCCATGAAGAATCAAAAAGTTT 10573

RESULT 6
US-08-770-379-17
; Sequence 17, Application US/08770379
; Patent No 5849564
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-17

Alignment Scores:
Pred. No.: 2,89e-23 Length: 35100
Score: 1727.60 Matches: 302
Percent Similarity: 10.41% Conservative: 35
Best Local Similarity: 9.33% Mismatches: 5
Query Match: 71.74% Indels: 2895
DB: 2 Gaps: 250

US-10-017-084A-523 (1-344) x US-08-770-379-17 (1-35100)

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Db	6628	ATGGCAAGGAACTGGCGCGGTCTATGCCGATGTGTACGCCCTAGCCATGACCTCTGT	6687		
QY	3	-----	ThrIle	-----	4
Db	6688	CTTCTTAGTTACGCAGACCCGCGCAACACTGGACACTAAAAGTCTGGCCCTCACTACAGG	6747		
QY	5	-----	Gln	-----	6
Db	6748	AAGTTTCAGAGCCTTTCAGGCACACTACTCCGCCCTCTCAGACGCAAAAGCACACGAA	6807		
QY	7	-----	LysMet	-----	9
Db	6808	TGCTCAGTCTGTCACTAGATTTGAGCAGCTTTTGGAAAAGTGGCTGATGCTGTGGCCA	6867		
QY	10	-----	Asn	-----	12
Db	6868	CGTTGGAGTGTGCACTAGCAGAAAAGTGTCTCCAGAGAGCAATTTTCCCTCTGCATT	6927		
QY	13	-----	Ser	-----	15
Db	6928	TGGACAAATGCAACAGCAACCGGAGCGTTAGGTTTAATTTTACGSAATTTGGGCC	6987		
QY	16	-----	IlePhe	-----	17
Db	6988	TTGGAGTTAAAGCTGTCACTAATAACGACGTTGAAATTTCTTTAAACGCTTAGTAGC	7047		
QY	17	-----	-----	-----	17
Db	7048	GTTTTATTATAGATCGGCAGTCTCTGGAGGGTTTAGGGAGGATTCGTTTC	7107		
QY	17	-----	-----	-----	17
Db	7108	GTTGGGAAGCTGAGGGTATCTCACCCGTACTCTGGCGGACCTATATGTCTCAAAATCTG	7167		
QY	18	-----	Thr	-----	20
Db	7168	CCCTGCTTAGAATGCTTTCAGGAAGTGTCTGACTCCCAACACGAGGACACGCTGTCG	7227		
QY	21	AlaAlaLeu	-----	-----	24
Db	7228	GCCATGCTCCGACACAGCSCCTGCAGTCACATATGTACCCCGCATGGGTGAGCCTGTC	7287		
QY	25	-----	LeuPhe	-----	30
Db	7288	CGGGCCCTCTTTGAGACGAGCTAAACAGCTCGGGCTTCAAAACCCCTGAGTCCATACCT	7347		

QY	31	-----	ValArg	-----	32
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QY	32	-----	-----	-----	32
Db	7408	CGGTAGGAGATCACCACATTTTCGGAGAGGTGACCAGATCTGCTCTGGAATCTCAAAAC	7467		
QY	33	-----	SerGly	-----	37
Db	7468	CTGATCTATTGGAGCTCTGGCCACTTCGATGCCACTTCGACGCGGAGACAGAGACTGCTCT	7527		
QY	38	-----	Phe	-----	38
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QY	39	-----	ProLys	-----	40
Db	7588	GGATGCTTGGCGGAACGGCGCACGCCCAACACTTTTGTGACTGCTTTCGCCGACAGCTCC	7647		
QY	40	-----	-----	-----	40
Db	7648	CTAGAAACCTTTTCTGTGTGTGTTCTTTTAGCTCCGTGGAGGACACCATAGAAGTCTC	7707		
QY	41	AlaMetAsp	-----	AsnValThr	46
Db	7708	CAAAAGGACTGCTCTCTGCTTCTTACCAACAGGTAAACTACACTACTGCACTGCAAAA	7767		
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Db	7768	CAGAACGAGTTTACGTCGCACTCAGCAAACTGCTGGCAGCTGCTGCTAAATTTGGGC	7827		
QY	51	-----	GluSer	-----	53
Db	7828	AAATGTTCCACTGAAAGTTGCCAATCCGAGGCCGTAGCAGCTGTTAGTGGGGCAAA	7887		
QY	54	-----	ThrLeuArg	-----	56
Db	7888	CCAGAGGAGTGTGAGGGATGCAAAACACCGGCAAGCACTATATCTTCAGAAAAGTGCA	7947		
QY	57	-----	Cys	-----	57
Db	7948	CGGACGCTTTTAAAAAACCTCTGATTTGATTAAGACACACGAGGCCACATCTCTCTCAG	8007		
QY	58	Thr	-----	Ile	59
Db	8008	ACCCTGGTCTAAGACTGTGGGGTCTGTCTATCTACAACAGGAGCATCTGCCCTACAAAAC	8067		
QY	60	-----	Asp	-----	60
Db	8068	CATTTTTCACAGAGCAGATTCATATCCCTCCCTGGCAGGACCTGACGGTCACTGT	8127		
QY	61	-----	Asn	-----	61
Db	8128	CCACGCGTTTGAAAATTTCTAAATATATCAAAATTTCTCTGTACTCCAGCGTCTGGG	8187		
QY	62	Arg	-----	ValThr	64
Db	8188	CGGGAACACGTAGAGATCTCTGACACTGGAGTTCTTACAAACTTATCACGGGCGCGTCA	8247		
QY	65	-----	Val	-----	66
Db	8248	AAGGACATCTTTATTTCCAGTCTCCAAATGTGACGCTGCTCAGTCTGCTCGAGGCT	8307		
QY	67	Ala	-----	-----	67
Db	8308	CGCGGATGCTTCCCATCAAAAGATGATGATCAGAGATGATCTGCGCCAGCATAGAG	8367		
QY	68	-----	Trp	-----	Leu 69
Db	8368	CCGAGGACTGGATAGAGCCCAACTTCAACAGTTCTTATAGCTTTGAGAATCAAGACATA	8427		
QY	70	Asn	-----	Arg	72

8428 AACCATCTGCAAGAGAGCTTGGGAATATATACAGAGAGCTGGTATTATTCGGTTTCTCTG 8487
73 ---Thr---
8488 TACAACAACTTGGGAGGAGGAGCTAAAAATACTTCTCACGCTCAGGGCTCACCGGG 8547
75 ---LeuTyr---
8548 TTTGAGGACCGAAACCGGACAGGACTCAACACGGGGCTGTACCTAACATTGTGACATCT 8607
77 Ala---
8608 GCGCCCTTGGTGGTGGATATAAAATATGCTGGATATTAAAGACCTGTACGCCCT 8667
79 ---AsnAsp---
8668 CTGTACCACCACTGCAACTGAGCAACCAATGACTCCAGGTCTAGATTGGCCACCT 8727
81 ---Lys---
8728 GGGGACTGTATCTGTGTCTGCTTTTGGCAGGCGGGCGCACTCGAGGGGTGACAC 8787
81 ---
8788 CTTTCAGAGCTCCAGTTCCGCCACACCCAGAGATCTTCTCTAAGGCCCCCAACCAACC 8847
82 ---Tyr---
8848 TGGTGAAGAGCATCTGGTCTTAAGAGTGTGGACTTTTACAGTTTCAGAGTGTGTAGTGC 8907
85 ---Asp---
8908 ATCGATCACCGGGAGCTTTTTCGGTTCACTTGGACGACAGCTGCCCAACCAACCAAGA 8967
88 ---Val---
8968 CAAGTACCACCAAGAGGAATTTTACTGGTGTACAAAAAACAATAGTGCCTCATATCTT 9027
91 ---
9028 TAAGTGGCGGCTATAGGAAATGCCACTCTGTCAAGGCTTACAGGGGCTTGACAGA 9087
91 ---
9088 GTCCGCATCACCAAGATATGAATCCCGAGACCGTGCCTCTATGAGATAGCCA 9147
92 ---Ser---
9148 CATGGACAGCACTATCAGTGTCTTGTAGTCCATGAAGGTAAATGTCAACGGGTAGAAA 9207
93 ---AsnThr---
9208 CACATTACTGACAGACGATGTAAACCAACAGTATTTCTCCACCACTAGAGGGCT 9267
96 Thr---
9268 TACGGATAACATTCAAAGGTACTTTAGCCAGCGGTCTATACCGGGAACCGCGTGGTT 9327
102 ---Ile---
9328 TCCGGCATATACAGATTAGGACCACTGTCAATTGGAGATAGTGGACATGATAGCCAG 9387
108 ---Tyr---
9388 GTCTGCTGAACCATACATTTACTTTGTACGTCACCTGGGTGACACGGTGAAGTCTCCCC 9447
110 ---Glu---
9448 TTTTGTATACGAATCTCTATGACGACAAACCCCGACCAACAAAATGGCCTTAGCT 9507
111 ---Gly---
112 ---Pr---

9508 CCAAGTAGTTCTCAACACCACTGTGTGCTACGTACTCTGACAGAGAACCACTCCCACTCC 9567
112 O---
9568 CCAAAACAGGATCTTTGTGAAACGGGAGGCTACACGCTTTCGTGGCCTCCAGAGCAA 9627
115 ---Cys---
9628 GACCACGGCGTGTGCTCGCTGCACTGTGAAACGCTTCCCGCTTCCATCCAGACTAC 9687
119 ---
9688 CCAGGAGACAGCTTCCACTTTGTGGCCAAACGAGATCACGGCCACCTTACGGCTCCTCT 9747
120 ---
9748 AAGCCAGTGGCCAACTTTTACGACACGACTCTTCTGTGACCTCGGATATCAACACCAC 9807
121 ---Asn---
9808 GTTAAACGCCAGCAAGGCCAAACTGGCGAGCACTCACGTCCTTAACGGGACGCTCCAGTA 9867
125 ---ThrSer---
9868 CTTCCACACACAGCGGAGTCTATTGTGTGGCAGCCCATGTCCGCGATTAACTGAC 9927
129 His---
9928 TCACGCTCAGGGCGACAGGGGAAACCCACGTCATCGCGCCCTCCGATCCCCCAT 9987
129 ---
9988 GACCACCTTGCAGCGCCGAGAAAGACGTCAGCCAGTACCGTGTGTCGGCGGGCG 10047
130 ---Leu---
10048 GGGTCCACGACAACTCTCTTACAGCAGCTGCAGTTTGGCTAGCAAACTGGCGGA 10107
131 ---Ile---
10108 TGGCATTAACTAGGTGTAGAGAACTCTCAGGGCATGTGTGCGGACGAGTCAGGGA 10167
135 ---Ser---
10168 CAACCTATGTGTAGAGCTCAGTAAATCAACCCACGCTTATGACAGCCATCTA 10227
136 ---Pro---
10228 CGTGCACCTGTATCCGCAAGTTCGTAGGAGACGCCATTTCCGTGACCGAGTGCATTAA 10287
141 ---Ile---
10288 COTGGACAGAGCTCGTAAACATCCACAGAGCTCAGAACAATAGTAGAGAGCTGTG 10347
142 ---SerSer---
10348 TTACGGCGCCCTGGTGCAGCTTTAAGTTTGAACAGTTTCCAACTATTCCCGGCCA 10407
143 ---
10408 GCTGGCGCGCGCAANTGAGATAATACTGACCAACCAACAGGTGGAAACCTGCAAGACAC 10467
143 ---
10468 CTGGCAACTACTTATCATACCCGCAACGAGACTCTGGTGTATAGGACTACGCGTACCT 10527
144 ---AspIleSer---
10528 GGCCTATAACACCACTGACATATCCCTGAACTTTTATCGCCCTGAATCTATC 10587
147 ---Ile---
10588 CTTTATCAAAACATAGACTTCAAGGCCATCGAGCTGTACAGCAGTGCAGAGAACGACT 10647

QY	149	-----Glu-----	149
DB	10648	CGCGAGTAGCGTGTTCACCTGGAGACGATGTTCCAGGAGTACAACACTACTACACATCG	10707
QY	150	-----Gly-----Asn-----	152
DB	10708	TCTCGCGGTTTGGCGGAGGATCTGGACAAACACCATAGATATCAACAAGGAGCGCTTCGT	10767
QY	153	-----Ile-----	153
DB	10768	AAGGCACTTGTTCGAGAGTAGTGGCGGACCTGGGTGGCATTCGAAAAACGGTGGTGAACGT	10827
QY	154	-----Ser-----LeuThr-----Cys-----	157
DB	10828	GGCCAGCAGCGTGGTCACTCTAATGGCTCATTTGGCTTACCGGATTCATAAATTTATTAA	10887
QY	157	-----	157
DB	10888	ACCCCTAGTGGCATGCTGATGATCATTTATCGTTATAGCAATCATCTCGTATCATTTT	10947
QY	158	-----Ileala-----	159
DB	10948	TATGTCAGTCGGCGCACCAATACCATAGCCAGCGCCGGTGAAGATGATCTACCCGA	11007
QY	160	-----Thr-----	160
DB	11008	CGTAGATCGCAGGCGACCTCTTAGCGGAGGCCCCAACACGGGAGGAAATCAAAACAT	11067
QY	161	-----Gly-----Arg-----	162
DB	11068	CTGCTGGGAATGACCCAGCTACAACAGAGAGGAGGAGGCGGATGATCTGAAAAA	11127
QY	163	-----Pro-----	163
DB	11128	AAGTACACCTCGTGTTCAGGTCACCGAAACGCCCTTCGTAGCGTCTGAGAGGATA	11187
QY	164	-----GluPro-----Thr-----Val-----	169
DB	11188	TAAACCTCTGACTCAATCGTAGACATCATGTCGGAAACGGGGAGTGACAGTGGATTCTG	11247
QY	170	-----Arg-----	170
DB	11248	AGTTATTGTTGATGTAAATTTAGGAAACACGGCCCTCTGAAGCACACATACAGA	11307
QY	171	-----His-----	171
DB	11308	CTGAGTTATCAACCTACTCGTTGCAACAGACAAATTTACCGTCCGAGATCATGGA	11367
QY	172	-----Ile-----	172
DB	11368	TTTTTTCAATCCATTATTCGACCAACTCGCGAGGCCCGAGAAACACTGTGAGGCAACC	11427
QY	173	-----SerPro-----Lys-----	175
DB	11428	CAGCGGTACAGTCGCCCAACTGTCCCTCGGAGACAAGAGTATGCAAGCTTATACCGGC	11487
QY	176	-----AlaVal-----	177
DB	11488	CTGTTTCCAAACCCCGGGGAGCCCGGTGGTTCGGCTGGACACCAATTTCCACCCAC	11547
QY	178	-----Gly-----PheValSerGlu-----	182
DB	11548	CTACTTCCAGGGCCCAAGCGGGAGAGTATTTCCGGGAGAGACTGGGTCTATCTCGAA	11607
QY	183	-----As-----	183
DB	11608	AACAAGGCGGACAGGCAAGCAATGCTCCTATGTGCAACCTCATATTTCCAGGTATACGA	11667
QY	183	p-----Glu-----Tyr-----LeuGlu-----	187
DB	11668	CATCGTGGAGACCACTACACGGCGCAGCGGTGGGAGCGTGCATTTAGTCTCCAGAC	11727

QY	188	-----Ile-----	188
DB	11728	TGATATCATTTCCAGCGGCACCGTCTCAAGCTGCTCGGAGAACTAGATGGCGCCAG	11787
QY	189		
DB	11788	TGTCGTGCGTGAACGTTTTTCAGGAGCGCTGCTACTTCTACACACTAGCAACCCAGGGGGT	11847
QY	191	e-----Thr-----	193
DB	11848	AAACCTGCACCCAGCTCTCCAGCAGGCCCCTCCAGGCTGCTTCGGTCGGCATCTCTGCGG	11907
QY	194	-----Glu-----	194
DB	11908	CTTCTCCACCGAGCCGGTCAGAAAAAATCTTGGCGGCTAGCAGACACACAACATATGC	11967
QY	195	-----Gln-----	196
DB	11968	TGTGCAAAAAATAACCGTGTCACTCCAGTCCGATGATGCGAACGCTTAGCGACCGCCTAAC	12027
QY	197	-----Gly-----	198
DB	12028	AACCTGTGGGTGCGAGGTGTTTTCAGTCCAAATGTGACGCCATTAGCGCCTTCGTGCTGGA	12087
QY	198	p-----TyrGluCysSer-----	202
DB	12088	CCACGGGTCTTCGACATTCGGGTGGTACGAGTGCAAGCAATCGGCCCCCCCGCACCCAGGC	12147
QY	202	-----	202
DB	12148	CAGAGACTCTTGACCGAACTGGAGTTTGACTGTCAGCTGGGAGGACCTTAAAGTTTATCCC	12207
QY	202	-----	202
DB	12208	GGAGAGCGAGTGGCCCCCATCTCAATCCTATCTTGTATAGTAATGTATGGGGA	12267
QY	203	-----Ala-----	204
DB	12268	GAAGGGTTTTCCCAACGCGACTCAAGACGAGGACATGATTACAAATCTCGTGTGTTT	12327
QY	205	-----AsnAsp-----	206
DB	12328	ACACACAGTCGGCAACGATAAACCGGTACACCGCATGCTACTGGGCCTGGGACATGCGA	12387
QY	207	-----Val-----	209
DB	12388	CCCCCTTCCTGGGTGGAGTCTTTTGAGTTTCTTCGGAGTACGACATGCTGGCGCGCTT	12447
QY	209	-----	209
DB	12448	CCTCAGCATGCTCCGCGATTACAATGTGGAGTTTATAACGGGTACAACATAGCAAACTT	12507
QY	210	-----Pro-----	210
DB	12508	TGACCTTCCATCATCATAGACCCGGGCAACTCAGGTGTACGACTTCAAGCTCGAGGACTT	12567
QY	211	-----Val-----	213
DB	12568	CACCAAAATAAAAACTGGGTGCGTGTGAGTTCACCAACCCAGAGGCGGTTCGGATGG	12627
QY	214	-----Arg-----	216
DB	12628	GGGCAACTTCATGAGTCCCAAGTCAAAAGTCAAAATATCGGGATCGTCCCATAGACAT	12687
QY	217	-----Val-----	219
DB	12688	GTAACAGGTTTGCAGGGAAGAACTGAGTCTGTGAGACTACAAGCTGGACACAGTGGCTAA	12747
QY	220	-----AsnTyr-----	223
DB	12748	GCAATGCCTCGTCACAAAAAGATGATCTCATCAAGACATACCCCCGCTTTTAA	12807
QY	224	-----Tyr-----	224

Db	12808	ATCTGGGCTGATGTCGCGCAAGGTGGGAACTACTGTGTTATTGACTCGGTCCTGGT	12867	Db	13888	CATACTGGGAGCCGAGCGCTCAAGGCGCGGCCAAAGCTTATTTTCGGGGCAGGCGACAGA	13947
QY	225	-----IleSerGlu-----	228	QY	255	-Tyr-----Lys-----	257
Db	12868	TATGATGTTCTGCTACGGTTTCAGACCCATGTTGAGATCTCGGAAATAGCCAGCTGGC	12927	Db	13948	CTGGGTGTACAGGGAAGGGCTCCAGAGGGGTTTCGTCAGATAATTTCAAGTGTCTCAAGC	14007
QY	228	aLys-----Gly-----	230	QY	258	-----Asp-----	258
Db	12928	CAAGATCCCAACCGTAGGTACTGACGGAGCGCCACAGATCAGGGTATTTTCTGCCT	12987	Db	14008	GAGCCACCGGAACTGTGGAACGACGCGTACCAGTAGACAACTGACGTTTACCACCGA	14067
QY	231	-----Thr-----Gly-----ValPro-----	234	QY	259	-----Asp-----	259
Db	12988	CTTGGAGGCTGCTGCCACGGAAGGTATCAATTCTCCCGTCCCAAGAGGAGCGGTTAG	13047	Db	14068	GCTAAGCCCGCCGCTCGGAGCTACAAAGAGGCAAAACCTCCCGCACTGACCGGTACCA	14127
QY	235	-----Val-----Gly-----	236	QY	260	-Lys-----Arg-----Leu-----Ile-----	263
Db	13048	CGGATATCAGGGGCCACTGTAAATAGACCCCTCTCCGGGATTTCTATGACGACCCGTA	13107	Db	14128	AAAGTCTCAAGCTAGACAGAGGAGCTTCCACAGATACACGACAGAAATCCCTACGTGT	14187
QY	237	-----Gln-----	237	QY	264	-----Glu-----	264
Db	13108	CGTGGTGAATTTGCCAGCTTGTAACCCAGTATCATCCAGCGCAACTTGTTGCTACTC	13167	Db	14188	CGTCGAGCCCGAGGTAGCTCGCTCCGAGCTGGCAGACACCCCGAGTAGCTTAAAGCA	14247
QY	238	-----Lys-----	238	QY	265	-----Gly-----Lys-----	266
Db	13168	CACACTGATACCGCGGATTCGCTCCACCTGCACCCACACTCTCCCGGACGACTAGCA	13227	Db	14248	GCAAGGACTCGCGTGGCGGTGACCTGTACTTCGACAAAGCTGGTACACGGGTAGCCAA	14307
QY	238	s-----Gly-----	239	QY	266	-----	266
Db	13228	AACCTTGTCTCAGCGAGGTCCGGTCCACTTTGTAAATAAAACACAAAGAGGAGTCCCT	13287	Db	14308	CATCATCAATGCTCTTCCAGAACAAACGTCGCAACCGTAGCTATGTTGTATAACTT	14367
QY	240	-----ThrLeu-----	241	QY	267	-----LysGly-----	268
Db	13288	TCTTGCAAGCTTCTGACGATATGGCTCGGAGAGAAAGAAATAGAAAGACCTGGC	13347	Db	14368	TTTAGACATTCGGTGACHTTCCACGCGCTAGTGACTCAGACGCGGAAACAGCGCTCA	14427
QY	242	-----Gln-----	242	QY	269	-----Val-----	269
Db	13348	ATCATGACGGACCGCCGACTGAAACTATTCTAGACAAACAACTGCGCATCAAGT	13407	Db	14428	GAAAGTTTCTCTGTGCTATGTGGGACAACTAGTAGTCCAACTGSCAAGCAGTGAGCA	14487
QY	243	-----Cys-----	243	QY	270	-----LysVal-----	271
Db	13408	TACCTGCAAGCGTTTACGGCTTACGGCTTACGGCGTTGGCTTGGCATACTGCTTGCCTAAA	13467	Db	14488	AGACGCCAGACAGCCGATCTCGAAAAAATAATGACAGACAGAGGCAACGTTTCATCTAGG	14547
QY	243	-----	243	QY	272	-----Glu-----Asp-----	273
Db	13468	CATAGCGAGACCGTGACACTACAAGGGGGAAGATGCTGGAGAGATCTCAGGCTTTGT	13527	Db	14548	TGACTGGGAGATAAGGTGTCTAATCTGCGGTTTACTTGACGACGCTTAACATGTGGGCC	14607
QY	244	-GluAla-----Ser-----Ala-----Val-----Pr	249	QY	274	-----Arg-----ProPhe-----	276
Db	13528	AGAGGCCATCTCCCGAAGCGCTAGGGGTCTCCTGCGAGGCCAATAGACGTCTCACC	13587	Db	14608	CCTTTACAGATCTAGCGGCGACTACACGCGCTAAGAAATCCCTTCTCTCTGATCGACT	14667
QY	249	o-----	249	QY	277	-----Leu-----	277
Db	13588	CGAGCGCCGATTCAGGTATATACGGGACACTGACTCTCTTTTCATATGCTGATGG	13647	Db	14668	AATACGTGACCATCTTTGGGCTATGTGCAAAATATTGAGGATCTGTTAACCCATGG	14727
QY	249	-----	249	QY	277	-----	277
Db	13648	TTTCAATGGAACAGGTGTACAGACTTCGCGAGGAGTACGTCATCAACACCAACAC	13707	Db	14728	GTCATGCGTCGCGTAGTGGCGAGCGCAAAACGCCACAGCGCGGCAACGCGACGATCGT	14787
QY	250	-----Ser-----AlaGlu-----	252	QY	278	-----Ser-----	278
Db	13708	GCTGTTTCTAGCCCATCAGCTGGAGGCTGAAAGATCTTCAAGTGCTTCTGCTCT	13767	Db	14788	CGCGCTGGCTGATAAACAATTTTTCAGAACCCATCGGCATTTGGGTACGCGGCCCTCC	14847
QY	252	-----	252	QY	279	-----LysLeu-----IlePhePheValSer-----	286
Db	13768	GACTAAAGAGATACGTGGGGTACTCAGTGACGACAAAGTTCTGATGAAGGGCGTAGA	13827	Db	14848	GCCGAAACCGCAAGGAAGTATTAGTTCTGCATATTTTTT---GTACGTCCCTGCC	14904
QY	253	-----Phe-----	253	QY	286	-----	286
Db	13828	CCTCATTAGAAACAGCCTGTGTTTTTGTCCAGGAAAGACGTCAGTCTCTGACCT	13887	Db	14905	CCCGGGGAGATGACCACATATGTTCAGGGCGGCGATTGCTCCCGGAGCAGAGA	14964
QY	254	-----Gln-----	254	QY	287	-----Glu-----	287
				Db	14965	ACCCGAAACACTACACTCCGCGGAGGCCCTTACCGTCGCGGAGACGCTGTTAACTGG	15024

QY 288 -----His----- 288
Db 15025 ACAGTGGCATCACTCGCCGGAACGATACGGGATATCTTCACAGCTGCTGTCCTCGCT 15084
QY 289 -----AspTyr-----Gly-----Asn----- 292
Db 15085 CTCTTTTGGACCTCTGACATTCGAGTTCATTTGGTGTGACACAGTGAAGGTGACCC 15144
QY 293 -----Tyr-----Thr-----Cys--Va 296
Db 15145 CGAGCAATTGACACCAAGTACTTGACGTTACGCGAGCGGAGAGAGACTTTGCAAGT 15204
QY 296 lalaSer-----Asn-----Lys----- 300
Db 15205 A---ACGGTTTACAAACCACTCGACAGCATGCAAGAGGCCGCTGTTGCTGCTTA 15261
QY 300 ----- 300
Db 15262 CAGACCGAGCGCTCGCCGCTCAGCTTGTTCATGGTCAAGCTTCACCCCTCATACAC 15321
QY 301 -----LeuGly----- 302
Db 15322 CCCTCTGGAGCGAGGTATTCGAGTCTATCCAGACTGTGAGAAACTATCCACCTCA 15381
QY 303 -----His-----ThrAsnAla----- 306
Db 15382 GGAACCAACCACTGAGGATCAATTGCTGTTGCGAGCAGTGTGCGCAACCGCGAGA 15441
QY 307 -----Ser----- 307
Db 15442 CTGCGCTTTTGTCATCGGGCTCGCCGCTGAAACAAAGTTGTCTCTATTTCCGCA 15501
QY 307 ----- 307
Db 15502 ACTCTTCGGGGAAGCAAGAACACTTATTTATTCATCAACCCACAGACATCTCTGAC 15561
QY 308 -----Ile-----Met----- 309
Db 15562 CATTCACGGGACACATAGTGGCGTGGCATGCTTCTATATCCACCCGCTAAGC 15621
QY 310 -----Le 310
Db 15622 AGCCAGCCAGCACCATACAGCTTCTACGACTGCAAGGAAGAGCTGCGACGTGGGCT 15681
QY 310 uPhe-----GlyProGly-----AlaVal----- 316
Db 15682 CTTCCAGATCAACCGCGGACCGGAGGGGTCTGTACACCACTTGCACCGTAGCGATTAG 15741
QY 317 -----SerGlu--Val----- 319
Db 15742 GGCCGACGCCACGAGGAACCATGCAATCGTGACTGTCGAGACATATGCGCGAGGAG 15801
QY 320 -----Ser-----Asn----- 321
Db 15802 TCAGAGAGTGTCCCGTGGTTCGAGTGTGCAAGTGAAGACGACGCTGGGCGCGC 15861
QY 322 -----Gly-----ThrSer----- 324
Db 15862 GAGCCGCTGGGATTCGTCATTCACCGGCGCATCTGTCATCTTAATCGATGACCC 15921
QY 325 -----Arg----- 325
Db 15922 CTCTTACTAAGAGAACAGCACATATGTCCTCTGTCGCCAGCGTGGCGAGATCTTC 15981
QY 326 -----Arg--Ala----- 327
Db 15982 CACAGAGCTACCCCAACTTTACATTTGACACAGCGCACCGCAAGCAGCAACGAGACC 16041
QY 328 -----Gly--Cys-----Va 330
Db 16042 TACACTGCATTTACGCTTTTGGGACCAAAATAACAGGTTAGGATCTTGCCCACTGTT 16101

QY 330 lTrp-----Leu-----Leu----- 333
Db 15102 GTGGAAGAGCTCTCGAGCGTGTGATTTTACACTGCGTGCATCGGTCTCTCGAACATC 16161
QY 334 -Pro-----LeuLeu----- 336
Db 15162 GCGTGGGAGGCTCAAAATAATAATACTTGTCTCTCACCTGTCATGCCAAGGAGTG 16221
QY 337 -----Val-----LeuHis-----LeuLeu----- 341
Db 15222 TACCTGCGTGGGTAAAGGACCTTTCTACACCACTGGCGACCGGCTATTGTCAGCGT 16281
QY 342 -----LeuLysPhe 344
Db 16282 GAGGTGCTGAGCAGCGGGTTTGAGCGCGAGTTTACGTAACGTGGCATTC 16330

RESULT 7

US-08-757-669A-17
; Sequence 17, Application US/08757669A
; Patent No. 6183751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,669A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-669A-17

Alignment Scores:
Pred. No.: 2,89e-23 Length: 35100
Score: 1727.60 Matches: 302
Percent Similarity: 10.41% Conservative: 35
Best Local Similarity: 9.33% Mismatches: 5
Query Match: 71.74% Indels: 2895
DB: 3 Gaps: 250

US-10-017-084A-523 (1-344) x US-08-757-669A-17 (1-35100)

QY 1 Met---Lys----- 2
||| |||

6628 ATGGCAAGAACTGGCGCGCTATGCGGATGTGTGACGCTTAGCCATGACCTCTGT 6687
QY 3 -----ThrIle----- 4
6688 CTTCTTAGTACGACACCGGCAACACTGGACACTAAAGTCTGGCCCTCACTACAGG 6747
QY 5 -----Gln-----Pro----- 6
6748 AAGTTTCAGAGCTTCAGGCACACTACTCCCTCCTCAGACGACAAACGACACGAA 6807
QY 7 -----LysMet-----His----- 9
6808 TGCTCAGGTCTGTCACTAGATTGGAGCACCTTTTGGAAAAAGTGTGCTGTCTGGCCA 6867
QY 10 -----Asn-----SerIle----- 12
6868 CGTTGGAGTGTGCACTAGCAGAAACTGTCTCCAGAAAGCAATTTTCCCTCTGCAAT 6927
QY 13 -----Ser-----TipAla 15
6928 TGGACACAATGCAACAGCAACCGAGCGTTAGGTTTAATTTTACGGAATTTGGCC 6987
QY 16 -----IlePhe----- 17
6988 TTGGAGTTAAAGCTGTCACTAATAAACGACGTTGAATTTTCTTAAACGCTTAGTAGC 7047
QY 17 ----- 17
7048 GTTTTTATTGTATAGGATCGGCAGTCTCTGGAGGGTTTAGGGAGGATATGCGTTTC 7107
QY 17 ----- 17
7108 GTTGGGAAGCTGAGGGTATCTACCCGTACTGGCGGACCTATATGTCTCAAACTG 7167
QY 18 -----Thr-----Gly-----Leu----- 20
7168 CCCTGCTAGAAATGCTTCAGAAAGTGTGTGACTCCCAACGAGGCACAGTCTGCG 7227
QY 21 AlaAlaLeu-----Cys----- 24
7228 GCCATGCTCCAGACAGCGCTGCAGTCACATATGTATCCCGCATGCGGTGAGCCTGTC 7287
QY 25 -----LeuPhe-----Gln-----Gly-----Valpro 30
7288 CGGGCGCTCTTTGAGAAGAGCTAAACAGCTCGGGCTTCAAAACCCGTAGTCCATACCT 7347
QY 31 -----ValArg----- 32
7348 ACTACCCCTGTCACTCCCGGTAAAGCAAGATGATGAATTCAGACAGAGCTCTTAATG 7407
QY 32 ----- 32
7408 GCGGTAGGATCACCACATTTTCGGAGAGTGACAGATCTGTCTTGGAAATCTCAAC 7467
QY 33 -----Sergly-----AspAlaThr----- 37
7468 CTGATCTATTGGAGCTCTGGCCACTCGGATGCCACTTGCAGCGAGACAGAGACTGTCT 7527
QY 38 -----Phe----- 38
7528 CACCTGCGCTCGTGTCTTACTCAGAGGCTGACATGATGAATAAAGGCGCGCTCGACCTGGCC 7587
QY 39 -----ProLys----- 40
7588 GGATGCTTGGGCAACGCGGACGCCCAACACACTTTTGTACTGCTTTCCGCCAGACTCC 7647
QY 40 ----- 40
7648 CTAGAAACCTTTTCTGTGTGTCTTTTATGCTCCGTGGAGGACACCATPAGAAAGTCTC 7707
QY 41 AlaMetAsp-----AsnValThr----- 46
7708 CAAAAGGACTGCTCTTCTGCTTCTACCAACAGGTAAATCTACTACTGCACTGCACTG 7767

QY 47 -----ValArg-----Gln-----Gly 50
7768 CAGAACGAGTTTTTACGTCGACTCAGCAAACTGTGGCAGCTGTCTCAGTAAATTTGGGC 7827
Db
QY 51 -----GluSer-----Ala----- 53
7828 AAATGTTCCACTGAAGTTGCAATCCGAGCCGCTAGCAGCTGTGTAGTGGGGCAAA 7887
Db
QY 54 -----ThrLeuArg----- 56
7888 CCAGAGGAGTGTGAGGATGCAAAACACCGGCAAGAACTATATACCTTCAGAAAGTGCA 7947
Db
QY 57 -----Cys----- 57
7948 CGCAGCGTTTTTAAATAACTCTCTGATTGTATAGACACACGAGCCACATCTCTGTCTCAG 8007
QY 58 Thr-----Ile----- 59
8008 ACCCTGGTCTAAGACTGTGGGGTCTGTCACTTACAACGAGGCATCTGCCCTACAAAAC 8067
Db
QY 60 -----Asp----- 60
8068 CACTTTTACACAGACACAGTTCATATCCCTCCCTGGCAGGACCTGCGTGTGACTGT 8127
QY 61 -----Asn----- 61
8128 CCAACGCGTTTGAATAATCTAAATATATCAAAATTTCTCTGTACTGCCAGCTGTGGG 8187
QY 62 Arg-----ValThr----- 64
8188 CGGACACCTAGAGATCTGACATGAGTTCACAACTTATCAGCGGCCGCTGTCA 8247
Db
QY 65 -----Arg-----Val----- 66
8248 AAGCGACATACTTTTATTTCCAGTCTCTCAAAATGTGACGCTGTGCTGTGAGGCT 8307
QY 67 Ala----- 67
8308 GCGGCGATGCTTCCCATCAAAAGATGATGTATCAGAGATGATCTGGCCACCATAGAG 8367
QY 68 -----Trp-----Leu 69
8368 CCGAAGACTGGATAGAGCCCACTTCAACAGTCTTATAGTCTTGAGAATCAAGACATA 8427
QY 70 Asn-----Arg-----Ser----- 72
8428 AACCATCTGCAAAAGAGAGCTTGGGAATATATCAGAGAGCTGTATATATCGGTTTCTG 8487
QY 73 -----Thr-----Ile----- 74
8488 TACACAGAACTTTGGGAGAGGAGCTAAATAATCTTCTCAGCCTCAGGCTCACCGGG 8547
QY 75 -----LeuTyr----- 76
8548 TTTGAGAAACCGAAACCCGAGGACTCACACGCGGCTGTACTTAACATTTGAGACATCT 8607
QY 77 Ala-----Gly----- 78
8608 GCGCCCTTGGTGTGGTGAATAAATAATGCTGGATATTTAAAGACCTGTACGCGCTT 8667
QY 79 -----AsnAsp----- 80
8668 CTGTACCACCACTGCAACTGAGCAACCAATGACTCCAGGTCTAGATTGGCCACCCT 8727
QY 81 -----Lys----- 81
8728 GGGGACTGTCCTCTGTGTGCTTTTGGCGAGCGCGGCACTCGAGGGGTGACAC 8787
Db
QY 81 ----- 81
8788 CTTTCAGAGTCCAGTTTCCCCACACCCAGGATCTTCTCTAAGGCCCCCACCACCAACC 8847
Db

QY 82 -----Trp-----Cys-----Leu----- 84
Db 8848 TGGTGAAGAGATCTGGCTTAAGAGTGTGGACTTTTACAGATTTCAGAGTGTGTAGTGC 8907
QY 85 -----Asp-----ProArg----- 87
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Db 8968 CAAGTACCACCAAGAGAAATTTTACTGGTTAGTACAAAAAACAATAGTGCCTCATATCTT 9027
QY 91 ----- 91
Db 9028 TAAGTGGCGCGCTATAGGAATTCACCTCTGTACGGTCTACAGGGGCTTGACAGA 9087
QY 91 ----- 91
Db 9088 GTCCGCCATCACCACCAAGTATGAATCTCCGAGACCGGTGCCACTCTATGAGATAAGCCA 9147
QY 92 -----Ser----- 92
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QY 93 -----AsnThr-----Gln----- 95
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QY 130 -----Leu----- 130
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QY 342 -----LeuLeuPhe 344
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RESULT 8

US-09-230-371A-17
; Sequence 17, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND

; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 35100
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-17

Alignment Scores: 2.89e-23 Length: 35100
Pred. No.: 1727.60 Matches: 302
Score: 10.41% Conservativity: 35
Percent Similarity: 9.33% Mismatches: 5
Best Local Similarity: 71.74% Indels: 2895
Query Match: 4 Gaps: 250
DB: 4

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 Db CCACGAGACAGCTTCCACTTTGTGGCCACGAGATACGGCCACTTCACGGCTCTCT 9747
 QY 120 -----Asp----- 120
 Db AACGCCAGTGCCAACTTTACCGACACGTACTTGTCTGACCTCGGATATACACACCAC 9807
 QY 121 ----Asn-----His--ProLys----- 124
 Db GCTAAACGCCAGCAAGGCCAAACTGGCGAGCACTCACGTCCCTAAACGGACGGTCCAGTA 9867
 QY 125 ----ThrSer-----Arg-----Val----- 128
 Db CTTCACACACAGCGGACTCTATTGTGTGGCAGCCCATGTCCGGATTAACTTGAC 9927
 QY 129 -His----- 129
 Db TCAGCTCAGGGCAGCAGCGGAACCCACGTCATCGCGCCCCCTCCGCATCCCCCAT 9987
 QY 129 ----- 129
 Db GACCACCTCTGCCAGCCGACAGAAAGACGGTCAGCCAGTACCGCTGTCGCGCGCGG 10047
 QY 130 -----Leu----- 130
 Db GGGTCCACGAGCAACCTGTCTTACACGAGCTGCAGTTGGCTTACGACAACTGCGGGA 10107
 QY 131 ----Ile-----Val-----GlnVal----- 134
 Db TGGCATTAATCAGGTGTTAGAAGAACTCTCCAGGGCATGGTGTGCGGAGCAGTTCAGGA 10167
 QY 135 -----Ser----- 135
 Db CAACCTAATGTGTACAGCTCAGTAAATCAACCCACAGCGCTTATGACGCCATCTA 10227
 QY 136 -----Pro-----Lys-----Ile--Val--Glu----- 140
 Db CGGTGCACTGTATCCGCCAAGTTGGTAGGAGAGCCATTTCCGTGACCGAGTGCAITAA 10287
 QY 141 -----Ile----- 141
 Db CGTGGACAGAGCTCCGTAAACATCCACAGAGCTCAGAACCAATAGTAAGGACGTGTG 10347
 QY 142 -----SerSer----- 143
 Db TTACGCGCGCCCTGCTGAGCTTTAAGTTTGTGAAACAGTTTCAACCTATTTCACGGCCA 10407
 QY 143 ----- 143
 Db GTTGGCGGCGCAATAGATAATACTGACCAACACACAGGTGGAAACCTGCAAGACAC 10467
 QY 143 ----- 143
 Db CTGCGAACACTACTTCACTACCCGCAACGAGACTCTGGTGTATAGGACTACGCTACCT 10527
 QY 144 -----AspIleSer----- 146
 Db GCGCACTATAAACACCACTGACATATCCACCCTGAAACATTTTATCGCCCTGAACTATC 10587
 QY 147 ----Ile--Asn----- 148
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QY 149 -----Glu----- 149
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 QY 150 -----Gly-----Asn----- 152
 Db TCTCGCGGTTTGGCGGAGGATCTGGACAACACCATAGATATGAACAAGGAGCGCTTCGT 10767
 QY 153 -----Ile----- 153
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 QY 154 ----Ser--LeuThr--Cys----- 157
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 QY 160 -----Thr----- 160
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 QY 161 -----Gly-----Arg----- 162
 Db CTGCTGGGAATGCACCAAGAGGAGAGGAGCGGATGATCTGAAGAA 11127
 QY 163 -----Pro----- 163
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 QY 164 -GluPro--Thr-----Val-----Thr-----Trp----- 169
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 QY 170 -----Arg----- 170
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 QY 171 -----His----- 171
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 QY 183 -----As----- 183
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 QY 188 -----Ile----- 188

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QY 189 -----GlnGly11 191
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QY 194 -----Glu-----194
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Db 12868 TATGATCTTCTGTCTACGGTTTCAGACCCATGTTGAGATCTCGGAAATAGCAAGCTGGC 12927
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QY 260 -Lys-----Arg-----Leu----- 263
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QY 264 -----Glu----- 264
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QY 274 -----Arg-----ProPhe----- 276
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QY 277 -----Leu----- 277
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QY 278 -----Ser----- 278
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QY 286 ----- 286
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QY 288 -----His----- 288
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QY 289 -----AspTyr-----Gly-----Asn----- 292
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QY 293 -----Tyr-----Thr-----Cys-----Val 296
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QY 296 lAlaSer-----Asn-----Lys----- 300
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QY 328 -----Gly-----Cys-----Val 330
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QY 330 lTrp-----Leu----- 333

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Qy	334	-----LeuLeu-----	336
Db	16162	GCCGTGGGAGGGCTCAAAATAATAATACITGCTCTCACCTGGTGCATGCCCAAGGAGTG	16221
Qy	337	-----Val-----LeuHis-----LeuLeu-----	341
Db	16222	TACCTGCGTTGCGGTAAAGACCTTTTACACCACACTGCGCACCGCGCTATTGTCAGCGT	16281
Qy	342	-----LeuLysPhe 344	
Db	16282	GAGGTGCTGACGACGGGTTTGAGCGCGAGTTTACCGTAACGTGGCATTC	16330
RESULT 9			
US-09-661-596A-76			
; Sequence 76, Application US/09661596A			
; Patent No. 6528066			
; GENERAL INFORMATION:			
; APPLICANT: Grose, Charles			
; APPLICANT: Santos, Richard			
; TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE			
; FILE REFERENCE: 140.0011 0101			
; CURRENT APPLICATION NUMBER: US/09/661,596A			
; CURRENT FILING DATE: 2000-09-14			
; PRIOR APPLICATION NUMBER: US 60/153,779			
; PRIOR FILING DATE: 1999-09-14			
; NUMBER OF SEQ ID NOS: 80			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 76			
; LENGTH: 124884			
; TYPE: DNA			
; ORGANISM: Varicella zoster			
US-09-661-596A-76			
Alignment Scores:			
Pred. No.: 7.19e-21 Length: 124884			
Score: 1725.90 Matches: 291			
Percent Similarity: 11.93% Conservative: 41			
Best Local Similarity: 10.46% Mismatches: 8			
Query Match: 71.67% Indels: 2442			
DB: 4 Gaps: 245			
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Db	75448	TAATTGTAATACACTGGATCGGCTTCTAATGGAGCAAGGCTGTGGCTCGCAAGCTC	75507
Qy	7	-----	7
Db	75508	CACCGACACTGAATATCAATTTAAACGCCCTCCCGGTTCTACCGAAATGACACAGGATCC	75567
Qy	8	-----Met-----His-----	9
Db	75568	GTGTGGCCTTTTCAAGAAGCATATCCACCCTATGCTCAAGCGATGCGGCATGTTCAG	75627
Qy	10	-----Asn-----	10
Db	75628	AACGGCTACGCGGGAGAAACCGGGGCAGATGAAGTTCCTTAGCCCAATATCTGATTCG	75687
Qy	11	-----Ser-----IleSer-----	13
Db	75688	AGACGGTCGCGCCCTTAGGGGATGTCTTCCTCTTCGCGGATAATTTACACAGCCCAT	75747

QY 62 -----Arg-Val-----ThrArg-----Val----- 66
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QY 67 -----Ala----- 67
Db 76888 GAACTGCCAATATACACGGACATAATTAATGCAACATCAGATCATCTGACATGTTCC 76947
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QY 72 ----Ser-----Thr----- 73
Db 77008 TCTGTCAGGTTATCCAACTGTTTACATAGATATCCACGGGGTCTACACCTAATTTACT 77067
QY 74 ----Ile-----LeuTyr----- 76
Db 77068 GTTAGGATACAGCTCCTGTGAGGCTATTATTTCCGGAGTTAAATCGTTTAAACAAA 77127
QY 77 -----Ala-----Gly----- 78
Db 77128 TAGTCTACGCGCGCGTCTTTTGTGTAATAAAAAAGGGTACGCCACGCTACAT 77187
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QY 82 -----Trp----- 82
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QY 89 1-----Leu----- 90
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QY 91 -Leu-----SerAsn-----Thr-----Gln 95
Db 77425 GCTCTAAGAAAAAAGTGCTCCAATCCAATATAATCCCAATCCGATTTATACGACCAACA 77484
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QY 129 -----His-----LeuIle----- 131
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QY 132 -----Val-----Gln-----Va 134
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QY 134 1-----SerPro-----LysIle-----Val----- 139
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QY 140 -----Glu-----Ile-----SerSer----- 143
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QY 143 ----- 143
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QY 144 -----Asp-----Ile----- 145
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QY 145 ----- 145
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QY 146 -----Ser-----IleAsn----- 148

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Qy 149 -Glu- -Gly- -Asn- -Ile- 153
79045 TGAGCCGCTGGACAGGGCGATTACGGGAAGAAACAATTCGTCCGCGACATCCC 79104
Qy 154 - - - - -SerLeu- - - - - 155
79105 ACCTTTACAGACGTTCTATTGTTTACCCAGCTTCGACAGAACCCCAAGCTCTTATGGA 79164
Qy 156 - - - - -ThrCys- - - - -IleAlaThrGly- - - - - 161
79165 ATGTTGACATCTGTTATGCCCAATTAGTTAGGGGACACTCCAGCAGATTTCTGGAA 79224
Qy 162 - - - - -ArgPro- - - - -Glu- - - - -ProThr- - - - - 166
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Qy 167 -ValThr- - - - -Trp- - - - -Arg- - - - - 170
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Qy 171 -His- - - - -Ile- - - - - 172
79345 TCATCTGCACAGGCTATTATTGATGCTGTATATAAATCCCGGTTGACAAATCCCCA 79404
Qy 173 -Ser- - - - -ProLys- - - - -Ala- - - - -Va 177
79405 AAGCTCATGTGACAGTCCCAAGAGCTAGTCGCGGTTTACGGTTTGGCTAAGT 79464
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79465 CCTAAATATCAAAACCCCTTACCCTGCTTAAACACGCGCGGAATGTTTAAACCA 79524
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Qy 182 - - - - -Glu- - - - - 182
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Qy 183 -AspGlu- - - - - 184
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Qy 184 - - - - - 184
79705 AATGTCATGGATCGGTTTATAACAGCTCCTTGATGATGCGGTTTGGGTATCTGTC 79764
Qy 185 - - - - -TyrLeu- - - - - 186
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Qy 187 - - - - -Glu11 188
79825 ATGCTGTTAGGTAATCGTTCTATATATTTTGACTATTATAATTCAGGAGGGAAT 79884
Qy 188 e - - - - - 188
79885 ACTTAAGCTTCCAGGTCCTCCGTTCCGTAGCCTTAGAAGGTTGGTATGTAATTC 79944
Qy 189 - - - - -Gln- - - - -IleThrArg- - - - - 193
79945 CACAAACTGAGGGTAAATTTATA- - -CGACGCGGATATTGTTGATATGGAATTG 80001
Qy 194 - - - - - 195
80002 TTCTAAGTATTTACCGGTCAATGTTACGGGTACATTTGTCTAGGATTTAAACGCAATT 80061
Qy 195 - - - - -GluGln- - - - - 195
80062 ACRATCCATTTAGTTTACCGGGGATTTGGCGATGTTTGTATATACCGATACCT 80121

Qy 196 - - - - -Ser- - - - -Gly- - - - -Asp- - - - - 198
80122 ACAGGACAGCTACCTGCATCGTTAATCGGACCTATTCTAGACAGATTTCTCTCTCTAT 80181
Db 198 - - - - - 198
80182 TCCCAACCCCATATAAATAATTAGTGTCACTATAAAAAACAATACACAGCAATCTCTTCAT 80241
Qy 198 - - - - - 198
80242 ATGTAATTTTACGTCAATTTCTCCGTTTCCACCCCTCTTAAATAATAAATAACCGGT 80301
Qy 198 - - - - - 198
80302 GGTGGCATTTAAACCCACAAGTACCCCGGCGCAATCCGTAGACTGTTTTCTGCTCAT 80361
Qy 199 - - - - -Tyr- - - - - 199
80362 GGAATTACAACGCATATTTCCGCTGTACACCGCTACGGTGCAGCGCAAAATTAACCCC 80421
Qy 200 -Glu- - - - -CysSerAla- - - - -Ser- - - - - 204
80422 CGAGCGAGTTTACAGACTCTCGCATGCAATTAACGCTGATATGGATATGGAATCCAT 80481
Qy 205 - - - - -Asp- - - - -Val- - - - -Ala- - - - -Al 209
80482 CCTGACCGATCCCGGGTGAATAATATGCATCACTGCTTTTATAACTTTAAGGATCGC 80541
Qy 209 aPro- - - - -Val- - - - -Val- - - - - 212
80542 TCGTTTATCCCTTCAAACGGATACTACTAATAATTGCGGTTGTTGTAGCCACAATTA 80601
Qy 213 - - - - -Arg- - - - -Arg- - - - -Val- - - - - 215
80602 CATCACGCGCCACGTACAGATGAATTAACCTCGAAGACTTTTCATGTAATGTAATTT 80661
Qy 216 - - - - -LysVal- - - - -Thr- - - - - 218
80662 TAATTACGAGTCTCGTACCAATGACGGGACTTTAAGAATTTATCCGGTTGAACAT 80721
Qy 219 - - - - -Val- - - - - 219
80722 AGACCATGTTTGTGGAGCAAGTTTAAAGCCGATCGGTACCCCTTCCACATCTAT 80781
Qy 220 - - - - - 220
80782 TCCGATCTCTGACAGATCCACCCCGCAGATCTTACACCAACGCAAACTTAACCA 80841
Qy 220 nTyr- - - - -Pro- - - - -ProTyr- - - - -IleSer- - - - - 226
80842 CTACTTACACCCCGCGGCTTCCGAAATCCATAGCATGTAAAGTTATTTCTCCGG 80901
Qy 227 - - - - -Glu- - - - -AlaLys- - - - - 229
80902 AGTGTGTGTGTCAGACGAAAGCGGCTTTATATGATGCTATGCTATGGAACCTAATTAAT 80961
Qy 230 - - - - -GlyThr- - - - - 231
80962 AGGCTATGTCGCGCGGATGCGATGCTCGATATCTGCTCTGTATTAATTCGACTCT 81021
Qy 232 - - - - -Gly- - - - -Val- - - - - 233
81022 CAGCCATGCGGAGGATGTGATGAATGTAATCATAGATTCAGTGGGGCACTGTATGC 81081
Qy 234 - - - - -Pro- - - - -Val- - - - - 235
81082 GTTACCCCATGTCAAAATCATCGGAAGTTGTGTGTGTGGCTCCGTTATGTGGAG 81141
Qy 236 - - - - -GlyGln- - - - -Lys- - - - -Gly- - - - -ThrLeuGln- - - - - 242
81142 AAAGCGGTGTCAGCGGAATTAAGAGGTAGACATTTGGCGCCACG- - -CAGGTCT 81198

QY 243 -----Cys-----Glu----- 244
Db 81199 TTTTGTAGATGTCACCACTGCAATTCGAATTACAGTACTAAAAATCCTCGCAATTACCGC 81258
QY 245 -----AlaSer-----AlaValPro-----Se 250
Db 81259 AAATCTTGGCGAGTTATAGCGGGAACCAACGCGAGTGGTCTCTCTGTACCAATAATTC 81318
QY 250 rAla-----Glu----- 252
Db 81319 ATCTGGTGGCAGCTTTATATGTTTGGAGAAACATTAAGCCGGCTATTATTAAACGGCTG 81378
QY 253 -----Phe----- 253
Db 81379 TGGTCTGCTTCAGCGAATTGCTTCCCGGAGACACAAAGATTATCGGGTGAACCGGAACC 81438
QY 254 -----Gln-----Trp----- 255
Db 81439 TACAACCACTAGTATACCTTAACCAACCGCGTGTGGAAAGGTATATGTCAACATTT 81498
QY 256 -----IleLys-----Asp----- 258
Db 81499 ACAGTAATATATTAAAGTTAAATTTATAAAACACTCACGTTTGTGTGTGACTTGACGC 81558
QY 259 -----Asp-----Lys----- 260
Db 81559 GAACACCGCTGTGCTGTAGACCCGCTGGTAAATGAAGACGTAAATAGATTTCGCTTTTAC 81618
QY 260 ----- 260
Db 81619 ATGATCCACGTAATTTGCCCAACCACTGTTCCAGGCGAGACTTGATACCTTCAAACAC 81678
QY 261 -----Arg-----LeuIle----- 263
Db 81679 GGGTTCGGTTGCTTTCGGTATATGACCGGTATACCCACTTTAAATTCCTCTAAACGTGC 81738
QY 263 ----- 263
Db 81739 CATTACTAAAGCTATTAAATGTTACAAAGAACCACTGTTTCCCATGCTACGTGGTACCAA 81798
QY 264 -----Glu-----Gly----- 265
Db 81799 AAACACAGTTGATTTTGTGTTGAAGTGTCTTAAACACTGTCAAGAAACACTTGGCGTGT 81858
QY 266 -----Lys----- 266
Db 81859 AAACACTGTACGAGAAAGCAGTCAACTCTGTCCGATGATCCCCCAATAGCACCGATGA 81918
QY 267 -----Lys----- 267
Db 81919 AATAAAATGCGTGTGTCATGAGGATCAATTTTGAACAGTTCCAACGTCCTCCCTATA 81978
QY 268 -----Gly----- 268
Db 81979 TCTGCCATAGATTGGACGTCACCTTTGCGCGTTTGGCATGACTTCCACACTCTTCAAT 82038
QY 269 -----ValIleVal----- 271
Db 82039 ACTCTCAAAAGATGTTTCCAAAGGTACGAAACCGTGTGTAAAGGTAGACAACTGACA 82098
QY 272 -----GluAsn-----Arg-----Pro-----Phe----- 276
Db 82099 GAAACTATCCGACAGAAACCGCGGAATGTGTTTCAATAACACCCGCTATACGCAATTCG 82158
QY 277 -----LeuSer-----LysLeuIle-----PhePh 283
Db 82159 ATGAGGTGCTCTTCTCCGGTGAATATTCATAAACTGTACACTACTGACAGCCCTTTT 82218
QY 283 eAsn-----ValSerGlu-----His----- 288
Db 82219 TAATTCAGGCTTACGTTTGCATTTACCGAATATCGCCATGTTTCAAACACTACATGGS 82278
QY 289 -----Asp----- 289

Db 82279 GGTACAGTTGTACCCCTGTTGACATAGAAACCGGCCAAACATTTGCCGTCGAGCAGTAGC 82338
QY 290 -----Tyr-----Gly----- 291
Db 82339 CGAGAACAGTGGAAATATATTCACACAGTTGTGAAGCGTTCCAAATTCGCGGAATAACGCG 82398
QY 292 -----Asn-----TyrThr----- 294
Db 82399 CTGATGACGTCGGGTTACATCTATAGCAAAATTCAGAAACGGGATTTGGTTGCGTTTCC 82458
QY 295 -----Cys-----Val-----AlaSerAsn----- 299
Db 82459 CAGAGACCTTTCGCGGTGAACACGGGTAGGGACTCCAAAGTCCCAAGAGCGTTTCATC 82518
QY 300 -----Lys-----Leu----- 301
Db 82519 CCTACGACGTTTACAGCTTCAAAATATCTTACAGATTCTTACCAGCGGTACGACCAA 82578
QY 302 -----Gly-----His----- 303
Db 82579 CATTATCAATGACATTTAAACATCAATTCACGAATCCGGCTCATCTCTTGTAAAGCAGTAA 82638
QY 304 -----Thr-----Asn-----Al 306
Db 82639 AACAGGAACGCGCTCATCTTACGTACTCGTTACGTATATATATCATATAACATTTTCAGGC 82698
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Db 82699 CGCATTCATTCAC-----TTTGGTCATGTCAGGCCACACTCCAACTACGTTTCTCATAGC 82755
QY 313 -----Pro-----GlyVala-----Val----- 316
Db 82756 GTAACCGGTCAAACTAGTTGAGCGGCTAAACCGCGCGGGTTATTAAAGAACGAGACC 82815
QY 317 -----Ser-----Glu-----Val----- 319
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QY 319 ----- 319
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QY 320 -----Ser-----Ser-----As 321
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QY 321 n-----Gly----- 322
Db 83056 CAGAAGACGTAATACCGATATATAGACAGACTGGAAGACGCGGTAGGACGGAACATCG 83115
QY 323 -Thr-----Ser-----ArgArg----- 326
Db 83116 AACACGAAATCATACTTGGTTTGGAGAGACGACGAGCGTTACTTACAAATGGATGC 83175
QY 326 ----- 326
Db 83176 TGACGACACACCCCAACCTCAAATATCTCAAACCTGAGGACCTTTCGTTCCCAACA 83235
QY 327 -----Ala----- 327
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QY 328 -----GlyCysVal-----Trp----- 331
Db 83296 CAACCCACACACGAGTGTGTAAATCATCCATGGCCCAATCGTCAACTGCAACATGCAT 83355
QY 332 -----LeuLeu----- 333

Db 83356 GGAATCACCAGACGATCACACAGACAGCTATTTTATTAAAGCAGCGCTTAACGAG 83415
QY 334 -----Pro-- 334
Db 83416 AGATCCAATACATCAACGCGAAAGGTGGACGTTTTTCCACAATTTAAACAAACCCCATG 83475
QY 335 -----LeuLeuVal 337
Db 83476 GGTTTTAGAATTTCCAAATATCCCGTTTAAATGTACCCATCTTCAGCTCAATGAACA 83535
QY 338 -----Leu 338
Db 83536 GTTATGTTTTCTAAATACAGATTGAGATAGACCCAGGTTTGGGAGCGGGAACGTA 83595
QY 339 -----HisLeuLeu 343
Db 83596 TGGGCGTTTCATATATATACCATCCATCGTCAAAAATAGCTGTAAAAACCATCGGACGTCGTGT 83655
QY 344 -Phe 344
Db 83656 TTTT 83659
RESULT 10
US-09-913-514-1
; Sequence 1, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913,514
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(124884)
; OTHER INFORMATION: Dumas Strain
US-09-913-514-1
Alignment Scores:
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Score: 1725.90 Matches: 291
Percent Similarity: 11.93% Conservative: 41
Best Local Similarity: 10.46% Mismatches: 8
Query Match: 71.67% Indels: 2442
DB: 4 Gaps: 245
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QY 6 -----Lys 6
Db 75388 AGGCGCTTCTCCTATCTACGCCCATGCTTTAAGTTTTTTTACACCAGCGAGGTTAAAC 75447
QY 7 -----Lys 7
Db 75448 TAATTGTAATACATCGGATCGGCTTCTAATGAGGCAAGGCTGTGGCGTCGCAAGGCTC 75507

QY 7 ----- 7
Db 75508 CACGCACATGAATATCAATTTAAACGCCCTCCGGTTCTACCGAAATGACACAGGATCC 75567
QY 8 -----Met-----His----- 9
Db 75568 GTGTGGCCTTTTCAAGAAGCATATCCACCACATATGCTCAAGCATGGGCCATGTTACG 75627
QY 10 -----Asn----- 10
Db 75628 AACGGCTCACGCGGAGAAAACCGGGGAGATGAAGTTTCACTTAGCCCAATATCTGATTCG 75687
QY 11 -----Ser-----IleSer----- 13
Db 75688 AGAGCGTCGCGCCCTTAGGGGATGTCTTCCTCTTCCCGGATAATTTCCACACGCCACAT 75747
QY 14 -----Trp----- 14
Db 75748 ACCCACTCCCAATAAAGCCCTGTAGAGCGCATTTGGCATCTTACTTGAGATTGGATACG 75807
QY 14 ----- 14
Db 75808 CTGGCCGACTTGTCTGTCTTTTCAAGCTTCTTAAACAACATGGCTATGCCAATTGAGATA 75867
QY 14 ----- 14
Db 75868 GAGGTATTGTACAGGAGAACTATATCCCGGGGGAACATCTGCATTACAGAAATGTGAG 75927
QY 15 -----Ala--- 15
Db 75928 GGAATAATTTACTTCTCAACCTCGCTATCGAGCTTCACTGGTGGATATAGCGCTG 75987
QY 16 -----Ile----- 16
Db 75988 TCGTCATATTACATTAAACGGTGTCCACAGACACAGCTCTCGCTGTAGAGCATACCGA 76047
QY 17 -----Phe-----Thr-----Gly-----LeuAla---Ala--- 22
Db 76048 ATGGATTTCGGGCGAGTATATAACACGGGTATCCCGGGAAGTGTGTGGCGCATGCCATT 76107
QY 23 -----LeuCys 24
Db 76108 GGGTGGGTACTCTACACCGGGTGTGTTTATTCAAATAATATATCCCGCTGTGATCTTGT 76167
QY 24 ----- 24
Db 76168 AATGGCGATTACATCTGCTTACTTCTCTCGGTTTTTGGGTCCGAGACTCAATTCGGTTG 76227
QY 25 -----Leu-----Phe-----Gln----- 27
Db 76228 GACTCTGAGGACTGGAAATGTTTTCCCTTTAAACCATCCCGAGACTTAATGCGAGAA 76287
QY 28 -----Val---Gly---Val--- 29
Db 76288 ATCATCGCCAAAGTGTGTGACGCGCGGTTGAGCGCAGCGCGGGTGTCTCAAAATTTA 76347
QY 30 Pro-----Val----- 31
Db 76348 CCCACGAAGTTCTACAGGCGCGGATGTCATTTGTTACAATGGAAGGCGTTATGAACCTC 76407
QY 32 -----ArgSerGly---AspAla-----Thr----- 37
Db 76408 GAAACAAATTTTCAACATCGGACGATCGATCGGCTATTTCGCACATTTGGTTTTAAAT 76467
QY 38 -----Phe-----Pro----- 39
Db 76468 CTAATGTTTCCATAAAGAGGATGTCTCTTTTATTGGCGCTGATTCCAACTTTGTTA 76527
QY 40 -----LysAlaMetAsp-----Asn-----Val---Thr-----ValArg 48
Db 76528 GTCCAAGGAGCACACGAGGTTATGTAATTTATGATACAAACGCGCAATTCGTTAGA 76587
QY 49 -----Gln---Gly----- 50

Db 76588 GAAACCGCCAGTAAATATATACCGCCAAATCGCGGGATTCAAGACGGCCATCGCGGA 76647
QY 51 -----Glu-----SerAla----- 53
Db 76648 TTTCCTATATGAAACTATTCATCTTGATATCAACATCATCTAGACTGGGGATACC 76707
QY 54 -----Thr-----LeuArg-----Cys-----ThrIle----- 59
Db 76708 TTGGGAACCTCGCAATTTTACCGCTCTGTGTTTGATGAGACCCCTACTGTTCATCCG 76767
QY 60 -----Asp-----Asn----- 61
Db 76768 GGAGACCGCGCCGCTGATTCAGGTAAACACAGGTGTTAATAAABACACACACAGCTCTA 76827
QY 62 -----Arg-----Val-----ThrArg-----Val----- 66
Db 76828 GTTACATTTACCGCTCTGTGTTTATTAATAGGCATAAACACAGGAATCCGGTATACAT 76887
QY 67 -----Ala----- 67
Db 76888 GAACTGCCAATATACAGGACATAATTAATGCAACCATCGATCATCTGACATGTTCCG 76947
QY 68 -----Trp-----LeuAsn-----Arg----- 71
Db 76948 GTGGTACCTTTACCCGTGAAGTTTGTGCTGATATACCCATACCGCTTTAATACC 77007
QY 72 -----Ser-----Thr----- 73
Db 77008 TCTGTAGGTTATCCAACTGTTTACATAGATATCCACGGGGTCTACACTAATTTACT 77067
QY 74 -----Ile-----LeuTyr----- 76
Db 77068 GTTAGGATACAGCTCCTGTGAGGCTATATATTTCCGGAGTTAATCGTTTACAAAA 77127
QY 77 -----Ala-----Gly----- 78
Db 77128 TAGTCTACGGCGCGCTTTTGTGTTTGTATAAAAAAAGGGTACGCCACGCTACAT 77187
QY 79 -----AsnAspLys----- 81
Db 77188 CCGGAGGTATGGAATGATAAACAAGTAACTGAGGCGGAAGATAGACAGTTTCCCTTT 77247
QY 82 -----Trp----- 82
Db 77248 TCGAGACAGCAAACTGTTGTGCTATAGCAACAGATATGCAACTGCAGAACTCTGGCTG 77307
QY 83 -----CysLeuAspPro-----ArgVal-----Val 89
Db 77308 CTGTTTC-----CCTCTATAGAAAGTGTACGTTTGTAAATGTATGGGGTGTAAAGCGAGT 77364
QY 89 -----Leu----- 90
Db 77365 ATGTGSCCTAAGCATGAGTAAGCAACGCCCTATCTCACTGGAAGACGTGCGAGTAAA 77424
QY 91 -----Leu-----SerAsn-----Thr-----Glu 95
Db 77425 GCTCTAAGAAAAAAGTGCTCCCAATCCAAATATAATCCAAATCCGACTTATAACGACCAACA 77484
QY 95 -----GlnTyr----- 98
Db 77485 ATCGCTACACAGTACACAGCTCTGTGTTTGTAGGTAATGCAAGGGTCTACGTAACGG 77544
QY 99 -----Ser-----IleGlu----- 101
Db 77545 TACAACACTGACGATAATATAGCAATTCGCAACGGTTGACGGCGGATATAAATAAAC 77604
QY 102 -----Ile-----GlnAsn----- 104
Db 77605 CTCTACGGGCGAGTTTGTGTAATAATAGCGCGTCAAAACCCACACCCAGAAATCTGT 77664
QY 104 ----- 104

Db 77665 TTACGCCCACTTACAAATTTCTGCAAGAGAGTGGGCCATAAATAAATCTCGAGTGGCG 77724
QY 104 ----- 104
Db 77725 CGCATGGCTCCATCCATCTGTGATGAAGAACCGGCTTTATTAAATACATAACACGAACAGCT 77784
QY 105 -----Val----- 105
Db 77785 GTGACATCGCTATGTGCTAAACACGCGCATGTGATCGTCGCATACATATATGTAACAACG 77844
QY 106 -----Asp-----Val----- 107
Db 77845 TTTAACACTGATCCGACGATCCAGTAAGTTATACAAAAAACTTGTTACTGCTTTCCG 77904
QY 108 -----Tyr-----Asp----- 109
Db 77905 GTATTGTTGATGAACCAAAAAATAATTTTACAAATGGTTGATTTTAAAAATCCGACTATA 77964
QY 110 -----Glu----- 110
Db 77965 GTTTGTACAGCATCAGGTGCGAATAAAATAGCTTCATCCAAACAGAGATTAAAAATCT 78024
QY 111 -----Gly-----Pro-----Tyr-----Thr----- 114
Db 78025 TGACCTCGGATACCTCGGAACGATAGAAAGATATATAGTTACCCACCAAGTTTAAATG 78084
QY 115 -----Cys-----Ser-----Val----- 117
Db 78085 TATCCTTAATACACGATACGTAATAAAATGTTTGAATAGTACATATTTCTTTTCTTTT 78144
QY 118 -----Gln-----Thr----- 119
Db 78145 CCAGTACACCATATCCGGTGTATTAATGGAAGCCCATTTGGCAATGAACCAACATGC 78204
QY 120 -----Asp-----Asn----- 121
Db 78205 ACTTTGGCATAATGATCACAAAAAGGATTACTACACGTGTGTGATACCTAACCGCGGCT 78264
QY 121 ----- 121
Db 78265 TATTCGGCGCGAATPAGATCCGCAATTACTGATTTTAAAGAAACCCGGAACAGCTTCAA 78324
QY 122 -----His----- 122
Db 78325 GGTGAAGTACAAACAGATATCATGCTACAGGTCAATGCGAACCGTGTGTCAGTTTT 78384
QY 123 -----ProLysThr----- 125
Db 78385 CGCCGCTACATTCGCGATAACCGCTTAACAAATCTCTTAATACCAAAACCGAACCATT 78444
QY 125 ----- 125
Db 78445 TGTTTACACAGTTTTTTTCGGCCACGCATAAATTCAGGGGGATGATTTTATCATTTGCCCTGT 78504
QY 126 -----Ser-----ArgVal----- 128
Db 78505 TTATCTTAGCCCGGTTTATTTCTTTGATGATTTAAACGTTGAGCATACGATAACGATAAC 78564
QY 129 -----His-----LeuIle----- 131
Db 78565 TGGAAACGCAAGCACCGCTGATATTTGTATTATGTATGACAGACTAATCCCAACCGGAAC 78624
QY 132 -----Val-----Gln-----Va 134
Db 78625 CGTTATTTTCTGATGACAAACCGGTACTTTTATATATGCAACAGCTGATTTGGGTATAT 78684
QY 134 -----SerPro-----LysIle-----Val----- 139
Db 78685 CCGATGCACCCCTCGTCTGTGATCGTCTATAAATAATATACGACGAGCATATGTTGGCAGC 78744
QY 140 -----Glu-----Ile-----SerSer----- 143
Db 78745 CATGGTGAATCACACAGTCAGGCAATATTTGGACCCGTTTCCATCCATAATCGA 78804

Qy	188	e	-----	188					
Db	79885	ACTTAAGCTTCC	AGGTC	CCCGTTCCCGTAGCTTAGAAAAGTTGGTATTGGTAATTC	79944				
Qy	189	-----Gln-----	Gly-----	Ile	Thr	Arg-----	193		
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Qy	194	-----	Glu	Gln-----	-----	Glu	Gln-----	195	
Db	80002	TTCTAAGTATT	TACCGGTC	CAATGTTACGCGTAC	ATTGTCTAGGATTTACACGACAATT	80061			
Qy	195	-----	-----	-----	-----	-----	-----	195	
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Qy	196	-----	Ser-----	Gly-----	-----	Asp-----	198		
Db	80122	ACAGG	CAGCACTACCTGC	ATCGTTTAATCGGAC	TATTCTAGACAGATTCTGCTTCTCTAT	80181			
Qy	198	-----	-----	-----	-----	-----	-----	198	
Db	80182	TCCCA	ACCCCATAAATAA	TAGTGTCACTATAA	AAACATAACACAGAA	TCTTCTCAT	80241		
Qy	198	-----	-----	-----	-----	-----	-----	198	
Db	80242	ATGTA	TTTTTAAGTCAT	TTCTCCCGTTTCCACCCCTCTTAA	ATATAAAATAACCGGT	80301			
Qy	198	-----	-----	-----	-----	-----	-----	198	
Db	80302	GGTGG	CATAAACCACA	AGTACCGCGGGCGCAATCCGCTAG	ACTGTTTTTCTGCTCAT	80361			
Qy	199	-----	-----	Tyr-----	-----	-----	-----	199	
Db	80362	GGNA	TTACACGATATTTCCGCTGTAC	CCGCTACGGGTG	CAGCGCGCAAA	TTAACCCC	80421		
Qy	200	Glu-----	Cys	Ser	Ala-----	Ser-----	204		
Db	80422	CGAGG	CAGTTCCAGAC	ACTCTCGATGCATTAACGCTGG	ATATGGGATATGGAATCCAT	80481			
Qy	205	-----	Asn	Asp-----	Val-----	Ala-----	Al	209	
Db	80482	CTGAC	CCGATCCCGGGTGA	AAATAATCGATCA	ACTGCTTTTATACTTTAAGGATGC	80541			
Qy	209	aPro	-----	Val	Val-----	-----	212		
Db	80542	TCGGTTAT	CCCCCTTCAACG	GATACTAATAATTCGCTGTTGTTG	ATGACCAATTA	80601			
Qy	213	-----	Arg-----	Arg-----	Val-----	Val-----	215		
Db	80602	CATC	AGCGCCCA	CGTCAGATGAACTTACCTCCG	AAAGACTTTTCATGTAATTGTAAATTT	80661			
Qy	216	-----	Lys	Val-----	Thr-----	-----	218		
Db	80662	TAATTAC	GAGGTC	CGTACGCAATGACGCG	CACTTAAGAATTTATCGGTTGAAAACAT	80721			
Qy	219	-----	Val-----	-----	-----	-----	219		
Db	80722	AGAC	CATGTTTTTGGG	CAACGTTTTAAGAACCCG	ATCGCTACCCCTTCCACATCTAT	80781			
Qy	220	-----	-----	-----	-----	As	220		
Db	80782	TCCG	GATCCTCGACG	ATCCACCCCGCAGATCTTAC	ACCAACGCAAACTTAAGCA	80841			
Qy	220	nTyr	-----	Pro-----	Pro	Tyr-----	Ile	Ser-----	226
Db	80842	CTACTT	CAACCCCGCGGCTCCG	AAAAATCCATACG	ATGTAAGTATTTCTCGGG	80901			
Qy	227	-----	Glu-----	-----	Ala	Lys-----	-----	229	
Db	80902	AGTGTG	GGTCAGACG	AACGAGCGGTTTTATATG	TACTGTGCTATGGAACTTAATTAAT	80961			
Qy	230	-----	-----	-----	-----	Gly	Thr-----	231	

80962	AGGGCTATGTC	CGCGCGGATGGCATGCTCGGATAC	TGTGGCTCTGTATTAAATCGACTCCT	81021
232	-----Gly-----	Val-----	-----Phe-----	276
81022	CAGCCATGCGGACGGATGTGATGAATGTAATCATAGAGTTACGTTGGGGGCACTGTATGC	81081	-----Val-----	233
234	-----Pro-----	-----Val-----	-----Phe-----	235
81082	GTTACCCCATGTGCACAAATCATCGGAAGGTTGTGTGTGTGGCTCCGTGTATGGGAG	81141	-----Val-----	233
236	-----GlyGln-----	-----Gly-----	-----ThrLeuGln-----	242
81142	AAAGCCGGTCACGGGAATTAAGATGGAGGTAGACATTTGGCCACG	81198	-----Val-----	235
243	-----Cys-----	-----Glu-----	-----Val-----	244
81199	TTTTGTAGATGTCAACACCTGCATTCGAAATACGAGTACTAAAAATCCTCGCATTAACGC	81258	-----Val-----	233
245	-----AlaSer-----	-----AlaValPro-----	-----Ser-----	250
81259	AAATCTTGGCGAGTTATAGCGGGAACCAACGCGTGTCTCTGTACCAAGTAATTC	81318	-----Val-----	233
250	-----Glu-----	-----Glu-----	-----Val-----	252
81319	ATCTGGGTGGCAGCTTTATATGTTGGAGAAACATTAAAGCCGGCTATTATTAAACGGCTG	81378	-----Val-----	233
253	-----Phe-----	-----Glu-----	-----Val-----	253
81379	TGCTCTGCTTCAGGAATTTGCTTCCCGGAGACAAAGATTATCGGGTGAACCGGAACC	81438	-----Val-----	233
254	-----Gln-----	-----Gln-----	-----Val-----	255
81439	TACAACCCCTAGTATACCTTAACTCAACCGCGGTTGTGAAAGGTATATGTCAACATTT	81498	-----Val-----	233
256	-----TyrLys-----	-----Asp-----	-----Val-----	258
81499	ACAGTAATATATAAGGTTAAATTTATATAACACTCACTGTTGTGTGTGTGACGC	81558	-----Val-----	233
259	-----Asp-----	-----Lys-----	-----Val-----	260
81559	GAACACGGCTGTCTGTAAAGACCGTCGGTAAATGAACAGTAATAGATTGCGCTTTTAC	81618	-----Val-----	233
260	-----Val-----	-----Val-----	-----Val-----	260
81619	ATGATCCAGTAATTTGCCCAACCACTGTTCCAGCGAGACTTGTATACCTCAACAC	81678	-----Val-----	233
261	-----Arg-----	-----LeuLeu-----	-----Val-----	263
81679	GGGTTCCGTTGCTTTGGGTATAGCCGCTATTAACCCACTTTAAATTCCTCTAAACGTGGC	81738	-----Val-----	233
263	-----Val-----	-----Val-----	-----Val-----	263
81739	CATTACTAAAGCTATTAAATGGTACAAGAACCACTGTTTCCCATGCTCAGTGGTACCAA	81798	-----Val-----	233
264	-----Lys-----	-----Glu-----	-----Gly-----	265
81799	AAACACAGTTGATTTTGTGAGTGTTCTAAACACTGTCAAGAACACTTGGCGTGT	81858	-----Val-----	233
266	-----Lys-----	-----Lys-----	-----Val-----	266
81859	AAACACTGTACGAGAAAGCAGTCAACTCTCGCGCATGATCGCCCAATAGCACCGATGA	81918	-----Val-----	233
267	-----Lys-----	-----Lys-----	-----Val-----	267
81919	AATAAATGCGGTGTCATGAGATCATTTTGAACAGTTCACACGTCCCTTATA	81978	-----Val-----	233
268	-----Gly-----	-----Gly-----	-----Val-----	268
81979	TCTGCCATAGATTGAACGCTCAACCTTTGGCGTTTGGCATGACTTCCACACTCTTCAAT	82038	-----Val-----	233
269	-----Val-----	-----Val-----	-----Val-----	271

82039	ACTCTCAAAAGATGTTTCCACAGGTTACGAAAAACCGTTGTGTAAAGGTAGACAACTGACA	82099	-----GluAsn-----	272
272	-----GluAsn-----	-----Arg-----	-----Pro-----	276
82099	GAAACTATCCGACAGAGAAACCGCGCAATGTGTTCATAACACCGCTATACGCAATTTTCG	82158	-----Val-----	233
277	-----LeuSer-----	-----LysLeuLeu-----	-----PhePh-----	283
82159	ATGAGGTGCTGCTTCTTCCCGTGAATATTATATAAACTGTACACTACTGACAGCTTTTTT	82218	-----Val-----	233
283	eAsn-----	-----ValSerGlu-----	-----His-----	288
82219	TAAATTCAGGCTTACGTTTGTCAATTTACGATATCGCCATGCTTCAAACACTCAATGGG	82278	-----Val-----	233
289	-----Asp-----	-----Val-----	-----Val-----	289
82279	GGTACAGTTGTACCCCTGTTGACGATAGAAAACGCGCCAAACATTGCCCCGTGACGAGTAGC	82338	-----Val-----	233
290	-----Tyr-----	-----Gly-----	-----Gly-----	291
82339	CGAGAACAGTGGATATATTACAAACAGTTGTGAGAGGTTCCCAATTCGGGGAATAACGGC	82398	-----Val-----	233
292	-----Asn-----	-----TyrThr-----	-----Val-----	294
82399	CTGATGACGTCGGGTTACATCATATAGCAAAATTCAGAAACGGGATTTGGGTTGGTTTCC	82458	-----Val-----	233
295	-----Cys-----	-----Val-----	-----AlaSerAsn-----	299
82459	CAGAGACCTTTGCGCGGTGGAAACACGGGTAGGGGACTTCCAACGCTCCCAAGGCTTCATC	82518	-----Val-----	233
300	-----Lys-----	-----Leu-----	-----Val-----	301
82519	CCTACGACGCTTAGACGTTCAAAATATCTTACAGATTCTTACCAGAGCTAGACCAAA	82578	-----Val-----	233
302	-----Gly-----	-----His-----	-----Val-----	303
82579	CATTATCAATGACATTTAAACATCAATTCACGGAATCCGCTCATCTCTGTAAGCAGTAA	82638	-----Val-----	233
304	-----Thr-----	-----Asn-----	-----Al-----	306
82639	AACAGGACGCGCTCATCTTACGCTACTCGTTAGTATATATATAAACATTTTCAGGCG	82698	-----Val-----	233
306	aSer-----	-----IleMetLeuPheGly-----	-----Val-----	312
82699	CGCATTCATTAC-----	-----TGTGTCATGTACGCGCACCTCCAACTCCTCATAGGC	82755	316
313	-----Pro-----	-----GlyVala-----	-----Val-----	316
82756	GTAACCGGTCAAACACTAGTTGAGCGGCTATAACCGCGGGGTATTATTAAGAACGGACCC	82815	-----Val-----	319
317	-----Ser-----	-----Glu-----	-----Val-----	319
82816	TCGATCTAATCCGTGGGGTGCAGGTGTACAGATCCAGCATTTGTGTATGCTTTTACTG	82875	-----Val-----	319
319	-----Val-----	-----Val-----	-----Val-----	319
82876	CTGCAAAAGAGCCTGCGCGATTTAAATACAGCTCCGCTCTGACAGCTCGCATAGCTT	82935	-----Val-----	319
319	-----Val-----	-----Val-----	-----Val-----	319
82936	CAGTTGAACAGAGATTCGTGATATACATCCAAAGTTTGAGGAACAAACAAGTATTCAAC	82995	-----Val-----	319
320	-----Ser-----	-----Ser-----		

QY	326	-----	326
Db	83176	TGAGGACACACCCCCCAACCTCCAAATATCTCCAACTCGAGGACCTTTGCGTTCCACCA	83235
QY	327	-----Ala-----	327
Db	83236	CAATACCGAGGACATGAACCAATGCAACCGCAGCGCATCAGCAAGAACGAGAATCCAC	83295
QY	328	-----GlyCysVal-----Tyr-----	331
Db	83296	CAACCCACACACGCGATGTGAATCATCCATGGGCCAATCCGTCAACTGCAACATGCAT	83355
QY	332	-----LeuLeu-----	333
Db	83356	GGAATCACCAGAACGATCAACAGACAGACTATTATTTATTAAAGCAGCGCTTAACGAG	83415
QY	334	-----Pro-----	334
Db	83416	AGATCCAAATACATCAACGGGAAGGTGGACGCTTTTCCACAATTAAACAAACCCCATG	83475
QY	335	-----LeuLeuVal-----	337
Db	83476	GGTTTTAGAAATTCCAAATATTCCGGTTTAATTGTACCCATCTTCACGCTCAATGAACA	83515
QY	338	-----Leu-----	338
Db	83536	GTTATGTTTTCTAAATTACAGATTGAGATAGACCCAGTTTGGGGACGGGGAACGTA	83595
QY	339	-----HisLeuLeu-----	343
Db	83596	TGGCGGTGTTTATATATACCATCGTCAAAATAGCTGTAAAAACCATGGACAGTCGTGT	83655
QY	344	Phe 344	
Db	83656	TTTT 83659	

RESULT 11

US-09-661-596A-76/c

 ; Sequence 76, Application US/09661596A

 ; Patent No. 6528066

 ; GENERAL INFORMATION:

 ; APPLICANT: Grose, Charles

 ; APPLICANT: Santos, Richard

 ; TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE

 ; FILE REFERENCE: 140.0011 0101

 ; CURRENT APPLICATION NUMBER: US/09/661,596A

 ; CURRENT FILING DATE: 2000-09-14

 ; PRIOR APPLICATION NUMBER: US 60/153,779

 ; PRIOR FILING DATE: 1999-09-14

 ; NUMBER OF SEQ ID NOS: 80

 ; SOFTWARE: PatentIn version 3.0

 ; SEQ ID NO 76

 ; LENGTH: 124884

 ; TYPE: DNA

 ; ORGANISM: Varicella zoster

US-09-661-596A-76

Alignment Scores:													
Pred. No.:	7,44e-21												
Score:	1725.30												
Percent Similarity:	11.34%												
Best Local Similarity:	9.89%												
Query Match:	71.65%												
DB:	4												
<table border="0"> <tr> <td>Length:</td> <td>124884</td> </tr> <tr> <td>Matches:</td> <td>293</td> </tr> <tr> <td>Conservative:</td> <td>43</td> </tr> <tr> <td>Mismatches:</td> <td>8</td> </tr> <tr> <td>Indels:</td> <td>2618</td> </tr> <tr> <td>Gaps:</td> <td>253</td> </tr> </table>		Length:	124884	Matches:	293	Conservative:	43	Mismatches:	8	Indels:	2618	Gaps:	253
Length:	124884												
Matches:	293												
Conservative:	43												
Mismatches:	8												
Indels:	2618												
Gaps:	253												

US-10-017-084A-523 (1-344) x US-09-661-596A-76 (1-124884)

QY	1	Met-----lys-----	2
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QY	2	-----	2

Qy	124	LysThr---Ser---Arg-----Val---	128
Db	51522	AAAACCTCTCCGATAGACCTGTGATGAGTGTGTAATGGGTACGACGGTTAAAC	51463
Qy	129	---His-----Leu-----	130
Db	51462	ATCGGCATGAAAGTTGTACCGGAAATACCGGTATACGTATAACATCCCATGGTTAAT	51403
Qy	131	-----Ile-----Val-----	132
Db	51402	ATGAACAATATCGAGTCTCCCATATGCAGAACACGTTGCACATAAATACGGCTTCCTT	51343
Qy	133	-----GlnVal-----	134
Db	51342	AAACAATGCCGTGACCAACCAAGTAAATATGTTATTTCTGGCTCTAATCAAGCGGGT	51283
Qy	135	-----Ser-----	135
Db	51282	GCATATCTCAGCGCCGTCGTCTCAACAGCACCGTCAACAGAGAGCCCTTGGCAGCGTGA	51223
Qy	136	---ProLys-----IleVal-----GluIle-----	141
Db	51222	AAACCAACCCGTTCTCGAGCGCGGTTCACGCGGTGTGAGATTGGGGCGCGGAGCT	51163
Qy	142	-----SerSer-----Asp-----	144
Db	51162	GGGTAAACCGTGTTCCTCCGTGAAAGACAAAGACAGATGGATAGATAAATGACTGGTAGT	51103
Qy	144	-----Val-----	144
Db	51102	GAGTTTTAAGTAAATACAGCTCCGGCAAGACCCGTAGTGGCTGCCAGAAACCAACGC	51043
Qy	144	-----Val-----	144
Db	51042	CAGCTGGATGTAAGAAGTTTTTCCACGCTCAAAATTACGCATCAAGGTAAATAAGCAA	50983
Qy	145	Ile-----Ser-----	146
Db	50982	ATCAGAGTCCGTGCTACGAGCGGCCAAAAATGAAATTTCTCCAGATCCAAATCTTCAAC	50923
Qy	147	-----IleAsn-----	148
Db	50922	CCGGCAGCATAAACGTAAACCCAGGGCCCGTGGCACTGTCAGTCTTCTGAGTATT	50863
Qy	149	-----Glu-----Gly-----	150
Db	50862	TTCCATTTTGGTGAAGTACTCGTAAATAATGGGGGTTGTGGCAGGGTCAATGACCACC	50803
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Db	50802	CAAAACCCAGTGTGATACATTAAGAAGAGAGGCTTTTAAACGGGTATTACATATCGG	50743
Qy	152	-----Asn-----Ile-----	153
Db	50742	GAACCAACAACAAATCAGCGGATTACACTTATGTATTAGAAGGCGTGGGTGTGTGTTA	50683
Qy	154	-----SerIleuThr-----	156
Db	50682	CTCAGTAACACTGGCTTTTACAAGATTATCAATCGTTAAACATAAAATGGCGATCAGAAC	50623
Qy	157	-----Cys-----IleAla-----ThrG1	161
Db	50622	GGGGTTTGTAACTCCCTTTTAAACCAAGCATCAGGGATTAAATATAACCCAGAACCGG	50563
Qy	161	YArg-----	162
Db	50562	GCGGGTAGTAACAGAGAAATTTCTTCATAGTTACAAAACTACCATGTCACTCTTCAATT	50503
Qy	163	---Pro---Glu---Pro---	165
Db	50502	TTTGGCCCTTAATGTTTAGATGAAGATGTGCCCATGGAGAACGAAAGGGGTTACGT	50443
Qy	166	---Thr-----Val-----	167

Db 49362 CGAGCTATTAAATTGCATTTATGACCTCGTAAACAGTAGCTCCCGAGTTTGCCACAGG 49303
QY 211 -----Val----- 211
Db 49302 TTATAACATGTGTTAAATTTGATTGGCGTTTATTATGAGAAACTTAATTTCTATATACAG 49243
QY 212 -----Val----- 212
Db 49242 TCTCAAGCTTGATGGTTATGGCAGTATAAACCGTGGGGTCTGTTTAAAGATATGGATGT 49183
QY 212 1-----ArgArg-----ValLysVal----- 217
Db 49182 TGGCAAAATCCGGATTTTCAGCGACGCAAGGTAAAGATCAACGGTCTCATATCTCTGGA 49123
QY 218 -----Thr-----Val-- 219
Db 49122 TATGTATGCAATTGCAACTGAAAAATTAAMAACTCTCGAGTTATAATTAGATTCGGTTGC 49063
QY 220 -----Asn-----Tyr-----Pro----- 222
Db 49062 ACGTGAAGCTCTAAATCGATCCAGAGAGATTGGCCCTACAAAGACATTCGCGGATATTA 49003
QY 223 -----Pro-----Tyr--Ile-----Ser----- 226
Db 49002 CGCTAGTGGACCGAATACACAGAGGAATATTGTGTGAATATTGTATATCAAGACTCGGCTCT 48943
QY 227 -----Glu----- 227
Db 48942 TGTGGGGAACTGTTTAAATATTATACACACCTTGAGTTATCCGGTTCGAAGGT 48883
QY 228 -Ala-----Lys-----Gly-----Thr-- 231
Db 48882 AGCTAGAATTACTTTAACCAAGGCTATTACGACGACAGCAGGTTAGGATTTACACCTG 48823
QY 232 -----Gly----- 232
Db 48822 TTTATTAGACTGGCTCGCTCGAGGATTTATTTACCGATGGGGGATACCCAGCTAC 48763
QY 233 -----ValPro----- 234
Db 48762 TTTTGAATATAAGATGTTATTTCCGATGTCGGGGATGTTGAGGAGAGATGATGAAGA 48703
QY 235 -----Val-----GlyGln-----LysGly----- 239
Db 48702 CGAGAGCGTTTCTCCCACTGGTAGCTCAAGTGGCGGAAATGATAGATATTAAGAGCCAG 48643
QY 240 -----Thr----- 240
Db 48642 GGTTTTGGCCCTGATACGGGATTTTATATCGATCCGGTGGTGGTATTTGCAAG 48583
QY 241 -Leu-----Gln-----Cys----- 243
Db 48582 TTTTATCCAAGTATAATTTCAGGCCCATTAATTATGTTTTCACCGCTAACGTTAAATTT 48523
QY 244 -Glu-----Ala----- 245
Db 48522 TGAGACGGTTAAACGTTTGAATCCATCCGATATGCCACCTTTACAGTTGGAGAAAACG 48463
QY 246 -----Ser----- 246
Db 48462 TCITTTTTTTGTGGCTCTAACGTTTCGAGAAAGTCTGCTGGGTGTTCTTTTAAAGACTG 48403
QY 247 -----Ala--ValPro-----SerAlaGlu----- 252
Db 48402 GTTGGCTATGGCAAGGCTATTAGAGCGCGCATACCCGGAAGTCTTCAGATGAAGCAGT 48343
QY 252 ----- 252
Db 48342 GTTATTAGACAAACAACAGCCGCGATAAAAGTAGTTTGTAAATTCGCTACGTTTAC 48283
QY 253 -----Phe----- 253
Db 48282 TGGAGTTGCGCAGGGAATTTCTGCCATGTTTATACGTAGCGGCCCACTGTCACATAATTGG 48223

QY 254 -----Gln-----Trp----- 255
Db 48222 CCGTCAAAATGTTATTAAAGTACCAGAGATTAATTATTAATAACTGGCGGATTTGAACG 48163
QY 256 -----Tyr----- 256
Db 48162 TTTTATTACAGGTTTCCAGACATTTGAAAGTAGCGTTCTCTCCCAAAAAGCGTACGAGT 48103
QY 257 -Lys-----Asp--AspLys-----Arg----- 261
Db 48102 AAAGGTTATATGAGATACGAGATTCTGTGTTTATCCGATTCAAGGGTGTAGTGTGA 48043
QY 262 -----Leu----- 262
Db 48042 GGGGATAGCTAAATCGCGAGAAAATGGCACATATAATTTCAACGGCTCTGTTTGTCC 47983
QY 263 -----Ile-----Glu----- 264
Db 47982 TCCTATAAAGTTGGAGTGTGMAAAAACTTTTATAAACTTTTGTCTTATAACAAGAAAAA 47923
QY 265 -----GlyLys-----LysGlyVal----- 269
Db 47922 GTACATGGGGTAAATTTACGCGGAAAGGTTTAAATGAAGGGAGTCGACTTGGTTAGAAA 47863
QY 270 -----Lys--ValGlu----- 272
Db 47862 AAACAACCTGCTCAATTTATTAAACGATTATGCCCGCAAACTTGTAGAACCTGTTGTATATGA 47803
QY 273 -----AsnAr 274
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QY 274 g-----Pro-----Phe----- 276
Db 47742 ACGGGCATGCGCTCTGGGATGGCGGGTTTGGACGATAATTGACATGACATCGCCA 47683
QY 277 -Leu--Ser--LysLeu--Ile-----Phe----- 282
Db 47682 GATTACATCACCCAAATTCGATATTAAATGATTTTGTATGACGGCGAGCTTAGTCGTCC 47623
QY 283 -----Phe----- 283
Db 47622 ACCATCCGCTACATAAACCGTCTGCTGCTCATTAAACAGTATATTATAAATAGTAAT 47563
QY 284 -----AsnVal----- 285
Db 47562 GAGACAGGTCAAATCCCAAAAGTTTCGAGAACGATCCCTTATGTTTGTGGCCCCAC 47503
QY 285 ----- 285
Db 47502 AGACGAAGTGGAGCTGTATGCAAAAAGTGTAGCTTTGCTACGTGGAGATCCTTTACAGAA 47443
QY 286 -----Ser-----G1 287
Db 47442 TACCGCAGGTAAACCGTGTGGGAGCAAGCGTAAGTTAATAATCTGACTTAGCGGA 47383
QY 287 u-----His-----AspTyr----- 290
Db 47382 AGATCCCATTCACGTAACATCACACGGGCTGCTTTAAACATTGACTATTATTTTCTCA 47323
QY 291 -----GlyAsn-----TyrTh 294
Db 47322 TCTCATTTGGAGCGGAGTGAACCTTTTAAAGCGTTATTTTGGAACGACACTAAACTCAC 47263
QY 294 r----- 294
Db 47262 AGAAGCGCTTTTAAACGTTTATTCAGACACGAGTGTGTAAAGTAAATGTCAA 47203
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Db 47202 CCGCTTGCAGGCGGAGGCTTTGTTTGTATACACGCCCGCTGCTGGGATAATAATGA 47143


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Db 47082 TATTCCAAAGCAATCTCCATCAAGTTAAGTTCACACATTTTACAGTAACGTCGAT 47023
QY 305 ----- 308
Db 47022 GTTCCAAATGGATGGACACACAGTCTCTGTTTGTCTGTCTGGGTTCGGACATACCCGACAGT 46963
QY 309 ----- 311
Db 46962 AAAAAATGTTGTCTGCCAAAGTGTGGGACTATTTTATACCCCGGACACGGCGCTGTATA 46903
QY 312 ----- 312
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QY 313 ----- 313
Db 46782 CTCATAATATGATACATAAAAAATATTCGGTGTGCCAATACGCTCGACATAGGGT 46723
QY 314 ----- 314
Db 46722 TCAGCGGACGCTGCTTGCAATGTTGGCTCGTCTGATAGCGCCAAATGGATGCAAGAAC 46663
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Db 46602 TCGGTTGACATAGACGCGGTTCTCCAGATGAGTGCATGTCGGACATAAATCTCCGAGA 46543
QY 321 ----- 322
Db 46542 CCTAATGATACCCATTCGGGATACGACAGGAGTATTCGCCCATCTGCTGACCCAAAG 46483
QY 323 ----- 326
Db 46482 TTAACGGAAGGGTGACAGGGGTCGTTTAATAATTGGCACGATTAAGCTCTAACGGTA 46423
QY 327 ----- 329
Db 46422 GCTAGTCTCTCGGGGGACCTTGCATGTAATAATAATGCGGTACACAGACCGC 46363
QY 330 ----- 331
Db 46362 TCCTTTGACATAAGTTTCTCCTGAATGTTTGACGGCGCATGGCGTTCTGAGCGTACA 46303
QY 332 ----- 333
Db 46302 CGCATCGAAGGCCGCTCCGAGATACGGATTTATATCGCCTAGACATACATTCGATAGGGT 46243
QY 334 ----- 334
Db 46242 GTGTTGAGGAGACAGCATATTGCATGCTCGAAGCATTAAGTCTCCATCTCGTAT 46183
QY 335 ----- 338
Db 46182 GAATGCGGCATTTGCGGTTGTTTGTGCGTGAAGAAATCTGTTAGGCTTTAAATGCATACGC 46123
QY 339 ----- 339
Db 46122 CAATGTCCAAGGCCACACATACACACCTTCAAATCTGTTTGTGACGCCAGTGGGC 46063
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QY 344 -Phe 344
Db 46002 GTTT 45999

RESULT 12
US-09-913-514-1/c
; Sequence 1, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccin
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913.514
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00678
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 124884
; TYPE: DNA
; ORGANISM: Varicella virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(124884)
; OTHER INFORMATION: Dumas Strain
US-09-913-514-1

Alignment Scores:
Pred. No.: 7,44e-21 Length: 124884
Score: 1725.30 Matches: 293
Percent Similarity: 11.34% Conservative: 43
Best Local Similarity: 9.89% Mismatches: 8
Query Match: 71.65% Indels: 2618
DB: 4 Gaps: 253

US-10-017-084A-523 (1-344) x US-09-913-514-1 (1-124884)

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Db 54822 CCGGAGAAACAGCTTTTAATAATACGAACTGTCAACAGTTAGCGCTAACCGATATA 54763
QY 3 -----Thr-----Ile-----GlnPro----- 6
Db 54762 AAAAGCGACACGCCACCTTGGATCAGTCGAGTAGCAGTTTCAACCTGAAAGATGTACG 54703
QY 7 ---Lys-----Met----- 8
Db 54702 TATAAACTTGACCCAGTAGAACCAACATGTTTCGATTAATATATCCATTCATGTTATCGG 54643
QY 8 ----- 8
Db 54642 GCTGTTACTGTCCACTGGACTGTAACTGAATGTTGGAGACACACTATATTACAGGTCA 54583
QY 9 -----His-----AsnSer-----Ile----- 12
Db 54582 TATGGGTAAGGACTACACACAAAAAAGAAAAACACACAGAAATATGTAATATTGACTGT 54523
QY 13 -----Ser-----TyrPala----- 15
Db 54522 TTATTAGTACACTCACCGCGTGTGGGCTTTAAATTTGGATAAAGAGGGAGGTTAAATCAT 54463
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QY 16 -----Ile 16
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QY 17 Phe -----Thr
Db 54402 TTCGGGGGTCGTTTAAGACACGGGACAGTTGACCTGGAATGTTTGACCTGAAATGTT 54343
QY 19 -----GlyLeuAlaAla----- 22
Db 54342 TAATACGTTAGATGTGTGTCATGCTTGTGTTACAGAAATCAAATTAATAATCTAGGTT 54283
QY 23 -----LeuCysLeu----- 25
Db 54282 TGTGGGGGTTCCCATCTCCCGCTGCTGTTTTTTCATCTAGAACTCTTTACTGCTCTAG 54223
QY 26 -----PheGlnGly----- 28
Db 54222 AGCGCCTTCTACGGTCCAGGGCGTTTCAGGGTTTGGATAATCTGTCGTGTAACCTCTC 54163
QY 29 -----Val-----ProVal----- 31
Db 54162 CAAGTCTCTGGCTAAAAACATCGTCTGTAAGACTTTAACCGAGTCGTCAAATGCCATATG 54103
QY 32 -----Arg----- 32
Db 54102 TTGTGCTCGAGCGCCCACTGCACGACACCGTGGCGTATATGGCTAAATTAACCATGGC 54043
QY 33 -----Ser----- 33
Db 54042 CCGCCACTGACAAATATACCGGAACTTGTGTCGATAGGTGTTTTCTCGATTTCCCGA 53983
QY 34 -----Gly-----Asp-----Ala 36
Db 53982 CGAGGGACCTGTTACGGGGCGAGATAAAACCTCTCTAGGACATGCTATTATAAAACGGCG 53923
QY 37 Thr -----Phe----- 38
Db 53922 AGTCGGATCAAAATGTAATAGCGGCATACATTTTTTACCCCGTTTTAAACCGCTCCAATT 53863
QY 39 Pro -----Lys----- 40
Db 53862 CCCTGCCTGAAGACGCGGTTGTTTCCTCGCGCTCCGTGATTAATTAATGCTTAATCC 53803
QY 41 -----Ala-----Met----- 42
Db 53802 TAAACGACCATGGACGTTGATTCATGCGCGCGGACTAAATGAGTTGAAGTAAAGC 53743
QY 42 ----- 42
Db 53742 CGTAGTCCATAATCCCGTAAGTTTTTCGTTTTTTTCAAGAGCGCCTTTGCTGGGTTTC 53683
QY 43 -----Asp-----Asn-----ValThr 46
Db 53682 TATGTCCGCGCGGACGTCATCTTTACGAATCCAATGCAAAACGGATGATGGTCACG 53623
QY 46 ----- 46
Db 53622 CGGGCGCTGCGCACCCGTAATATAGAGTTAAGGTATTTATAGGTACTGTGAATGATC 53563
QY 46 ----- 46
Db 53562 GCAGTATTTAAGAAATAGATTTGCCATATAAACTGGGCTAATTTCTCCTATGCGAGTTGG 53503
QY 46 -----Val-----Arg-----GlnGly 50
Db 53502 GGGTAGATTAATAAGTTTATTTGTCGATATTCCTCGGTAAACCGTTTAAACAGCTGCAAT 53443
QY 47 ----- 50
Db 53442 AGTGTATATCTCTTCGTGTGAAGTTTTATCTGCGCGCATCTGGTTGCGTTGTAACAGGT 53383

QY 50 ----- 50
Db 53382 CCAAAACCACTCGGGTTCGGGGATTTACTGTTTGGTGCATACCCCGAGGAAATAACAG 53323
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Db 53322 GCGGTGAACCTGTTTAAGCAAAAACCCCTAGGCCCCCGGTGTAACATATCCACTCTTTTTC 53263
QY 53 -----Ala-----Thr-----LeuArg----- 56
Db 53262 TTGGCCTTGGTAGGCACTTGCAGGCTACAAGCCTTGCCTGGGCTGCTCAGAGAGAT 53203
QY 57 CysThrIle-----Asp-----Asn----- 61
Db 53202 TGTACAGTTACGTGAAAAAACGACCTATTTTTAACCTGATATCCGGAATAACTTCCAC 53143
QY 62 -----Arg-----Val-----Thr-----ArgVal----- 66
Db 53142 GCTTACGCGCGCTAAATCCCATCAAGGTACGCCCGCGCGCGCTCTTGTCCCAATGT 53083
QY 67 -----AlaTip-----Leu 69
Db 53082 CGGATTTGGCGCGGATACAGGACCTTCAGATAATGTTACGGTTATAGAGCGTGTGATAT 53023
QY 70 -----AsnArg----- 71
Db 53022 AAACCCCCCAATTAACAGGTCAACAAACGCGCGCCGCAAAACAGGTTTGAATTTGTTACG 52963
QY 72 -----Ser-----Thr----- 73
Db 52962 AAGTTTCGCGCCCTCAACTTGTGTCCTCGTAAATAACAATGACATGCGTTAATGCTAA 52903
QY 74 IleLeuTyr----- 76
Db 52902 GTCTTGTACACGCGTAGTGTGTTTAACTAAATAATGGTAATGGGACAAATGCG 52843
QY 76 ----- 76
Db 52842 TCCTGATATGATCAAAAGTTAAACGCCATTAAGTGGTGGCTTCGGATAATCCTTCACG 52783
QY 77 -----AlaGly----- 78
Db 52782 GATCTTATATCCGGGTCTCAACCAACACTTTCATAAATGTTGTTGTTCTGTTCTAT 52723
QY 79 -----AsnAspLys----- 81
Db 52722 ACGCGACGCGAGTGTCTTAATATGCGACGAAACGTTGGATGATCCACAATGACAGCGA 52663
QY 82 -----Trp----- 82
Db 52662 TAGTCCCTCGGAAGAACATGGGGCACCGCGATCCAGTAGTCGCTCTTGTCTAGATCGAT 52603
QY 83 -----CysLeu----- 84
Db 52602 AAACAGCGTTCTAGTGTAGCCCTATAAGTGTCTCTGATGTTGCCCTTTCCTGCTCCGT 52543
QY 85 -----Asp----- 85
Db 52542 TTGATCCCGGGTTTTTGAAGGATTAATAATGAGCATAGTTTCTCTAGAGATCGCAGTC 52483
QY 86 -----Pro----- 86
Db 52482 GCTATATGGCTGTTCAATGTTTCCAAACACCCCAATAGTTTGAAGGTGGCTGTGTCGCA 52423
QY 87 -----Arg-----Val-----Val 89
Db 52422 TCGGGCATCGGTGTCTAAGTGTGCTGTTGTTGTTGAGCGCATACCGCGCGGTGTG 52363
QY 90 LeuLeuSer-----Asn----- 93
Db 52362 TTTTTCATAAAACTACATGGAATTTTCAGAGTCAAAGGTCCCGGTAAACATATTATTAACGC 52303
QY 94 -----Thr----- 94

Db	52302	ATCCCCGTGACCCCTGTAAACGCCACGCGGTACAGCGTTCCTAGATAAAAAAGCAGTCG	52243
Qy	95	---Gln---Thr---Gln---	97
Db	52242	CGCCACAGGGGTGCTCCAAATCCACAAATGAGTGCCCAATAATCCACGCTAAACTCTGT	52183
Qy	97	---	97
Db	52182	GTTTGATGAACCCGTAGACTGACTGGATAGAAACGTGGCCATCTCGATCTGTTGGGGATT	52123
Qy	98	---Tyr---SerIleGlu---	101
Db	52122	CGCAGCTAAATGAGGTCCGGCAAACTGGTAAATCGATTAAATGATGGAACCCGCTCCCC	52063
Qy	102	---IleGln---	103
Db	52062	ATCCTTGGCTTCGGTCATCCCGCTATCTCCACCTCAGTTAGATACACGCAAGATTGG	52003
Qy	104	---Asn---Val---Asp---	107
Db	52002	GCTGAAACCAATCGCACCAATGACCCCGGCCACACGAGCGGTATATGACCCGAGCGGT	51943
Qy	108	---Tyr---Tyr---Asp---	109
Db	51942	TAGCCTTGGCAAGTGCCCTCATGCCTATAAATGATGGCCATCTTTGATATCTGTTGG	51883
Qy	110	---Glu---	111
Db	51882	AGTTTCTTCGTAATTCAGTGTGAATATAACTTCTGGTCAAGGCTGTGTACGCGC	51823
Qy	112	---Pro---Tyr---	113
Db	51822	CATAATAGACGCAACCGTCTTCAAACCCCGCATGGGTAGGCTTAGCGTGAGTT	51763
Qy	114	---	114
Db	51762	GACATCGTTTCAGCGGCTCCAGGGCGGTAGTGTTCACCTTGAAGAGCCTGAAATA	51703
Qy	115	---Cys---Ser---Val 117	
Db	51702	CGTGTACGTAATGTCAGGGGGAGTACTGCCCTCGTGATTTTCATCAAAAGCAAGGTG	51643
Qy	118	---Gln---ThrAsp---Asn---His---	122
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Qy	123	---	123
Db	51582	AATAACACAGTCATGTAAATGGCAACCCGGTGTATATAAAGGGTGTGGGTATAC	51523
Qy	124	LysThr---Ser---Arg---	128
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Qy	129	---His---Leu---	130
Db	51462	ATCGGCGATGAAAAGTTGTACCGGAATAACCGGTATACGTATACATCCCCATGGTTAAT	51403
Qy	131	---Ile---Val---	132
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Qy	135	---Ser---	135
Db	51282	GCATATCTCAGCGCGGTCTCAACAGCACCGTCAACAGGAGGCCCTTGGCAGCGTGA	51223
Qy	136	---ProLys---IleVal---GluIle---	141
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Qy	142	---SerSer---	144
Db	51162	GGTAAACCGTGTTCCTCCGTGAAAGACAAAGACAGATGAGTGAATGACTGGTAGT	51103
Qy	144	---	144
Db	51102	GAGTTTAAAGTAATACCAGCTCCGGCAAGACCGGTAGTGTCTCCAGAAACCCGC	51043
Qy	144	---	144
Db	51042	CAGCTGGATGATAAAGTTTTCACCGTCAAAATTACGCATCAAGGTATAAAGCAA	50983
Qy	145	Ile---Ser---	146
Db	50982	ATCAGATCCGTCTACAGCGGCCAAAATGAAATTTCTCCAGATCCAAATCTTCAAC	50923
Qy	147	---IleAsn---	148
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Qy	149	---Glu---	150
Db	50862	TTCCATTTTGGTGAAGTACTCGTAAATAATGGGGGGTGTGGCAGGGTCAAAATGACCACC	50803
Qy	151	---Asn---	151
Db	50802	CAAAACCCAGTCTCGTCAATTAAGAGAGAGGCTTTTAAACGGGTATTACATATGCG	50743
Qy	152	---Asn---Ile---	153
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Qy	154	---SerLeuThr---	156
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Qy	161	Yarg---	162
Db	50562	GGCGGTAGTAACAGAGATTCTTTCATAGTTACAAACTACCATGTCTATCGTTCAATT	50503
Qy	163	---Pro---Glu---Pro---	165
Db	50502	TTTGGCCCTTAAATGTTTAGATGAAGATGTGCCCATGGAGAACGAAGGGGGTTCAGT	50443
Qy	166	---Thr---	167
Db	50442	CGGTACACTTAGTCGACCGCCTAAAGTTTACTGTAAATGGAAGAAAGTTCGATTCTGGA	50383
Qy	168	---Thr---Tyr---Arg---	170
Db	50382	TTTTCGTTGTCAGCGCCCTGGCTAGACGCGTGAATATTTGGGGGAAATCGACTTTCG	50323
Qy	171	---	172
Db	50322	TGGGGATAAGTTTGACCCCGCTTTTAAACATTCATGTATGATATTTGTGGAACAAC	50263
Qy	173	---Ser---	174
Db	50262	AGNAGCCGCTTAATGGAGATGATCCCGGTTTGCAACTGCAACACGACCGCTTGGTAC	50203
Qy	175	---	178
Db	50202	CGTTATTACTTTACTTGGCATGTCCCGATGTGAAAAGAGGGTGCAGTTTCATGATACGG	50143
Qy	178	Y---Phe---	180
Db	50142	CATCTGTCAATATTTTATATAAACAAGCCGAGGTGGATACCGCTTGTGGCATACGTTTC	50083

QY 181 ----SerGlu----- 182
Db 50082 CGGTAGCGAGTATCTGTATTACTTGCAGAGTGTTCACGAGTCTTATGATACACAAAA 50023
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Db 50022 TGATGCAACGTTAAATGGAGACAAAGAACGCTTTTCATGTGTACCTCGTTTAAAGAGCAGTC 49963
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Db 49962 TCCAGAAAGCTTCGGCTTGAGGTATTGAGCGCACAGAGTGTATTACTACGATACACA 49903
QY 185 ----TyrLeu----- 186
Db 49902 GCCATGTGCGTTTTTACAGGGGTGATTCTCCCTCATCTAAATTTACAAATTTATCTTTGTGA 49843
QY 187 ----Glu----- 187
Db 49842 TAACCTTCACCGGAGTTGAAAGATGAAAGGTGCGGTAGACGCTACCACTCGTTTCT 49783
QY 188 ----Ile-----Gln-----GlyIle----- 191
Db 49782 AATGATAAATCCCGCTTGTGTAGTTTGTGTGTATCACTAAACCTGAGTGTATGG 49723
QY 192 ----ThrArg-----Glu----- 194
Db 49722 GGAACGTGTTCGAGTCGACCGGCAAGTCGCCAATTAAAGTAAAGCGAGCTGGAATTGA 49663
QY 195 ----Gln-----SerGly---AspTyr----- 199
Db 49662 CTGCATGCGATAATCTGACGGCTATACCAACGATGACTCATGGCTGACTACAAAGTT 49603
QY 200 ----GluCys---Ser---AlaSerAsn----- 205
Db 49602 GTTATGTTTCGATATTGAATGAAATCAGGAGGATCTAATGAGCTGCGGTTTCCCGATGC 49543
QY 205 ----- 205
Db 49542 AACACATCTGGAGGATCTGTAAATCCAAATTTCTGTCTATATATTCATCCCTCGACA 49483
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Db 49482 GTCTTTAGACACATTTTACGTGTTTCCCTTGGCTCTTGTGCTGTGCTGAGTTTGTATGTAAT 49423
QY 206 -----Asp----- 206
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Db 49362 CGAGCTAATATGCAATTTATGACCCCTCGTAAACACAGTACGCTCCGAGTTTGCACAGG 49303
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QY 212 ----Va 212
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QY 212 1-----ArgArg-----VallysVal----- 217
Db 49182 TGGCAAAATCCGGATTTTACGCGAGCAAGCAAGGTAAAGATCAACGGTCTCATATCTCTGGA 49123
QY 218 ----Thr-----Val--- 219
Db 49122 TATGATGCAATTTGCAAACTGAAAAATTTAAAACTCTCGAGTTATAAATTAGATTCGGTTGC 49063
QY 220 ----Asn-----Tyr-----Pro----- 222
Db 49062 ACGTGAAGCTCTAAATGAGTCCAGAGAGATTTGGCCCTACAAAGACATTTCCGGATATTA 49003

QY 223 ----Pro-----TyrIle---Ser----- 226
Db 49002 CCCTAGTGCACCAATACACAGAGAAATTTATGGTGAATATGTATACAAAGACTCGGCTCT 48943
QY 227 ----Glu----- 227
Db 48942 TGTGGGAAACTGTGTTTTTAAATATTATACACACCTTGAGTTATCCGGGTTCGAAGGT 48883
QY 228 -Ala-----Lys-----Gly-----Thr--- 231
Db 48882 AGCTAGAATTACTTTAAACCAAGGCTATTACACGACAGCAGGTTAGGATTTACACCTG 48823
QY 232 -----Gly----- 232
Db 48822 TTTATTAGACTGGCTTCGCTCGAGGATTTATTTTACCCTGCGGATACCCAGCTAC 48763
QY 233 ----ValPro----- 234
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QY 235 ----Val-----GlyGln-----LysGly----- 239
Db 48702 CGAGACGCTTCTCCCACTGGTACGTCAAGTGGCGCAATGTAGGATATAAAGGAGCCAG 48643
QY 240 -----Thr----- 240
Db 48642 GGTGTTTGGACCTGTATACGGGATTTTATATCGATCGGTGGTGTGTTTGGATTGCAAG 48583
QY 241 -Leu-----Gln-----Cys----- 243
Db 48582 TTTATATCAAGTATAAATTCAGCCCATTAATTTATGTTTACCACGCTAACGTTAAATTT 48523
QY 244 -Glu-----Ala----- 245
Db 48522 TGAGACGTTTAAACGTTTGAATCCATCCGATATGCCACCTTTACAGTTGGAGAAAAACG 48463
QY 246 ----Ser----- 246
Db 48462 TCTTTTTTGTGCGCTCTAACGTTGAGAAAGTCTGCTGGGTGTTCTTTTAAAGACTG 48403
QY 247 ----Ala---ValPro-----SerAlaGlu----- 252
Db 48402 GTTGGCTATGCGCAAGGCTATTAGAGCGCCATACCCGGAAGTCTTCAGATGAAGCAGT 48343
QY 252 ----- 252
Db 48342 GTTATTAGACAAACAACGCGCGATATAAAGTAGTTTGTAAATTCGCTGACGTTTAC 48283
QY 253 ----Phe----- 253
Db 48282 TGGAGTTGCGCAGGGATTTCTGCCATGTTTATACGTAGCGGCCACTGTCTACATAATTGG 48223
QY 254 ----Gln-----Trp----- 255
Db 48222 CCCTCAATGTTTAAAGTACCAGAGATTATATCAATAAAGTGGCGCGCATTTGAACG 48163
QY 256 -----Tyr----- 256
Db 48162 TTTTATTACAGCGTTTCCAGACATTGAAAGTAGGTTCTCTCCCAAAAAGCGTACGAGGT 48103
QY 257 -Lys-----Asp---AspLys-----Arg----- 261
Db 48102 AAGGTTATATATGAGATACGGATTTCTGTGTTTATCCGATTCAAGGTTGTAGTTGA 48043
QY 262 -----Leu----- 262
Db 48042 GGGGATAGCTAAATCCGCGAGAAATGGCACATATAATTTCAACGGCTCTGTTTGTGCC 47983
QY 263 ----Ile-----Glu----- 264
Db 47982 TCCATATAAGTTGGAGTGTGAAAAAATTTTATAAACTTTTGTCTTATACAAAGAAAAA 47923
QY 265 ----GlyLys-----LysGlyVal----- 269

46842	DB	AACCTCCGCGATCTCCATCAGGATAAAAAAGTACGCGTATATCTCGCATGCCCCCTCC	46783
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46782	DB	CTCATAATGATACATATAAAATAATTCCGGTTGTGCCAATACGCTCGACAATAGGCGT	46723
314	QY	-----Gly-----	314
46722	DB	TCAGCGGCGCTGCTTCATGTTGGCTCGGCTCGATAGCGCAAAATGGATGCAAGAAC	46663
315	QY	-----Ala-----ValSerGlu-----	318
46662	DB	ACAGGATATTCGTATATGTTGTTAAGCTGCTGAACATATGCTAGTATCAGAGCCGCCGA	46603
319	QY	-----Val-----Ser-----	320
46602	DB	TCGTTTCGACATAGACGCGGTTCTCCAGATGCAGTGCATGTCGGACAATAACCTCCGAGA	46543
321	QY	-----Asn-----Gly-----	322
46542	DB	CCTAAATGATAACCACTTCGGATAACGACAGGCGATTATCGGCCACTGCTGACCCCAAG	46483
323	QY	-----Thr-----Ser-----Arg-----	326
46482	DB	TTAAACGGAAGGTGACAGGGGTCGTCTTAATAATTGGCAGGATTAAAGCTCTAACGGTA	46423
327	QY	-----AlaGly-----Cys-----	329
46422	DB	GCTAGTTCTTCGGGGGGACCTTCGATGATTAATTAATAATGCGGTACACAGACCGC	46363
330	QY	-----Val-----Trp-----	331
46362	DB	TCCTTTGACATAAGTTTTCCTCGAATGTTTGACGGCGCATGGCTCTGGAGCGTACA	46303
332	QY	-----LeuLeu-----LeuLeu-----	333
46302	DB	CGCATCGAAGCCCGCTCCGAGATACGGATTATATCGCTAGACATACTTCGATAGGGT	46243
334	QY	-----Pro-----Pro-----	334
46242	DB	GTGTTTCGAGGAGACCGGATATTGCATGTCGTCGAACATAAGTCTCCATCTCGTAT	46183
335	QY	-----Leu-----Val-----Leu-----	338
46182	DB	GAATCGGCAATTGGCGGTGTTTGGCTGGAAAAATCTGTTAGGCTTTAAATGCATACGC	46123
339	QY	-----His-----	339
46122	DB	CAATGTCCACAGGCCAGCACATACAGACCTTCAAATCTGTTTGTGACCCAGTTGGGC	46063
340	QY	-----LeuLeu-----Leu-----Lys-----	343
46062	DB	TTTATATAACTCCAACACTTCCTTATCCGCGGTTGTAGGATGGCAATAAAAAATTTTAGG	46003
344	QY	-----Phe 344	
45002	DB	GTTT 45999	

RESULT 13
US-09-913-514-2
; Sequence 2, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAWACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANISHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live
; FILE REFERENCE: 0216-0454P
; CURRENT APPLICATION NUMBER: US/09/913,514
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: PCT/JF01/00678
; PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: JP 2000-62734
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 125157

TYPE: DNA
ORGANISM: Varicella virus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(125157)
OTHER INFORMATION: Attenuated Oka strain
US-09-913-514-2

Alignment Scores:
Pred. No.: 8.62e-21 Length: 125157
Score: 1722.90 Matches: 284
Percent Similarity: 11.90% Conservative: 53
Best Local Similarity: 10.02% Mismatches: 5
Query Match: 71.55% Indels: 2491
DB: 4 Gaps: 245

US-10-017-084A-523 (1-344) x US-09-913-514-2 (1-125157)

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QY 1 Met-----Lys-----2
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QY 2 -----2
Db 32483 GTGGAACGCTGTTGTGCTTATATTATTCGAACAAGACGCTTGATGCCCTTCGGCA 32542
QY 3 -----Thr-----IleGln-----5
Db 32543 ACAATAGCTTTGCTCTTTTGATACACGGGGAATACAGCAAGCCTTGCTATCTTCATGG 32602
QY 6 -----Pro-----LysMet-----8
Db 32603 GCTCGGNTTATGATCCGGAACGCTGCCAATGCAGATGGATATCGCAAAACTATCT 32662
QY 9 -----His-----9
Db 32663 GCTCTTATAACAATATTAGAACCTTTTACCGGTACACACCCCCAGTACTTTTACCATCT 32722
QY 9 -----9
Db 32723 CACGTTTCTACTATAGATTCCCTTATATGCGAACTTCATCGCACTGTTGGCATTTGCCGTT 32782
QY 10 -----AsnSer 11
Db 32783 GACCTGCTTCCACGACGTCGTCCTTTGGTTCTCTGACCGTCCTTCTATTACAAATAGC 32842
QY 12 Ile-----Ser-----Tyr-----14
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QY 14 -----14
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QY 18 -----Thr-----18
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QY 19 ---Gly-----Leu-----Ala-----Cys 24
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QY 37 Thr-----37
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QY 46 -----ThrValArg-----Gln 49
Db 33683 AAAATAACGACAACGCTCAGAGACGTAATTTTCAGAGCTCCGACGTGATATAGGACAA 33742
QY 50 -----Gly-----50
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QY 50 -----50
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QY 53 -----Ala-----Thr-----54
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QY 55 -----LeuArg-----56
Db 34103 CTGGACCGCGCTCAGGTCTGTCTCATGTTTAAAGACATCTTTATCGTTTTTGCATATGACA 34162
QY 57 -----Cys-----57
Db 34163 TATGCGCATGGAATTAATGCAACCCCTGTCTCATCAGACATGATTTGATGATGTTTACAAGAG 34222
QY 58 -----Thr-----58
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Db	34343	TGCGTTTTGTCTAGAATATACGGCGATAGCCATTTTTTTTACCGTTCACAGACAGGGTTTT	34402
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Db	34403	ATGTGCACACAAATCCCGCTAGACGGTTTTTCGATGATGTGTGATGGAGCGTGAAGAG	34462
Qy	72	Ser---ThrIle-----LeuTyr---AlaGlyAsn-----	79
Db	34463	TGCTATACAAATTATACTGTAGACTCAACGGGAATGGCCATCTATCGTCAGGGAAACATA	34522
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Db	34523	TCTTTTATTTTTGATCCACATGGCCATGGGACTATAGACAGGCTGTAGTTGTCGGGTG	34582
Qy	80	-----Asp-----	80
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Qy	81	Lys-----Trp-----	82
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Db	34703	GAAGAAGCGTATCTTCGGCAGTAACGCTTATATACGGAAGCTGTGATACATATTTTACA	34762
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Db	34763	GATGAACAATATTGCGAAAACTGGTTACAGCTCAACATCCGTTGCTTCTTTCACCTCCT	34822
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Db	34823	AATTCACGACAAATTGTCTTAATAATCGTCTATAGTACCTCTTACCAGAAACGTTGGT	34882
Qy	84	-----LeuAsp 85-----	85
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Qy	86	ProArg-----Val-----	88
Db	34943	CCTAGATGTAGTTACAGCGAGGTTGTATCTTGGCATGCGGTTCTAGAAAAACACCTCGACT	35002
Qy	89	-----ValLeu-----	90
Db	35003	GGGTCTGGCGTTTGGATTCGTGTAGAGCGGCTCTTCATGGACTCTCTCTTCAGC	35062
Qy	91	-----Leu-----Ser-----Asn 93-----	93
Db	35063	GAGGAAATTTAGCTTGTATCGAGATGGCTTGTGTAATAATAACATATCCACGGATAAT	35122
Qy	93	-----	93
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Qy	94	ThrGln-----	95
Db	35183	ACACAAGTGGCAATGTATTATACCCGGCTACGAGAAGTTGCTAACACCCAGAGTTGTG	35242
Qy	96	-----Thr-----	96
Db	35243	TTAAATGTATCCAATGTAGATACGCTGAATCCAGTCCACTTTTTTTCACGGAACATGAAT	35302
Qy	97	-----GlnTyrSer-----	99
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Qy	100	-----Ile-----GluIle-----	103
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Qy	104	Asn---Val-----Asp-----ValTyr--- 108	
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Qy	109	-----AspGlu-----	110
Db	35480	ACAAGGCCCTTGGTCATGCCAGACGAAAGGATCCATTGGAGCTTTTATTAACTCACC	35539
Qy	110	-----	110
Db	35540	ATTTTTCGTTTAAACGGGATTTTGTGTGAAAAATGGAAACACGTACATCATGTGTCTACA	35599
Qy	111	-----GlyPro-----	112
Db	35600	AGCGTTGTATCAGACTTTTATAGGTCCCTTGGGAAAAATTTTAAACAGGATTTCCCTCCGCC	35659
Qy	113	-----Tyr-----	113
Db	35660	CGCGAACTTATACGGTTTACAAAGTTTATATTAACAAACATGCCGGGGCGGGAATATGCT	35719
Qy	114	-----Thr-----CysSer-----	116
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Qy	121	-----Asn-----HisPro-----	123
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Qy	124	LysThr---Ser---Arg-----Val-----	128
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Qy	129	-----His-----	129
Db	36020	GAGACAGCTATATGGTGAAACACACCGCGCTTGTTCAGTGTAAAGCTTTAGAGAAAT	36079
Qy	130	Leu-----Ile-----ValGln-----Val-----	134
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QY 190 -----Gly----- 190
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QY 193 ---Arg-----GluGlnSer----- 196
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RESULT 14
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; Sequence 19, Application US/08008216
; Patent No. 536887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barthorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVULVUS ARVENSIS PLANT CELLS
; CLONE: CLONE 7
; FEATURE:
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; LOCATION: complement (937..2262)
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OTHER INFORMATION: /label= ORF5SUBSEQUENCE
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NAME/KEY: misc feature
LOCATION: complement (18177..18743)
OTHER INFORMATION: /label= ORF17SUBSEQUENCE
FEATURE:
NAME/KEY: misc feature
LOCATION: complement (19031..19390)
OTHER INFORMATION: /label= ORF18SUBSEQUENCE
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Score: 1721.10 Matches: 293
Percent Similarity: 11.04% Conservative: 44
Best Local Similarity: 9.60% Mismatches: 6
Query Match: 71.47% Indels: 2709
DB: 1 Gaps: 241
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QY 3 -----Ile-----Thr-----GlnProLysMet----- 8
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QY 34 GlyAspAla-----Thr----- 37
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Db 8112 AGCCATGCGAAACACGACTCTGTTTGTATCCCGTGGTGAATAGCAAGAGGCGGG 8171
QY 150 ----- 150
Db 8172 AGATTGAGGTATGCTTGAACACAGCTCATTCGGTGTGTTTTCACAGGTCATCATGGC 8231
QY 151 ----- 151
Db 8232 GGCAGTCTGAGCGCGCTACAGTTGATACAGACTGGCGGGGATGAGACTTCTCTCAGC 8291
QY 152 ----- 155
Db 8292 TACAATATCGAACCCCGCTCGGAAACTCGTGTGCGCTGTCAATTACAGACCTTCATG 8351
QY 156 ----- 156
Db 8352 GTCAGAGCAAAAGTTTGGTTTAACTCCGGCATCCAGCAGTGATATGACCGATGGG 8411
QY 157 ----- 158
Db 8412 CTTGTGCGTGTGTTGCAATGACATCGCAATCGCCAGCTGGAGAGGCGCTTGTGTT 8471
QY 159 ----- 161
Thr-----Gly

Db 8472 TTTCACATGCTTTGGATGACTATCTATCCCGCGGATCGAGCATCATGACAGAAGGA 8531
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162 Arg-----ProGlu----- 164
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Db 8532 CGGTGCTTGGAAATGGTCAGGAGCTTGTCTGCTGCTTCTGAACTGGCTTGTACCTG 8591
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Qy 165 --ProThr-----Val-----Thr----- 168
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Db 8592 GTCCAGTCAACGAAGACTACGAACGATATGCTTTCGACGACCACTTAACGGATGGTTT 8651
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Qy 169 -----TpaIq----- 170
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Db 8652 AAGGAGCTTTGTGGAGGAAAAATCTCTGAAAAAGTCAATATCCAGGATCGCT 8711
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Qy 171 -----His----- 171
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Qy 171 ----- 171
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Db 8772 GTCACCGAGCTCGTTCGAGGAGCGGTGAAGGGGCGCATCAAGCGGCTGCGCCGTC 8831
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Qy 172 Ile-----Ser-----Pro----- 174
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Db 8832 ATCCGACACCGGGGAGCTCTCTTCACTCCAAACCGGTGGACTGGAATAAAAAATAG 8891
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Qy 175 Lys-----Ala-----ValGly----- 178
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Qy 179 -----Phe-----Val-----Ser----- 181
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Qy 182 -----Glu----- 182
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Qy 183 -----Asp----- 183
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Db 9072 AATTGGAATTCAAACGATTCCTTGATGCTATCTTCGTATGATGATGATGATGATAAAG 9131
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Qy 190 -----Gly-----IleThr----- 192
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Qy 215 -----ValLys-----Val----- 217
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Qy 219 -----Val-----AsnTyr-----Pro----- 222
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Db 10272 ATACTGCAATATATGTTAGTAGATTAGTATGATGATGATGATGCTGTTTTGGCAA 10331
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Db 10332 AATTACAGCAGGATCAACACAGAGAATAATTTAGTACAGAAAATAGTCAACACA 10391
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Qy 223 -----Pro----- 223
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Db 10452 ACTTATGACAACTCATAGATAAGTTGCCGTGCGAGGGAGTTCAAGTCGCTTTAGGC 10511
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Qy 231 -----Thr--Gly--Val-----Pro 234
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Qy 235 -----ValGly----- 236
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Db 10632 GAGGCGATTTTGGTGAATTTGTTGTCGCCCAAGCTACACATCATAGGGCGGTTTTTC 10691
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QY 237 -----GlnLys---Gly-----Thr----- 240
Db 10692 AGTCCCTCGCGCAGAAAGGTCAGAGTACTCTCTCCCGTAAACGTTGGTCACTTT 10751
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QY 254 ----- 254
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QY 280 -----LeuIlePhePheAsn----- 284
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QY 293 -----TyrThr-----Cys----- 295
Db 12012 GCTTTTAAGAGACCCATAATAAATGCGAGCTGTGTTGTTGGTGGCAGCAGGCTTAA 12071
QY 296 -----ValAla---Ser---AsnLys--- 300
Db 12072 CGTGGGTTTAGCTTGACAAAGTAGCGCTTTCCGAGCATATAATAAAGTAGCGGGTG 12131
QY 301 -----Leu---Gly-----His----- 303
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QY 306 ---AlaSerIle----- 308
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QY 313 -----Pro----- 313
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QY 316 ----- 316
Db 12732 CAACCTTCCCGGTACCAGCATGATGTGACTCTCGATGAGGTCAATAGAGGCTCAGGCA 12791
QY 317 -----Ser-----Glu-----Val--- 319
Db 12792 AGCATCAGGTTTTTTCGTTACGGGATCCTCTCGGAGCGCCTACTTTCGCTGCATTTTC 12851
QY 320 -----SerAsn-----Gly--- 322

Db 12852 TTTCCCTGGCGGTGTCATCAAGCTGAATGAGCAGATGAGCTAACTCGACAAGGGAA 12911

Qy 323 Thr-Ser-----Arg-----Arg-----AlaGly 328

Db 12912 GTGCTGACATTCGACCTCTATGCCAGCAGCCAGCTTAGGTTGCAACCTGGTGAGTTGGT 12971

Qy 329 -----Cys-----Val-----Tyr----- 331

Db 12972 GAGGCATGGCGAGTGCAAGTTTGCAATCGGCTAATGGTTAGTCATGGGCTGACGAGTTT 13031

Qy 332 -----LeuLeuPro-----Leu----- 335

Db 13032 GATGTCAGGAGAGCTGAGTGTCACCTTGTTCCTTTAAGAGATTAATGTAATAAA 13091

Qy 336 -----LeuVal-----Leu-----His----- 339

Db 13092 AATCAAGATCTGGTTTAATAACTGGATCTGATTTCATCGCGCTTTTGTGATAAATG 13151

Qy 340 -----Leu-----LeuLeuSph 344

Db 13152 TTTGTTGCTTGACTTTAAGATATCCTTTGAAATTT 13187

RESULT 15

US-08-459-569-19

Sequence 19 Application US/08459569

Patent No. 5543501

GENERAL INFORMATION:

APPLICANT: Slightom, Jerry L.

APPLICANT: Tepfer, David A.

TITLE OF INVENTION: R1 T-DNA Promoters

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: GRAY, CARY, AMES & FRYE

STREET: 401 B Street, Suite 1700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-4297

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,569

FILING DATE: 02-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/008,216

FILING DATE: 25-JAN-1993

APPLICATION NUMBER: US 06/725,368

FILING DATE: 22-APR-1985

ATTORNEY/AGENT INFORMATION:

NAME: Barnhorst, Marnie W.

REGISTRATION NUMBER: 36,740

REFERENCE/DOCKET NUMBER: P1020US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 699-2700

TELEFAX: (619) 236-1048

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 21126 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Agrobacterium rhizogenes

STRAIN: STRAIN A4

IMMEDIATE SOURCE:

LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS

US-08-459-569-19		US-10-017-084A-523 (1-344) x US-08-459-569-19 (1-21126)	
Alignment Scores:			
Pred. No.:	4.8e-24	Length:	21126
Score:	1721.10	Matches:	293
Percent Similarity:	11.04%	Conservative:	44
Best Local Similarity:	9.60%	Mismatches:	6
Query Match:	71.47%	Indels:	2709
DB:	1	Gaps:	241
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QY	3 -----Thr-----Ile-----GlnProlysMet-----	8	
DB	4095 GACCGGACATTCGAGAAAGCGCCACCGTCTGCATTTTCGTCGCGAGAAATGAGCTCC	4154	
QY	9 -----His-----	9	
DB	4155 AAGGGCTCTCCAGTTCTGTCTCAATTCACCCCTCAGTTTCGAGATCTGGAATCTTGTG	4214	
QY	10 -----Asn-----SerIle-----	12	
DB	4215 GATGCCAGATTCGAGAGTTACAAATTTATGAAAGGCAATGGCACAGTGCACCGCACCG	4274	
QY	13 -----Ser-----Trp-----	14	
DB	4275 GATTTGAAAGTCAATTCGAAAGACAGCGTATTGACAGGCCAGGCCACGCTCGGCCACG	4334	
QY	15 -----AlaIle-----	16	
DB	4335 TCCAAGTTGAATCTCTTTCGCGCTGTCCCGAGTGTCCCGCAACAGTAATTCGCGCCACGAT	4394	
QY	17 PheThr-----Gly-----	19	
DB	4395 TTTACCCATCTCGGCCCTGTGAGCGGTGATAGGAATCTACTCGCAGCACGGTATTGCGG	4454	
QY	20 LeuAlaAla-----LeuCysLeu-----	25	
DB	4455 ATTGCCGTAGAAACCTGGTACGATCGTTTATCCGTGCGAAAGAGTTCTCTGTTGGAG	4514	
QY	25 -----	25	
DB	4515 GTCAGCTACAGCGGATCGGCCCTAGAAAGTACTTCAACGCTTGGGGACAGGCTTAT	4574	
QY	26 -----PheGlnGlyVal-----Pro-----	30	
DB	4575 AGCAATGGCGGTGGCACTAGCTTC-----GGTCTTCAACAGCGTCCGTCTCTTGCCTTAAT	4631	
QY	31 -----Val-----ArgSer-----	33	
DB	4632 CTTTCCGCGCGCGCTCGCTACATATTTTCAACGCTCGGATCTCTGTCCCTTCCATTG	4691	
QY	34 GlyAspAla-----Thr-----	37	
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DB	4752 TTTCCGATCACTGCTTCTCCCGCCAGAGCACCAATCAGTTTCAACGCTCGGATCTCTGTCCCTTCCATTG	4811	
QY	42 -----Met-----Asp-----	43	
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QY	44 -----Asn-----ValThrVal-----Arg-----	48	
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QY	49 Gln-----	49	
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QY	53 -----AlaThr-----LeuArg-----	56	
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QY	57 -----CysThr-----	58	
DB	5172 GCGGACCGAGCCGCTTGGAAAGCATTTGTCAGCTCCAACTTCTGCTCAGAAGCACT	5231	
QY	59 Ile-----Asp-----	60	
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DB	5352 CFTCGATGCCCTTTTTCACGACAGAGCAGACCGCCCGGCATTCGCCCTGTGATGGCA	5411	
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QY	67 -----Ala-----Trp-----	68	
DB	5592 CTTTGGGAGAGCTTTCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5651	
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QY	72 -----Ser-----ThrIle-----	74	
DB	5832 TCACCGCATCAGAGTTTCATCGTTTTCATACGCGCATCGAGGCGGAACCTGCCAAAGA	5891	
QY	75 -----Leu-----	75	
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QY 82 ----- 82
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QY 83 ----- 85
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QY 86 -----Pro-----Arg--- 87
Db 6432 GTGTTTCGTGAACATGTCAACCCCTTCGGTATACATTAGCCTACAAGTAATAACGTGA 6491
QY 88 -----Val-----ValLeu 90
Db 6492 TAAATGTCATCTGTTGTAAATAAATTCAGCTTATTATGATATAACAGACCCCTGTGTA 6551
QY 91 -----LeuSer----- 92
Db 6552 ATCTAATTACAAAGAAATTCATCAITCTCCCAAGCAATCCTGAGTAGCTGCGTAGGAT 6611
QY 92 ----- 92
Db 6612 CTTCCATATCAGCGCCACGTTTCAACCCGTTTGCCTGCCATCCACGTCAGTAGTGAGTC 6671
QY 93 ---Asn-----ThrGlnThr-----Gln----- 97
Db 6672 AACCTGAACCGTGCATATTCTCAGGCTTGTCTGCTATGATCAGTTCCTGCGNACGGCTC 6731
QY 98 ---Tyr-----Ser-----Ile 100
Db 6732 TTGCGATATCAGCAAGCTGGACGGATTTGGGTGTTCCAGCTTGCCTTCATGGCCCCCGAATAGCGCG 6791
QY 101 Glu----- 101
Db 6792 GAAGAGTGGCGTGTGTTCCAGGTTGCACCTTGCCTTCATGGCCCCCGAATAGCGCG 6851
QY 102 -----Ile-----Gln-----Asn----- 104
Db 6852 CTCGAAGTGTGATACCTCGTCGCCACCGCTTCTCATTTATATGTCGAACAACCAATTG 6911
QY 105 -----Val-----Asp---Val----- 107
Db 6912 CAGCGCTTTGTTGCACACCAGTGCATTGCTCAACTTGGCGACGCCGTGCTTGTGTCATG 6971
QY 107 ----- 107
Db 6972 ATCCCGCCCTACCGGAGTGACCTCTCGCTGCAGGAAATGGCTCGGGCGCAACAGATTT 7031
QY 108 -----Tyr-----Asp----- 109
Db 7032 TGCCAGGAGTTACAGGAGTCCGAGAGGTACAGTGTCTTATCGCCATCCAACTCAGC 7091
QY 110 -----GluGly----- 111
Db 7092 AGCCGATTCTGTTGAGGAGGACATGTAACTGACGTCGCGGCGAAATGGCTTAAAGAAAC 7151

QY 112 ---Pro-----Tyr----- 113
Db 7152 TGCGCTTCTTTTCGTCGCCCTGCTGAGTTCCTCAGCCGTTATGATCATCGTTGCCATTTGGG 7211
QY 114 -----ThrCys-----Ser--- 116
Db 7212 CCGGTGCTCTTCCATGATGAATGCGGATTTGCCCAAAATGCAATGAGCCTCTTTTCTCGC 7271
QY 117 -----Val-----Gln----- 118
Db 7272 TTTGACCTCGGAGTACGACTATCAGTCTTCTCCAGGAGTCGATGCCATGATGGTGTG 7331
QY 118 ----- 118
Db 7332 GGGCATATCCGGAAGCGCACCACTACTAGTGTGCCATCGTAGGAGCGGGCTGCT 7391
QY 118 ----- 118
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Db 7452 ACCGTGATGAGATCCGTAAGTTTGGGCAATCGCGATGCCAAACGGCGAGCTCCACAG 7511
QY 123 -----Pro----- 123
Db 7512 GCCTTGACGTCGTTCGGTGTCTATGCTTCTCCGCAACCACTTTGCTGTCATACAT 7571
QY 124 ---Lys-----ThrSer---ArgVal-----His--- 129
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QY 130 ---Leu----- 131
Db 7632 GCATATATTTCCGCCAGAAACGCTACGATGGCAGCGGGGCAAGCTCCCGCGGGATA 7691
QY 132 ValGln-----Val----- 134
Db 7692 TTTCAAGCGGTACATGTCGGATGGAGACACTACTCTACAAAGGCTGTGAACGGAATGGC 7751
QY 135 -----SerProLys---Ile----- 138
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; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,831
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barthorst, Marnie W.
; REGISTRATION NUMBER: 36,740
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; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS
; CLONE: CLONE 7
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; LOCATION: complement (19031..19390)
; OTHER INFORMATION: /label= ORF18SUBSEQUENCE
US-08-458-831-19

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Score: 1721.10 Matches: 293
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Best Local Similarity: 9.60% Mismatches: 6
Query Match: 71.47% Indels: 2709
DB: 1 Gaps: 241

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Db 6912 CAGCGCTTGTGTCACACCCAGTGCATGCTCAACTTGGCGAGCCGTGCTTCTGCTGCATG 6971
QY 107 ----- 107
Db 6972 ATCCGCCCTTCGCGAGTAGACCTCTCGCTGAGGAAATGGCTCGGCGCAGCAACAGATT 7031
QY 108 -----Tyr-----Asp----- 109
Db 7032 TGCCAGGCGAGTTACAGGAGTCCGCGAGCTACAGTGTCTTTATCGCCATCCAACCTCAGC 7091
QY 110 -----GluGly----- 111
Db 7092 AGCCGATTGTTGAGGAGGSCACATGTAACGTGCACGGCGAAATGGCTTAAAGAAACC 7151
QY 112 -----Pro-----Tyr----- 113
Db 7152 TGCCGCTTCTTCGTGCGCTGCTGAGTCTTCAGCCGTTATGACATCGTTGCCATTGGG 7211
QY 114 -----ThrCys-----Ser----- 116
Db 7212 CCGGTGCTCTTCATGATGAATGATGCGCCAGCAACTGCAATGAGCTCTTTCTCTGC 7271
QY 117 -----Val-----Gln----- 118
Db 7272 TTTGACCTGCGGTACGACTATCAGGTTTTCCTCCAGGAGTGCATGCCCATGATGTGTG 7331
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QY 119 Thr-----Asp-----Asn-----His----- 122
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Db 7512 GCCTTGACGCTGTCGTTGTCATGCTTCTCCGCCAACCACTTTGCTGTCTACTAT 7571
QY 124 -----Lys-----ThrSer-----ArgVal-----His----- 129
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QY 130 -----Leu-----Ile 131
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QY 132 ValGln-----Val----- 134
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QY 135 -----SerProLys-----Ile----- 138
Db 7752 AGGAGACTGATGGCTCCGATGGATATCTCTTCATGTTGAAGAGCGTCTGCTGTATGAA 7811
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QY 139 ---ValGluLeu-----SerSer----- 143
Db 7872 TTGTCGAGATCTTCAGCTGTGGTAAATTCGATCTCTGTTGGCAAGGATGCGCAACACCC 7931
QY 144 ---Asp-----Ile----- 145
Db 7932 CATGATTTCCGAGGCTTTCCGGGATACTGAGTGGGATACGGCCGAGTTTGTCTCTATTAC 7991

QY 146 -----Ser-----IleAsn-----148
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QY 148 -----148
Db 8052 CTTTCTATTGTTGGGTTCAACTTTTGCAGGCTCTGATGCCATTTGAATAATTCAGAAA 8111
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QY 156 -----Thr-----156
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QY 157 -----CysIle-----158
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QY 159 -----Ala-----Thr-----Gly-----161
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QY 162 Arg -----ProGlu-----164
Db 8532 CGTCTTGGAAATGCTCAGGAGCTTGTCTGCTGCTTCTGAACTGGCTGTGTCACCTG 8591
QY 165 -----ProThr-----Val-----Thr-----168
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QY 169 -----TyrArg-----170
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QY 184 -----Glu-----Tyr-----185
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QY 186 -----LeuGlu-----Ile-----188
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QY 189 -----Gln-----189
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QY 193 -----Arg-----Glu-----194
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QY 210 -----Pro-----Val-----211
Db 9972 GGACCTTTGTGCGCGGAGCTGAAAAATTCAGACCTTACGGGATTAATACGCATTTTCGAAC 10031
QY 212 -----Val-----ArgArg-----214
Db 10032 AAACCTACGGGATTAATACGACGTGGCTGGCGGCTTCGATTTCATTTCCAGCCCGGAGA 10091
QY 215 -----Vallys-----Val-----217
Db 10092 TGAATATGATGTTCTGTTAAAGTTAAATAAGCTGGAGCCATGGCGGATTTGCTCTG 10151
QY 218 -----Thr-----218

QY	309	----	-----MetLeu	-----PheGly-	-----	312
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QY	313	-----	-----Pro-	-----	313	
Db	12432	GTACAAAGCAACCTGTTTCCTACTTTGTTAAACATGGCTGAAGACGACCTGTGTTCTCTCTT			12491	
QY	313	-----	-----	-----	313	
Db	12492	TTTCAAGCTCAAAGTCGAGGATGTGACAAGCGATGAGCTAGCTAGACACATGAAGAA			12551	
QY	313	-----	-----	-----	313	
Db	12552	CGCCTCAAATGACGPTAAACCTTGATCGAGCGGGTGAGAAATCAATCGATGGATATTGA			12611	
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Db	12612	CGAAGAAGGAGGTCGGTGGCCACGGCTGCTGTACTCTACGCTCGACTGCCCGCAGCAT			12671	
QY	316	-----	-----	-----	316	
Db	12672	GATGCTCTGCTTCTATGAGAGGTCCTTGGCTTACAATTGGATGCAAGGCGCATCCTCTCAC			12731	
QY	316	-----	-----	-----	316	
Db	12732	CAACCTTCCCCGTACCAGCATGATGACTCTCGATGAGGTCAATAGAGGCTCAGGCA			12791	
QY	317	-----Ser-	-----Glu-	-----Val---	319	
Db	12792	AGCATCAGGTTTTTTTCGGTTACGCGATCCTATGCGGAGCGCTACTTGGCTGCATTTTC		:::	12851	
QY	320	-----SerAsn-	-----Gly-	-----	322	
Db	12852	TTTCCCTGGCGGTGCATCAAGCTGAATGAGCAGATGGAGCTAACTTCGACAAAGGGAAA	:::		12911	
QY	323	ThrSer-----Arg-----	-----Arg-----	-----AlaGly	328	
Db	12912	GTGTCTGACATTCCGACCTTATGCCAGCACCCAGCTTAGGTTTCGAACCTGGTGGATTGGT		:::	12971	
QY	329	-----Cys-	-----Val---	-----Trp---	331	
Db	12972	GAGCATGGCGAGTGCAGTTTGCATTCGGCTAAATGTTAGTCATGGGCTCAGCAGTTT			13031	
QY	332	-----LeuLeuPro-	-----Leu-	-----	335	
Db	13032	GATGTCAGGAGAAGCTGAGTGTGTCACTTGTTTCCCTTTTAAGAAGTATTAAATGTAATAAA	:::	:::	13091	
QY	336	-----LeuVal-----Leu-	-----His-	-----	339	
Db	13092	AATCAAGATCTGGTTTAATTAACCTGGATCTGATTGATTTCATCGCGCTTTTTTGAATAAATG			13151	
QY	340	-----Leu---Leu-----	-----LeuLysPhe	344		
Db	13152	TTTGTGCTTGACTTTTAAGATATCCTTTTGAATTT			13187	

RESULT 17

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; Sequence 2, Application US/09913514
; Patent No. 6653069
; GENERAL INFORMATION:
; APPLICANT: GOMI, Yasuyuki
; APPLICANT: SUNAMACHI, Hiroki
; APPLICANT: TAKAHASHI, Michiaki
; APPLICANT: YAMANTSHI, Koichi
; TITLE OF INVENTION: Method for Quality Control of an Attenuated Varicella Live Vaccine
; FILE REFERENCE: 0216-0454p
; CURRENT APPLICATION NUMBER: US/09/913,514
; CURRENT FILING DATE: 2001-12-07
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; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: JP 2000-62734

Db 54332 TCACCTGAATGTTTAATACGTTAGATGTGGTTCATGGCTTGGTTCACAGAAATCAA 54273
QY 22 -----
Db 54272 ATTAATGCTAGGTTTGTGGGGTTTCCCATCTCCCGTGTGCTTTTTCATCTAGAAT 54213
QY 23 ---LeuCys-----
Db 54212 CTTTACTGCTTCTAGAGCGCTTCTACGGTCAGGGCGTTTTCAGGGTTTGATTAATCTG 54153
QY 29 -----ProVal 31
Db 54152 GTCTGTAACTCTCTCAAGTCTCTGGCTAAAACTCATGCTCTGTAAGACTTTAACCAAGTC 54093
QY 32 -----Arg-----
Db 54092 GTCAAATGCCATATGTTGTCTGAGCGCCACTGCAACGACAAACCGTGGCGTATATGGC 54033
QY 32 -----
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QY 33 -----Ser-----Gly-----Asp-----
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QY 36 -----AlaThr-----Phe-----
Db 53912 TATTATAAACCGCGAGTCCGATCAAAATGTAATAGCGGGGATACATTTTACCCCGGT 53853
QY 39 -----Pro-----Lys-----
Db 53852 TAAACCGCTCAATTCCTCGCTGAAAGACGGGTTGTTCTCGCGCTCCGATATTT 53793
QY 41 -----Ala-----Met 42
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QY 43 -----Asp-----Asn 44
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QY 49 -----GlnGly-----
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QY 51 -----Glu-----
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QY 52 -----Ser-----Ala-----Thr-----
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QY 55 ---LeuArg-----CysThrIle-----Asp-----
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QY 61 -----Asn-----Arg-----Val-----Thr-----Arg 65
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QY 69 -----Leu-----
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QY 103 Gln-----Asn-----Val---Asp----- 106
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QY 131 -----Ile-----Val----- 132
Db 51392 ATCCCATGGTTAATATGAACAATATCGAGTCTCTCAATAATGCAAAACACGTTGCACAT 51333
QY 133 -----GlnVal----- 134
Db 51332 AAATACGGCTCTCTTAAACAATGCGGTGACCCAAAGTATATAATTTGTATTTCTGCGTC 51273
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QY 154 -----SerIleuThr----- 156
Db 50672 CGTGGGGTTGTACTCAGTAACACTGGCTTTTACAAGATTATCAATCGTTAAACATA 50613
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Qy 184 ----- 184
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Qy 185 -----TyrLeu-----Glu----- 187
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Qy 210 o-----ValVal----- 212
Db 49292 CGAGTTGGCCACAGGTTATAACATTTGTTAATTTGATGGCGGTTTATTATGGAGAACT 49233
Qy 212 ----- 212
Db 49232 TAATCTATATACAGTCTCAAGCTTGATGGTTATGGCAGTATAACCGTGGGGTCTGTT 49173
Qy 213 -----ArgArg-----ValLysVal----- 217
Db 49172 TAAGATATGGGATGTTGGCAAAATCCGGATTTTCAGCGACGAAAGGTAAGATCAACGG 49113
Qy 218 -----Thr----- 218
Db 49112 TCTCATATCTCTGGATATGATGCAATTCGAACTGAAAAATTAACACTCTCGAGTTATAA 49053
Qy 219 -----Val-----Asn-----Tyr----- 221
Db 49052 ATTAGATTCGGTTGCAAGTCTAAATGAGTCCAAAGAGAGATTTGCCCTACAAGA 48993
Qy 222 ---Pro-----Pro-----Tyr---Il 225
Db 48992 CATTCGGGATTAATACGCTAGTGGACCGAATACACGAGGAATTTATGGTGAATTTGTAT 48933
Qy 225 e---Ser-----Glu----- 227
Db 48932 ACAAGACTCGGCTCTTGTGGGAAACTGTTTTTAATAATTTACCACACCTTGTGTTATC 48873
Qy 228 -----Ala-----Lys-----Gly----- 230
Db 48872 CGCGTTGCAAGGCTAGCTAGAAATTACTTTAAACCAAGGCTATTATACGACGACAGCAGGT 48813

Qy 231 -----Thr----- 231
Db 48812 TAGATTTACACTTGTGTTTATTAGGACTGGCTTCGTCTCGAGGATTTATTTTACCCGATGG 48753
Qy 232 -Gly-----ValPro----- 234
Db 48752 GGGATACCCAGTACTTTTGAATATAAGGATGTTATTCCCGATGTCGGGGATGTTGAGGA 48693
Qy 235 -----Val-----GlyGln----- 237
Db 48692 AGAGATCGATGAAGACGAGAGCGGTTTCTCCACTGTGTACGTCAAGTGGCGGAATGTAGG 48633
Qy 238 ---LysGly-----Thr----- 240
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Qy 241 -----Leu-----Gln-----Cys----- 243
Db 48572 ATTGGATTTTGAAGTTTATATCAAGTATAATTCAGGCCCAATAACTTATGTTTACCAC 48513
Qy 244 -----Glu-----Ala----- 245
Db 48512 GCTAACGTTAAATTTTGAGACGGTTAAACGTTTGAATCCATCCGATTTGCCACTTTAC 48453
Qy 246 -----Ser----- 246
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Qy 247 -----Ala---ValPro----- 249
Db 48392 TCTTTTAAAGACTGTTGGCTATGCGCAAGGCTATTAGAGCGCGCATACCCGGAAGTTC 48333
Qy 250 -SerAlaGlu----- 252
Db 48332 TTCAATGAAGCAGTGTATTATAGACAAACAAAGCGCGCATAAAGTAGTTTGTATATTC 48273
Qy 253 -----Phe----- 253
Db 48272 CGGTACGGTTTACTGGAGTTGCGCAGGATTTCTGCCATGTTTATACGTAGGGCCAC 48213
Qy 254 -----Gln-----Tr 255
Db 48212 TGTCACTACAATTTGGCGCTCAAAATGTTATTAAGTACACAGAGATTATATTCAATAACTG 48153
Qy 255 p----- 255
Db 48152 GSCCGCATTTGAACGTTTATTACAGGTTTCCAGACATTGAAAGTAGCGTTCTCTCCCA 48093
Qy 256 ---Tyr-----Lys-----Asp---AspLys---Arg----- 261
Db 48092 AAAAGCGTACGAGGTAAGGTTATATATGGAGATACGGATTCGTGTTTATCCGATCAA 48033
Qy 261 ----- 261
Db 48032 GGGTGTGGTTGAGGGGATAGCTAAATTCGCGGAGAAATGGCACATATAATTTCAAC 47973
Qy 262 ---Leu-----Ile-----Glu----- 264
Db 47972 GGCTCTGTTTGTCTCTCTATAAAGTTGGAGTGTGAAAAAACTTTTATAAACTTTTACT 47913
Qy 265 -----GlyLys-----LysGlyVa 269
Db 47912 TATAACAAAGAAAAAGTACATTTGGGTAATTTACGCGGGAAGGTTTAAATGAAGGAGT 47853
Qy 269 l-----ValG1----- 272
Db 47852 CGACTTGGTTAGAAAAAACAATGTCATTTATTAAAGATTATGCGCGCAAACTTGTAGA 47793
Qy 272 u----- 272
Db 47792 ACTGTTGTTATATGACACACCGTCTCGCGTGTGCGCGGAGCGGTCTGTTTCCAT 47733


```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,117
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Catherine R
; REGISTRATION NUMBER: 34,240
; REFERENCE/DOCKET NUMBER: 8589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6208
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Endothia parasitica (Cryptonectria)
; ORGANISM: parasitica)
; STRAIN: BP713
; US-08-459-146-1

Alignment Scores:
Pred. No.: 6,31e-25 Length: 12752
Score: 1718.90 Matches: 296
Percent Similarity: 11.19% Conservative: 39
Best Local Similarity: 9.89% Mismatches: 7
Query Match: 71.38% Indels: 2652
DB: 2 Gaps: 264

US-10-017-084a-523 (1-344) x US-08-459-146-1 (1-12752)

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QY 5 -----Gln-----Pro 6
Db 12473 GTATGGTAGCTTTACACAGGCGGTAGCCCATCTTCGGGCAACCCCTTTTCGCCCA 12414
QY 7 LysMet---His-----AsnSer-----11
Db 12413 TTCTTGAACATGTAGACGATCTCTACGTGACGCGATCCGGCTTACTTTTCCAGTCTGT 12354
QY 12 -----Ile-----Ser-----TtpAla---15
Db 12353 GCTTGCTCGGTCTTATTGCGGTTCCTACACAGCATCAGCCCTGGTCTCTCGGCGGG 12294
QY 16 -----IlePheThr-----18
Db 12293 GTCGTTCGGTACACGCTACCAACAGTTAAAGTATTAGTATTCTAGCCCTATTGCT 12234
QY 19 Gly-----Leu-----Ala-----21
Db 12233 GGCCGACAGTGTCACTGTGTTTCTGCTCTCTTTCGAGTGGTCTCATGGTCACGTGGG 12174
QY 22 -----Ala-----22
Db 12173 TGTGTGATGAGGCACAAATTGCATCTCCGAGGCGCTTAACCATTCGCGGGAATGGTGTG 12114
QY 23 -----Leu-----Cys-----24
Db 12113 TGTTCGCTCTGAGCTCTTCAGCGGGTTCCTCCCTGCGCAATCTCTCAGAGGAGCAAAACC 12054
QY 25 -----Leu-----Phe-----26
Db 12053 GTAGATTTAATCTACGTACCGTTCGCGGTTCGGGTGTTAAACAGATCAGTCCCGGGTTA 11994
QY 27 -----Gln-----27

11993 ACCTCTTACTACGGGCGAGTGACCATGTGCTATAGGCTTGAGTTATCCACTCAGGTGCTG 11934
28 -----GlyVal-----ProVal-----31
11933 GTTTTGGCGGTGTCACGGGGTCACTACCTCCCGTGGAAAGCAAGAAATGACAAATGGA 11874
32 -----ArgSerGly-----AspAla 36
11873 AGCGGTTTGTGTTAAACCCCAACAGGTATATCCCGAGGACGGGTGTGTCGTAAGATGG 11814
37 Thr-----37
11813 ACCTGCTGTGCTTCTTCGGGTGCATGCTGATCTCAGCTGTGATGAAGGCGAAGGTCTG 11754
38 -----PhePro-----39
11753 GGCTCTGAGCTCGTTGACCTGGCTTGCACATGCCGATCTCTGCATGTTCCGCTGGTG 11694
40 ---Lys-----40
11693 TAGAAGTACCTTGTGCGCATATGACTTACGGGAGGAGGATCTCCACCCACATCCCATC 11634
41 -----AlaMetAsp-----AsnVal----45
11633 ACAAGGATATCTTGTGCGCTTATTGTGGGACGCCACCGATGTAACGTGCC 11574
46 -----Thr 46
11573 GTTGGCCCACTGATGCCATGTCACACTGGTATGTGGTTAGCATACCTCAGTTTACC 11514
47 -----Val-----Arg-----48
11513 CGACGTTAAGATGCGCTCCAAATGATCTTCACTCTCCCGAAAGGAGGTGAAGTTCAAA 11454
49 -----GlnGly-----50
11453 GTATCGATTGTAACGCAAGGCCCATTCGGACTGCTGACGCCGCCAATGCCATGATGATG 11394
51 -----Glu-----Ser-----52
11393 GATAACAGGAGGATTTGTCGTCACGCTTGTTCCTCTCTCTCTTGTAGCGGGTCTGA 11334
53 -----AlaThr-----54
11333 AAGCTCGGATGTGACTTGAITGACATGTACGCGAGTTCGGGTGGACACACCAATGAC 11274
54 -----54
11273 TTTAGTTAATCGGGGACCTTGTACTGCCCCCGGACTAACTCTGAAGAAAAGAAATCCC 11214
55 -----Leu-----Arg-----Cys-----57
11213 ACTAGGATCTTACAGAGGAGGTGCTGTGCCAGCAGCTTGGCGGTGTATGACACACAC 11154
58 -----Threleap-----60
11153 ATCCATGCTCTACCGACAGGATTGACCTCTGTTGTTGCTTCTCTGCTCGTATAGGG 11094
61 -----Asn-----61
11093 GTGGGTGTGACTAGCTACCTTATGCAATGACATCTCGGCGCTGTGATCAAGAT 11034
61 -----61
11033 CGACGCGCGGGTTTGATATCGATGCCAGTTTGTATATATGCGGTGACACAGGCGCAC 10974
62 -----Arg-----ValThr-----64
10973 AGTCTTAGGACGAGGGGGCTATTACTGCTCACTCATGCCAGTGTATAGACCTGTCCAA 10914
65 -----Arg-----Val-----66
10913 GTTCTCCATCCAGCAATGCTCTTCTGAGTTCGTTATATGTGGGACTATGATCATTTGG 10854
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Qy	67	Ala	-----	67	Qy	108	Tyr	-----	Asp	-----	109
Db	10853	CGCGCCCAACAATT	CGGCTGATCAGCAAACTGATTCGGAGCCCGGTTCCACATTTCCAA	10794	Db	9773	TATCGTATTTCAGATGCCGTAAGGGGACTCTT	TAGCGACGGCATCAATTTGGCGAA	9714		
Qy	68	-----	-----	-----	Qy	110	-----	-----	-----	110	
Db	10793	CACGTATCGGAATCAAC	TTGTAAACGGTAAGATTGAAACGCTTTGGCAGTGTGGCTC	10734	Db	9713	CGTAGCTCGTCAACGGTCGTGGTTTCCAGCAACTT	GAGGTATATGAATTTCTCCACATA	9654		
Qy	70	-----	-----	-----	Qy	111	-----	-----	-----	111	
Db	10733	AAGAAAGGGATCGCGGCATTC	CATGAAGTGCACAGAGTTGCACATCATGAAGATGGT	10674	Db	9653	CTGGTTGTAGTGTGCCACCGAATTC	CGGCATACAGCATCTCCGTAGACGGCATGAACCT	9594		
Qy	73	-----	-----	-----	Qy	112	-----	-----	-----	112	
Db	10673	TGGTCTTCCAGTCTTCCAGTCT	CTGTCAGTCAAAACCGTCCATTTTCGTGAACATCATC	10614	Db	9593	TTTAAACTCCTCAGGTATCATGTC	CGGTAGCATACACCCGTCACATATACCGAT	9534		
Qy	76	-----	-----	-----	Qy	114	-----	-----	-----	114	
Db	10613	GAAGAACACAGGTTGTCCT	CGGACAGTCCACCTATCTCTCGTTCGGAATGTCGTA	10554	Db	9533	CCCTCATCTGGATTGCGCCAGCGGATCC	AGTTTGGCGATAAAGCATCATGCGCGGA	9474		
Qy	77	-----	-----	-----	Qy	114	-----	-----	-----	114	
Db	10553	CGTGTCACTAGATATCGGCGGAT	GGGTCTAGTGTTCGCGCGTTTCAGATTGAGA	10494	Db	9473	TGGTCAAGGATCCCTTATCT	CTGAGGTGTATGTCTAGAACTTGTGATAGATGGAACCTT	9414		
Qy	79	-----	-----	-----	Qy	115	-----	-----	-----	115	
Db	10493	TCGGATGTCAAAATGGAATCT	CCAGTTATCGCGAGGATCTTCTCTGGCATACGATCCA	10434	Db	9413	GGCTGCTGCTGATCCACCGAAGGAATG	CTTCTGTCTTGTGTGACAACTTGAAGTTCCGTTT	9354		
Qy	82	-----	-----	-----	Qy	117	-----	-----	-----	120	
Db	10433	CAGTTTCTGATCCGATGTCCT	CTCTCGGCCACACCGCTCGGGGGAAGATGGA	10374	Db	9353	CCAGTTCCGGTTCCGTTTATAACCTG	CACTTCTATCTTGTGACTGACGAGCTC	9294		
Qy	83	-----	-----	-----	Qy	121	-----	-----	-----	121	
Db	10373	CTTACCGGAAGCGGTTTTT	TGGGCTACAGTAAAGTACCGTGTCTGATGGTTTGTGTC	10314	Db	9293	GTAGCGTGATTGATGTGTGCTCTT	TGCAGACGATTCAGGTCTCTCGCGTACTCAAT	9234		
Qy	86	-----	-----	-----	Qy	122	-----	-----	-----	123	
Db	10313	GTACGTGTGGCGGTPACGCGG	CGCAAGGATTGGACGGCACATTTAACGATTTGCGAGATCG	10254	Db	9233	TGCGAACCTCTTGTACAGTGGGGT	TGGAATGCCGTACAGAGTGGTGACCGGACCCCG	9174		
Qy	89	-----	-----	-----	Qy	124	-----	-----	-----	125	
Db	10253	TGCGTCTGAAGTCGGTGCCT	ACCGATTCAGATTTCGAAACAGTCTCCACATGCGCCC	10194	Db	9173	TTCCACAGAGGTGACAGGAATTC	CGAGGACTGCTCTGATAATAACGGAAACAGTCTCT	9114		
Qy	93	-----	-----	-----	Qy	126	-----	-----	-----	128	
Db	10193	AAATAGAACTTCGATGATCT	CGCGAGACCATCCAGACCAAGTCTACGGGAACGATACC	10134	Db	9113	TCGCAATTAGAAATAGCGTGGG	TTCTGGACCATCAGGAATTGAGTAGTGTCTCGCGTTC	9054		
Qy	96	-----	-----	-----	Qy	129	-----	-----	-----	129	
Db	10133	GAGAGCAAAATCGTTCAGG	GATGAATCAGCCATCGTCTGACGAAACGTTTAGACCACAT	10074	Db	9053	AATGAGAGAAGTGTCTTCT	ACTGAACCGCTGAGGATCGCATCTTCTCGATCCTTCC	8994		
Qy	97	-----	-----	-----	Qy	130	Leu	-----	-----	133	
Db	10073	GTATGGTCTCTTGGCAGGAT	CGAGTGTCTCTCTCTCGAGCGGCTTACCATGCCA	10014	Db	8993	CTGCTCCATGCCCGATAGTCC	CGTGAATCTTCTGCGTTGGCGCAGGTGGCAACTTCGA	8934		
Qy	100	Ile	-----	-----	Qy	134	Val	-----	-----	134	
Db	10013	ATAAAAGTGTTCGCCAGT	CGTAGACTTTTGAACAATCCCGAGAACGACCATGAATAG	9954	Db	8933	TAAGTATCCACTTCTGTTAT	CTTCTTGTGCGACCGCATCTCAAGCAGGATGCCAAATC	8874		
Qy	102	Ile	-----	-----	Qy	135	Ser	-----	-----	136	
Db	9953	ATTATATAATGGCCCTAT	CAAGACAGTGAATGAAATAAACAGCTCGACCAATGCATTGC	9894	Db	8873	GGCGGAGCTTGTGTAAGCGAT	CAACCTCGGACAGGATAACAGGTCTCTTAGACCACCA	8814		
Qy	105	-----	-----	-----	Qy	137	-----	-----	-----	141	
Db	9893	GAAATACATGCCGAGATGAT	GACAGTCATGCCCTTGGTAGATGGCGACCTTATCTATCAT	9834	Db	8813	CACGTGTATCGCTCGTAT	TGTGAGCCCTGTTGAACAAAGAAATCTTTGGCGCGGTTT	8754		
Qy	107	-----	-----	-----	Qy	142	Ser	-----	-----	145	
Db	9833	GGCCTCGAGGCCAAGAGAT	CTCTTCAGATAGTCAGGCTCTCTTAGGTCTTCCCGAACCTT	9774	Db	8753	ACCAGTAGCGGTGCCCGCG	CTGATGACGCCAAGTTTGAATGTAGTGTATGTGCCA	8694		
					Qy	146	Ser	-----	-----	146	

Db 8693 CGAAGTGGCACTCTGACCACTGCTCCACCACGAGTTCTTGTTGGTGGACGTTGGATATGAC 8634
QY 147 -----Ile-----Asn----- 148
Db 8633 TTCGCGATTGGCGAAGACATACGCTTTATATCTCTCATTTGCGCGCTTGAATCATA 8574
QY 149 -----Ile-----Glu----- 149
Db 8573 GAATAAGTTTGGTATTTCCGGAATTCGTCCTTTTGGGTTTCGTTGGTGAAGAACCTTG 8514
QY 150 -----Gly-----Asn----- 152
Db 8513 CCATGACGAGCTTGAATCGCAATGCTGGATCATTTGTTGAAGGAAACCTTGCACGGAAC 8454
QY 153 -----Ile-----SerLeuThrCys----- 157
Db 8453 GGCTGTCATGTCAGAC-----ACATGCTTTCCTTCCCTCCCAAGATAAACCTTCCACTC 8397
QY 158 -----Ile-----Ala-----Thr----- 159
Db 8396 AGTGACGTTTACATTAATTTGAGCCAGAGCTCGCTGAAGCTGCAAGTGTGACGGTA 8337
QY 160 -----Thr----- 160
Db 8336 CTTGGATTCCAGTTTCATGCTCACCGCACGTCAGGAGCGTGGAAGTCAAGCGGTATA 8277
QY 161 GlyArg-----Pro-----GluPro----- 165
Db 8276 GGAAGGTTGCTTATCCCCATGACCAATGATTTGATGGCTCGAATTTGCACTGGAC 8217
QY 166 -----Thr-----Val-----Thr----- 168
Db 8216 AACTTGTGGAATTTGCTCTTTCGCTGCTGACCTCGGATGATTTTGAACCTTAACCTCAACCA 8157
QY 169 -----Trp----- 169
Db 8156 TTTGCCAGCCCCATGGAACAAATCTGTTTACAGTTTGAAGTGTAGTGTGAGCAGTCATCAGC 8097
QY 169 ----- 169
Db 8096 AATGATGAATGCTTCCCTTCGCTTCCCAATCATGACGCTCGTCCCAATGCGAGC 8037
QY 170 -----ArgHis-----Ile-----SerPro----- 174
Db 8036 CATCGATTGTGACAAAGGCTATGCCAGAACCGGACCGTACGTTTCCGAGGTATTGCTT 7977
QY 175 -----Lys----- 175
Db 7976 GTTGGCTCGATCTGAAGAATCTGGTGGACCATGTAAAGCGATAGATCTCGGAGACCAC 7917
QY 176 -----Ala----- 176
Db 7916 CGTTGCAAGTCTTCATGCGGGGAGCCAAAGGTTTGGCAGGAACCGCTTGTGACTT 7857
QY 177 -----Val-----Gly----- 178
Db 7856 CGCGAAGCGGTGTAATAATTTGCGTAGGGTATTATACCGGTACTGATGCACTCCAGTGGCTT 7797
QY 179 Phe-----Val-----Ser----- 181
Db 7796 TTTACGATCATATCATGACACGCTTGTCTTAAGAGCCTTTCTACTCTTATAGAACA 7737
QY 181 ----- 181
Db 7736 GCTTATGAACGGGTGCCCGGAGTACTTCTTTTGATGATAAAGTCTACACCTTTAGG 7677
QY 182 Glu-----Asp-----Glu-----Tyr-----Leu-----Glu----- 187
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Db 7615 ATCTCTCCCAAGGCGCTTCTCTCAGCGAAACAGCCAGAGTATTCGGTTCATATCGGCT 7557
QY 192 -----ThrArg-----Glu----- 194
Db 7555 TATGATCGCGGATCTCTGTCGGGATTCCTGTCCTCAAGAGAGACGCCATCGATCGCTG 7497
QY 194 ----- 194
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QY 195 -----GlnSer----- 196
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QY 195 ----- 196
Db 7375 TCGAATCGGACGCTGTTGGCCCTCCGATGGTGTATTATACCAGGTAGTCTTTTCCCGG 7317
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QY 199 -----Tyr-----Glu----- 200
Db 7255 TTCCATCATTTGATATGTTCTTGACGAGTATGGCTTTCTGACTGTCATGCCAGAGCCAC 7197
QY 201 -----Cys-----Ser----- 202
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QY 203 -----Ala----- 203
Db 7135 GTCTAGCAATGGCAGAGCAGTGTATACGGAACGTGTGGCAGCATCACTCACGATTT 7077
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QY 205 -----Asp----- 206
Db 7015 CTCCCTAGTCTTTCAACACACGAGTTCGTTGAGAACTCGCGGTGTATATTGAGT 6957
QY 207 -----Val-----AlaAla-----Pro 210
Db 6955 AAACCTGGGAGACACCGATGCTCTGCTCTATTAACTTGGCCAGTTGCCAGGCTTCA 6897
QY 211 -----Val----- 211
Db 6895 ATTGCGCATGTCCAGAACTTTAGTTCCTTGGTTCGTTGATGCGTTCCTTTTCGTCCTG 6837
QY 212 -----Val-----ArgArg 214
Db 6835 GACAACTGGGTGTAAAGCCAGTTTCGACTACATCGAGTTTGACTCTCTCAGGATCGCGT 6777
QY 215 Val-----Lys-----ValThr-----ValAsn----- 220
Db 6776 ATCTTTCAAGGAAGACAGCAAGTAACACAGGTCGTTAAACCACTGTGTCAATATGCTCTG 6717
QY 220 ----- 220
Db 6716 ACTCCCCACCAATCTTGTGTCTATAGTCAGAAATTTGTCAATTTGTCATGTTCCGCGCGTGG 6657
QY 221 -----Tyr----- 221
Db 6656 CTCTGACTGACAGCAACCGAAGGCTTTTCTCAACGTCCTCTCTCTATCACTTCCAT 6597
QY 221 ----- 221
Db 6596 TGGCACCGGTGCCACCTGCTGCGAAACCCAGCAGCAGATGATACAGCCTTTGATGTGTCCCA 6537
QY 222 -----Pro----- 222
Db 6536 CGATGCTCGGATACACCCAGTGATAAACGTAAGCGTAGCCGCGCTTGAGGAGCGGAGGAC 6477
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QY 223 -----Pro-----Tyr----- 224
Db 6476 CAGGTACACCGCCACGAAACCATATACGCGAATACAAACCTAGTGCACTACGGTACAT 6417
QY 225 -----Ile-----Ser----- 226
Db 6416 GATCCCTTGAGGATCACGGTCGTGCAATTGTGATTCGCGCTGTAAAGTAGTGTGCTC 6357
QY 227 -----Glu-----Ala----- 228
Db 6356 ATCCATTGAATCCAGNAGCTCTGGACGTGGAAAGGCACCGAGTGGAAACACTGCCACAG 6297
QY 229 -----LysGly-----Thr----- 231
Db 6296 TCGGACCGGTCTAACGGACTTCGCAACTTGAAGGAGAGACCGGATGAGGTCTCACTGG 6237
QY 232 -----Gly-----ValPro 234
Db 6236 GTTGACAAATTTCTCGTAAACAAATCATCGAGTTGGTTCACGCAACACACAGTGCCC 6177
QY 235 -----ValGly-----Gln-----Lys----- 238
Db 6176 GAATGGTAGGAAACGTGTGCTTACCCGAGTTACCGGTTGGAAGATCAATTCAAACG 6117
QY 238 ----- 238
Db 6116 TTTGCTCGGTAGTTAGCCCGTCTTGGGATTAACGCCACCAACCAATGTATACCGAAAC 6057
QY 239 -----Gly-----Thr----- 240
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QY 241 -----LeuGln----- 242
Db 5996 CGCCTTCAGCATTAGGAGACGGGTTCACTTAACACGCCATGCCAACCAAGTACTCTT 5937
QY 243 -----Cys-----Glu-----Ala----- 245
Db 5936 AACGAACCTTGGTGCCATGATCGCGCTGCCATGAATGGTAGTGTGCAAGCACCCATA 5877
QY 246 -----Ser-----Ala 247
Db 5876 CCACAGAACACCCAGCCCTGATCAGCAAGTCAGCGGGAATTCAGATGCTTAGCG 5817
QY 248 -----Val-----ProSerAla-----Glu-----Phe----- 253
Db 5816 GATGAGTAATGAACACTTCAGCCA---GCCTATGACGAGCAACACGCGTGGCAGTTTAA 5760
QY 254 -----Gln-----Tyr----- 256
Db 5759 ATCAAAACCTTCCTCCACAGCCATGCGGAAGTATGGCAGTATGGAGGGTTGGTGAAGTC 5700
QY 257 -----Lys-----AspAspLys----- 260
Db 5699 TTCTCGGTAGGCAATTGTGTGATAATCTGTCAAGTTGACGTCTGTGACGACGACTTC 5640
QY 261 -----Arg-----LeuIle 263
Db 5639 GCATCCACAAGCGAATTGCGGTTTGGACGCGCACCGGCTCCACGAGCATGTAAATCTTATC 5580
QY 264 -----Glu----- 264
Db 5579 ATAATGCCCTGAAGATCTCGTTGTGTGTCACCGTTCCGAAACCGGGGTACTGTGCCCTGAT 5520
QY 265 -----Gly----- 265
Db 5519 GTCTTAGGCAACACAGCTGGATCAGCGGAGCCATGTAGCCATCCGATTTCCCTGTGTTT 5460
QY 266 Lys-----LysGly-----Val----- 269
Db 5459 AAGGTTGGGTTGTTGGTGATCAGGGAAACACCATCCGCGAAACGCGGTAAATTCGAACC 5400

QY 270 ---Lys-----Val-----Glu----- 272
Db 5399 TCTRAAGCAACCAATTTGCCAGTGGGCCAGAACGTGTCTGCCAGTTCTTCGGCGAACCA 5340
QY 273 ---Asn-----ArgPro-----Phe----- 276
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QY 277 Leu-----Ser-----Lys 279
Db 5279 CTGTTGATGTAGCTGCGAGCGGTGTAAAGTTGTACGAAGTTGGTTCCGGCATGTCAAG 5220
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Db 5219 CTCGACATCGGAGTGAACGCGGCTTTGTAAACCCCTCAGCACCGAGTAATGGTTCTGAAG 5160
QY 281 Ile-----Phe----- 282
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QY 283 ---Phe-----Asn-----ValSerGlu 287
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QY 288 ---His----- 288
Db 5039 GAACGCTGGTGGCACGTGATCTCCTCTTGTTCCTATGTCGGGATCAAGAGCGTGGATGA 4980
QY 289 ---Asp-----Tyr 290
Db 4979 CGGTCACGTGAAACCTCCTCACTTGAATGACAAGTTCTTCTTCCGGCTCCTCTAC 4920
QY 291 ---Gly----- 291
Db 4919 GAAGAAATAAACGGCACCGGCTCACACGCTAGCGGTAGCAAGATGGTCCAGAC 4860
QY 292 ---Asn----- 292
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QY 292 --- 292
Db 4799 CAGGTACGGCACATAGAGTGTGAAGTATATGGCACTAGAAACCGCAGATGAAGCGAT 4740
QY 293 ---TyrThr-----Cys----- 295
Db 4739 CATGATGTTATATTGCCATACACTACACACCTTGCGCGCGTGTCTCCAGTTTGTCTG 4680
QY 296 ---ValAlaSer----- 298
Db 4679 CAAGTTTCTTCGGGGGGGTTGCGGC-GACAGGTTTTTGTATTTCGATTAACTGTCAA 4621
QY 299 Asn----- 299
Db 4620 AATCGTGGTGGTTTCGTGGACCTCAGTTCCAGTCGCGTCAACCAAAACCTTCTG 4561
QY 300 ---Lys-----Leu----- 301
Db 4560 CTTGCAACTTGTAGTTCTTGCAACGAGCGAAAGGAATCTCCCTCCCTCGACGGGAG 4501
QY 302 Gly----- 302
Db 4500 GGGATACACTCTCACATGATGCGTGAACGGAAGAGGTTCTCTCAGCGCATACA 4441
QY 303 ---HisThr-----AsnAla----- 306
Db 4440 CCGTCGAGTGTGACTAGATACCTCTAGTGTCTATCTACCTACCTAGGAGGAACCGAGTG 4381
QY 307 ---Ser---Ile-----Met 309
Db 4380 GGTACATTGATCTCCAGCGCGAGCGCTCCACGTAGAGAGTCCATCTGAGGCAATG 4321
QY 309 --- 309

Db 4320 GGATGACCGGATTGAACACTGCGCAACCAATAATTGTTCATAATCAGACTGCTACCGTTTA 4261
QY 310 -----Leu----- 310
Db 4260 ACAAGCCAGCGCCTGAAACGGTTTGGCACTCTGATGATAGAGGAGAGAGCTGATGC 4201
QY 311 PheGly----- 312
Db 4200 TTCGGTTGCGATGCGCCCTGCAAGAGGAGGATGTCAAAACCCCATCTTTCGCGAGGAC 4141
QY 313 -----Pro----- 314
Db 4140 GTGACTGAGCCTTGC CGGGTTGGTCAGAGATPAAATTTATCGTCTCTCTGACCGAACCC 4081
QY 315 -----Ala-----Val----- 316
Db 4080 AGTCGTGATTAGCAGTCAGCTTGAGCACCGGTGACAAATTGTCCCGAATTCAGCTTCA 4021
QY 317 Ser-----Glu----- 318
Db 4020 TCAGTATGCCGATGACATCATCCCAAAATCGCGAGGCGATGAATACAGGCGTAGGCA 3961
QY 319 Val-----Ser-----Asn----- 321
Db 3960 GTCTAGGTTAATTCGACAAAGAAATCCCGAGTAGCCCATGGATGCCGTGTTCCTCACAC 3901
QY 322 -----Gly-----Thr----- 325
Db 3900 TCCTAATGTGCGCATTTGCGTCATGTTGACGTAACTCGTCACCTTCAAGCGGTGACCC 3841
QY 326 -----ArgAla-----Gly----- 329
Db 3840 ATTGGTCGACCTCCCGGAGGGGCTGTCGGTTGTCAAAAGGATGAATGTAGTCAGCGT 3781
QY 330 -----Val-----Leu-----Pro----- 334
Db 3780 CTTCAATCGGCTAGGTGTCGAAGGGTTGGTATTATCTTTGGCCCTTTGGCCAGGTTTCAG 3721
QY 335 Leu-----Leu----- 336
Db 3720 CTAGACCTTCGCTAGCTTGAGCCCAATTCGACCCACTGCTGTTTTCAAACAGAGAGT 3661
QY 337 Val-----Leu-----His-----Leu-----Leu----- 342
Db 3660 GTTGGCCGCTTTCACATAATCAGCGACTGAACCTTCTTCAGCTCCCAACGAGGATGTGAG 3601
QY 343 -----Lys-----Phe 344
Db 3600 GCTCGTTTCTCAAGATGACCTCGAGACGGCTTTGATT 3562

RESULT 19

US-08-459-065-1/c
; Sequence 1, Application US/08459065
; Patent No. 5882642
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil Ho
; APPLICANT: Nuss, Donald Lee
; TITLE OF INVENTION: Genetically Engineered Transmissible
; TITLE OF INVENTION: Hypovirulence
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,065
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,117
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Catherine R
; REGISTRATION NUMBER: 34,240
; REFERENCE/DOCKET NUMBER: 8589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6208
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Endothia parasitica (Cryptonectria
; ORGANISM: parasitica)
; STRAIN: BP713
; US-08-459-065-1

Alignment Scores:
Pred. No.: 6,31e-25 Length: 12752
Score: 1718.90 Matches: 296
Percent Similarity: 11.19% Conservative: 39
Best Local Similarity: 9.89% Mismatches: 7
Query Match: 71.38% Indels: 2652
DB: 2 Gaps: 264

US-10-017-084A-523 (1-344) x US-08-459-065-1 (1-12752)

QY 1 MetLys-----Thr-----Ile----- 4
Db 12533 CTAAACTCTGAGATGTTGAACACTTAACATTTCAGTTGTGAGTGGCGGAGGTTT 12474
QY 5 -----Gln-----Pro 6
Db 12473 GTATGGTAGCTTTTACAAGAGCGGTAGCCCATCTTTCGGGCAACCTTTTCGCCCA 12414
QY 7 LysMet-----His-----AsnSer----- 11
Db 12413 TTTCTTGAACATGTAGACGATCCTACGTCGACGGATCCGGCTTACTTTCCAGTCTCTGT 12354
QY 12 -----Ile-----Ser-----TrpAla----- 15
Db 12353 GCTTGTTCGGTCTTATTGCGGTGCTTAACAGCATCAGCCCTGGTCTTCTGGGCGGG 12294
QY 16 -----IlePheThr----- 18
Db 12293 GTCGTTGCGGTACAGCCTTACCACCAAGTTAAAGGTATTAGTATTCTTAGCCCTATTGCT 12234
QY 19 Gly-----Leu-----Ala----- 21
Db 12233 GGCCGACAGTTGCACGTGTGTTTCTCTCTTTCGAGTGGTCTCATTTGGTCACTGGG 12174
QY 22 -----Ala----- 22
Db 12173 TGTGTTGATGAGGCAAAATTCATCTCCCGAGGCGCTAACCATTCGCCGAATGGTGTG 12114
QY 23 -----Leu-----Cys----- 24
Db 12113 TGTTCGCTCTGGACTCTTCAGCGGGTTTCCCGCTGCCAATCTCTCAGGAGGAGAAACC 12054
QY 25 -----Leu-----Phe----- 26

Db 12053 GTAGATTTAATCTACGTACCGTTCGCGGTGGGCTGTAAACAGAAATCAGCTCCCGGGTTA 11994
Qy 27 -----Gln----- 27
Db 11993 ACGTCTTTACTGACGGGCAGTGACCATGTATAGCTTGAGTTATCCACTTCAGGTGCTG 11934
Qy 28 -----ProVal----- 31
Db 11933 GTTTTGGCGTGTACAGGGGTCACTACTCCCGTGAAGAGACAAAGAAATGACAAATGGA 11874
Qy 32 -----ArgSerGly-----AspAla 36
Db 11873 AGCGGTTTGTGTAAACCGCAACAGGTATATCCGAGGACGGGTGTCTGTAAGATGCG 11814
Qy 37 Thr----- 37
Db 11813 ACCTGCTGTCTTCTCGGGTGATGTGATCTCAGCTGTGACTGAAGGGCAAGTTCTG 11754
Qy 38 -----PhePro----- 39
Db 11753 GGCTGTAGCTCGTTGACCTGGCTTGCCATGCGGATCTCTGCATGTTCCCGCTGGTG 11694
Qy 40 ---Lys----- 40
Db 11693 TAGAAGTACCTGTGCGCATATGACTTAGGGAGGAGGATCCTCCACCCACATCCCATC 11634
Qy 41 -----AlaMetAsp-----AsnVal--- 45
Db 11633 ACAAGGATATCTTGTCGCGTTATTGTGGGACGCCACCGATGCCCATGTAACTGTGCC 11574
Qy 46 -----Thr 46
Db 11573 GTTGCCAGCAACTGCATGGCCATGTCAACTGGTATGTGTAGCATACCTCAGTTTACC 11514
Qy 47 -----Val-----Arg----- 48
Db 11513 CGAGTTAAGATCGCTCCAATGATCTTCATCTTCCCGAAAGGAGGTGAAGTTCAA 11454
Qy 49 -----GlnGly----- 50
Db 11453 GTATCGATTGTAAACGCAAGGCCATTGCGACTGCTGACGCCGCCAATGCCATGAGATG 11394
Qy 51 -----Glu-----Ser----- 52
Db 11393 GATAAACAGGAGCGATTTCGTACAGCTTTGTTCTCTCCCTGCTTGTAGCGGGTCTGA 11334
Qy 53 -----AlaThr----- 54
Db 11333 AAGCTCGGATGTGTACTTGATTGATGTACGCGAGTTCCGGGTGGACACCACTTCAC 11274
Qy 54 ----- 54
Db 11273 TTTAGTTAATCGGGGACCTTGTACTGCCCGCGACTAACTCTGAAGAAAAGAAAATCCC 11214
Qy 55 -----Leu-----Arg-----Cys----- 57
Db 11213 ACTAGGATCTTGACAGGAGGGTTCCTGTGCCAGCCAGTTGCGGCTGTATGACCAACC 11154
Qy 58 -----ThreAsp----- 60
Db 11153 ATCCATCGTCTACCGACACGATTGACCCCTCTGTTGCTGTTCTCTGTCGTCGATAGG 11094
Qy 61 -----Asn----- 61
Db 11093 GTGGGTGTGTAGCTACCTTACCCTTATGCAAAATGACATCTCGCGCGCTGTGCAAGAT 11034
Qy 61 ----- 61
Db 11033 CGACGGCGGGTTGATATCGATGCCAGTTTGTACATATGGGTGTCACAGGCCACC 10974
Qy 62 -----Arg-----ValThr----- 64
Db 10973 AGTCTTAGCCAGGAGGGCTATTACTGCTCACCTCATGCCCACGTGTAGACCTGTCCAA 10914

Qy 65 -----Arg-----Val----- 66
Db 10913 GTTCTCCAATCCAGCAATCGTCTCTTGTAGTTCGTATATGTGGGACTATGATCATTTGG 10854
Qy 67 Ala----- 67
Db 10853 GCGGGCAACAATTCGGGCTGATCAGCAAACTGATCCGAGCCCGGTTCCACATTTCCAA 10794
Qy 68 -----TyrLeu 69
Db 10793 CAGTCATCGAATCAACCTTTGAAACGTTGAAGATTGAACGCTTTGGCAGTGTGGCTC 10734
Qy 70 -----AsnArgSer----- 72
Db 10733 AAGAAAAGGATGCCGCCATTCATGAAGTGCAACAGGAGTTGCACCTCATGAAGATGGT 10674
Qy 73 -----ThrIle-----Leu--- 75
Db 10673 TGGTCTTTCCAGTCTTCCAGTCTCTGTAGCATGAACCCGTCATTTCTGTAACATCATC 10614
Qy 76 -----Tyr----- 76
Db 10613 GAAGAACACCAGGTTGCTCCCTCGGACCACTCCACCTATCTCTGTCGGAATGTCGTA 10554
Qy 77 -----AlaGly----- 78
Db 10553 CGTGGTCACGTAGATATCGGCCGATGGTCTAGTGTGTTGCCCCGTTTTCAGATTGAGA 10494
Qy 79 -----Asn-----Asp---LysTrp--- 82
Db 10493 TCGGATGTCAATGAATCTCCAGTTATCGGAGGATCTCTCTGTCGATAACGATCCA 10434
Qy 82 ----- 82
Db 10433 CAGTTTCTGATCCGATGTTCTCTCTCGGCCACACCGCTCGGGGAGAAAGTGA 10374
Qy 83 -----Cys-----LeuAsp----- 85
Db 10373 CTTACCGAAGCGTGTGTCGCTACAGTAACGTGACCGTGTCTGATGGCTTTGTGTC 10314
Qy 86 -----ProArgVal----- 88
Db 10313 GTACGTGTGGCGGTACGCGGCCCAAGGATTGGACGGCACAATTAAACGATTTCGCAGATG 10254
Qy 89 -----Val-----Leu-----Ser----- 92
Db 10253 TGGTCACTGAAGTCGGTGCCTACCGATTTCAGATTTCGCAACAGTCTCCACATGCGCCC 10194
Qy 93 -----Asn-----Thr-----Gln----- 95
Db 10193 AAATAGAAGTCTCGATGATCTCGCGAGACCATCCAGACCAAGGTCACGGAACGATACC 10134
Qy 96 -----Thr----- 96
Db 10133 GAGAGCAATCGTTTCAGGATGAATCAGCCATCTGCTGACGAACGTTTAGACCAT 10074
Qy 97 -----Gln-----TyrSer----- 99
Db 10073 GTATGGTCTCTTGGCAGGATCGAGCTGATTCTCTGCTCGAGCGGCTTTACCATGCCA 10014
Qy 100 Ile-----Glu--- 101
Db 10013 ATAAACGTGTTCGCCAGTCCGTAGACTTTTGAAATFCCCAGAACGACCACATGAATAG 9954
Qy 102 ---Ile-----Gln-----Asn----- 104
Db 9953 ATTATATATGGCCCTATCAAGAACAGTGAATAACAGCTCGACCCCAATGCAATTGC 9894
Qy 105 -----ValAsp----- 106
Db 9893 GAAATACATGCCGAGATGATGACAGTCACTGCTCTGCTGAGTGGCACCCTTATCTATCAT 9834

Qy	107	----	Val	107
Db	9833	GGCTCGGAGGCCAAGAGATCCTTCAGATAGTACAGGGTCTCTTAGTGTCTTCCAGAACCT	9774	
Qy	108	Tyr-----Asp-----	109	
Db	9773	TATCGTATTATGCAGATGCCGTAAAGGGHACTCTTAGCGACGGCATCAAAATGGGGGAA	9714	
Qy	110	-----Glu-----	110	
Db	9713	CGTGAGCTCGTCAACGTCGTGGTTTCCAGCAACTTGAGGTATATGAATTTCTCCACATA	9654	
Qy	111	-----Gly-----	111	
Db	9653	CTGGTTGTGAGTGGCCACGGATTCTCGGCATACAGCATGCTCGGTAGACGGGATGAACCT	9594	
Qy	112	-----Pro-----Tyr-----Thr-----	114	
Db	9593	TTTAAACTCCTCAGGTATCATGTCCGTGTAGCGATACACCCCGTCCACTATATCACGGAT	9534	
Qy	114	-----	114	
Db	9533	CCCCTCATCTGGAATGGCCCAAGCGCGATCCAGTTTGGCGATAAAGCATCATGCGCGGA	9474	
Qy	114	-----	114	
Db	9473	TGGTCAGGATCCCTTATCCTGAGGTGTATGTCTAGAACTTGTTCGATAAGATGGAACCT	9414	
Qy	115	-----Cys-----Ser-----	116	
Db	9413	GGCTGCTCATCCACGGAAGGAATGCTTCTTGTCTTGGTGACAACTTGAAGTTCGGTTT	9354	
Qy	117	-----ValGln-----	120	
Db	9353	CCAGTTCGGGTACAGTTTATAACCTGCATCTTCATCCTATCTTGTGACTGACGAGCTC	9294	
Qy	121	-----Asn	121	
Db	9293	GTAGCGTGATGATGTGTGTCTCTTTCAGAGACGATTCAAGTCTCTCGGCTACTCAAT	9234	
Qy	122	-----His-----	123	
Db	9233	TGCGAACCTCTGTACAGTCGGGTGGAAATGCCGTACAGAGTCGTGACCGGACCCCG	9174	
Qy	124	-----Lys-----	125	
Db	9173	TTCACACGAGGTGTACAGGAACCTTCGAGGACTGCTCTGATAATAACGGAAGACAGTCTCT	9114	
Qy	126	-----SerArg-----Val-----	128	
Db	9113	TCGCATTAGAAATAGCCGTGGGTTCTGGACCATCAGGAATGAGGTAGTGTCTCGGTTTC	9054	
Qy	129	-----His-----	129	
Db	9053	AATGGAGAGAAGCTGCTTTCACTGAACGGCTTGAGGATCGCATGTTCTCGATCCTTCC	8994	
Qy	130	Leu-----IleVal-----	133	
Db	8993	CTGCCTCCATGCCGATAGTCCGCGTAATCTTCTGGGTTGGGCGAGCTGGCAACTCGA	8934	
Qy	134	-----Val-----	134	
Db	8933	TAAATTTCCACTTCTGTATCTTCTTGGTGCAGCCGATCTCAAGCAGGATGCCAAATC	8874	
Qy	135	-----Ser-----	136	
Db	8873	GGCGGCAGCTTGCTTGAAGCGATCAACCTCGGACGAGGATAACAGGTCTCTTAGACCA	8814	
Qy	137	-----LysIleVal-----	141	
Db	8813	CACGTGTGATCGCTCGTATTTGTAGACCTGTTTGAACAAAGAAATCTTTGGGCGGTTT	8754	
Qy	142	-----SerSer-----Asp-----	145	

Db	8753	ACCAAGTAGCGCGTGCACGGCGCTGATGACGCCAAGTTGAATGTAGCTGATTTGCCCA	8694
QY	146	-----Ser-----	146
Db	8693	CGAAGTGGCACTCTGACAGTGCCTCCACCAGGTTCTTGTGTGGACGTTGGATATGAC	8634
QY	147	-----Ile-----Asn-----	148
Db	8633	TTCCGATTTGGCGAAGACAATACGCTTTATCTCTCAUTGCCGCTTCGAATCATA	8574
QY	149	-----Glu-----	149
Db	8573	GAATAAGTTTGGTATTTCCGGAATTCGTCCTTTTGGTTCGGTGGTGAAGAACTTG	8514
QY	150	-----Gly-----Asn-----	152
Db	8513	CCATGACGACCTTGCATTCGCAATGCTGGATCATTTGTAAGGAAAACCTTCCAGGAAC	8454
QY	153	-----Ile-----SerLeuThrCys-----	157
Db	8453	GGCGTCATGTCAGAGC---ACATGCTTTCGGTTCCTCCCAAGATAAAGCTCTTCCACTC	8397
QY	158	-----Ile-----Ala-----	159
Db	8396	AGTGACGTTTCACATTATTTGAGCCAGAGCTCGCTGAACGTCGCAAGTGTGCAGGTA	8337
QY	160	-----Thr-----	160
Db	8336	CTTGGATTCCAGTTTCATGCTCTACCGCCAGCTCAGGAGCGTGGAAAAGTCAAGCGGTATA	8277
QY	161	GlyArg-----Pro-----GluPro-----	165
Db	8276	GGAAGGTTGGTTATCCCATGACCCATGCATTTTCGATGGCCCTCGAATTTGCACCTGGAC	8217
QY	166	-----Thr-----Val-----Thr-----	168
Db	8216	AACTGTGCGAATTGCTGCTCTTTGCCACTCGGATGATTTTGGAAAACCTTAACCAACCAG	8157
QY	169	-----Trp-----	169
Db	8156	TTTGGCAGCCCATGGAAACAATGCTGGTTTACAGTTTGAGTCGTAGCGAGTCGCATCAGC	8097
QY	169	-----	169
Db	8096	AATGATGAAGTGCCTCTTCGGGTTTCTCAAAATCATGCAGCTCGTCCCAATGCGAGC	8037
QY	170	-----ArgHis-----Ile-----SerPro-----	174
Db	8036	CATCGATTGTGACAAAGGATGCCAGACGGCACCAGTTCGTTTCCAGGTTATTCGCTT	7977
QY	175	-----Lys-----	175
Db	7976	GTTGGCTCGATCTGAAGACATCTGTCGACCATGTAAAGCGGATAGATCTTCGAGACCAC	7917
QY	176	-----Ala-----	176
Db	7916	CGTTCGAAGTCTTCATCGCGGGAGCCAAACAAAGTTGGCCAGGAACGCTTGTGACTT	7857
QY	177	-----Val-----Gly-----	178
Db	7856	CGCGAAGCGGTGTAATTCGTAGGTTATTACCGGTACTGATGCATCCAGTCCGCTT	7797
QY	179	Phe-----Val-----Ser-----	181
Db	7796	TTTACGATCACATCCATGACACCGATTGCTTTAAGAGCCTTCTACTCTTATAGAACGA	7737
QY	181	-----	181
Db	7736	GCTTATGAACGGGGTCCCGCGAGTACTTCTTTTGATGATAAGTTCTACACTTAGG	7677
QY	182	Glu-----Asp-----Glu-----Tyr-----Leu-----Glu-----	187

Db 7676 GAGCATGATGCTCGATCGCGCAACACTTCTGCGCAATGTTTGAACATGCGCCTGCGCGT 7617
Qy 188 Ile-----GlnGly-----Ile----- 191
Db 7616 ATCTCCACCAAGCGCTTGTCTCAGGCGACAGCCAGAGTATTCGGGTTCAATATCGGCT 7557
Qy 192 -----ThrArg-----Glu----- 194
Db 7556 TATGGATCGCGCGATCCTGTCTGGGATTCCTGTCTCCAAAGAGGACGCCATCGACTGCTG 7497
Qy 194 ----- 194
Db 7496 CGGATCCCTTCCCAAGGTAATCGTTTATCCTTTTCGTGATACCTATATCCACTTCATA 7437
Qy 195 -----GlnSer----- 196
Db 7436 CTCCCAGGCTTCAATCCACAGATTTCGGCAGCCTGGTGAGACATGACAGGGTCTTGTA 7377
Qy 196 ----- 196
Db 7376 TCGAATCGGAGCTCGTTGTGTGGCCCTCCGATGCTGTTTATACAGGTAGTCTCTTCCCGG 7317
Qy 197 -----GlyAsp----- 198
Db 7316 TTCTTGATGTGGAGACAAGTTGTCTATATCATCAAGGAATTCCTCTGCCCTCGTA 7257
Qy 199 -----Tyr-----Glu----- 200
Db 7256 TTCCATCATGCTATGTTCTGAGCGAGTATGGCTTCTGACTGTGTCATGCGAAGCCAC 7197
Qy 201 -----Cys-----Ser----- 202
Db 7196 CAGCCTGTGAGTCCCAACACAGCTTTCACCTGTGTAGGGCGGAGCCGCATACATCAC 7137
Qy 203 -----Ala----- 203
Db 7136 GTCTAGCAATGGCAGGCGAGTGATATACGAACGTGTGCGACGATCACTCAGGATTT 7077
Qy 204 -----Ser-----Asn----- 205
Db 7076 GGCAGCTCTCATCGACGTACTAATAGCATAAGAATGGTTTCAGCGACCTTATAGAGTT 7017
Qy 206 -----Asp----- 206
Db 7016 CTCCCCTAGTCTTCAACACACAGCAGGTTCGTTGAGAACTCGCGGTGTATATGAT 6957
Qy 207 -----Val-----AlaAla-----Pro 210
Db 6956 AAACCTGGGAGACACCGATCGCTCTGCTCTATTAACTTGGCCCCAGTTGCCAGCTTCCA 6897
Qy 211 -----Val----- 211
Db 6896 ATTCCGCATGTCCAGAACTTAGTTCCTTCGTTCTGTTGTTGTTCTTTCGTCCTG 6837
Qy 212 -----Val----- 214
Db 6836 GACAAGCTGGGTGAAGCCAGTTGCACTACATCGAGTTTGACCTCTTCAAGGATCGCCGT 6777
Qy 215 Val-----Lys-----ValThr-----ValAsn----- 220
Db 6776 ATCTTTCAGGAAGCAGCAGCAAGTAACACAGGTCTGTTAAACCAGTGTGTCAATACGTCTTG 6717
Qy 220 ----- 220
Db 6716 ACTCCCCACCATTTCTTGGTCATAGTCAGAAATTTTGTTCATTTGTCGATTTTCGGGGCTGG 6657
Qy 221 -----Tyr----- 221
Db 6656 CTCTGACTGACCAACCGAAGGCTTTTCTCAACGTGTCTTTCGTCTATATCATCTCCAT 6597
Qy 221 ----- 221
Db 6596 TGGCACCGTGCACCTGCTGGAACCCAGCAGCAGATGATACAGCCTTGTATGTGCCA 6537

Qy 222 -----Pro----- 222
Db 6536 CGATCGTCCGGATACACCCAGTGATAAACGGTAGCGCGCTTGAGGAGCCGGAGGAC 6477
Qy 223 -----Pro-----Tyr----- 224
Db 6476 CAGGTACACCGCCGCAAAACCATATACGGAATACAAAACCTAGTGCACATCGGTACAT 6417
Qy 225 -----Ile-----Ser----- 226
Db 6416 GATCCCCCTTGAGGATCACGGTCTGCAATTTGATTCGCGCTGTAAAGTATAGTGTGCTC 6357
Qy 227 -----Glu-----Ala----- 228
Db 6356 ATCCATTGATCCAGAAGCTTCTGGAGCTGGAAGGACCCAGGTGGNAACACTGCGCCAGG 6297
Qy 229 -----LysGly-----Thr----- 231
Db 6296 TCGGACCGGTCTAACCGACTTCGACAACTTGAAGGGAGACCCGATTTGAGTCTCCTTGG 6237
Qy 232 -----Gly-----Valpro 234
Db 6236 GTTGACAAATTTCTCTCGTAAACAATCATTCGAGTTGGTGTCTCAGCAAAACACAGTGC 6177
Qy 235 -----ValGly-----Gln-----Lys----- 238
Db 6176 GAATGGGTAGAAAACGTGTGCTTACCCCGAGTTACCGGTTTCGAAGATCAATTCAACCG 6117
Qy 238 ----- 238
Db 6116 TTGCTCGGTAGTTGAGCCCTTGGGATAACGGCCACCAACCAATTTATACCGAAAC 6057
Qy 239 -----Gly-----Thr----- 240
Db 6056 CGTTACAAATGAAACCGCAGCATCCACTTGGGGTGACCATGAAATTTGGAATAACCCACAG 5997
Qy 241 -----LeuGln----- 242
Db 5996 CGCTTCAGCATTAGGAGACCGGTTTCAGTTAACCCAGCCATGCCAACCAAGTACTTCTT 5937
Qy 243 -----Cys-----Glu-----Ala----- 245
Db 5936 AACGAACTTTGGTCCCATGATCGCGCTGCCATGTAATGTTAGTGTGCAAGCACCATA 5877
Qy 246 -----Ser-----Ala 247
Db 5876 CCACCAACAACCCAGCCCTGATGACGAAGTCAAGCGGGAATTCAGATGCTTTGAGCG 5817
Qy 248 -----Val-----ProSerAla-----Glu-----Phe----- 253
Db 5816 GATGGAGTATGAACCTTCAGCCA---GCCTATGACGAGCAACACGCGTGGCAGTTTAAAC 5760
Qy 254 -----Gln-----Tyr-----Tyr----- 256
Db 5759 ATCAAACTTTCCTCCACAGCCATGCAAGTATGTCAGTATGAGGGTTGGTGAAGTC 5700
Qy 257 -----Lys-----AspAspLys----- 260
Db 5699 TTTCTGGTAGGCATTTGTGTGATAATCTCTGTCAAGTTGACGCTGTGTGACGACGACTTC 5640
Qy 261 -----Arg-----Leuile 263
Db 5639 GCATCCAAAGCAGTTCGCGTTTGGACGCGCAGCGCTCCACCAAGGCATGTAAATCTTATC 5580
Qy 264 -----Glu----- 264
Db 5579 ATAATGCCTGAAGATCTCGTTGTGGTCAACGTTTCGGAACGAGGGGTACTTGTCCCTGAT 5520
Qy 265 -----Gly----- 265
Db 5519 GTCTTAGGCACACAGCTGGATCAGCGGAGGCATGTAGCCATCCGATTTTCCCTGTTTT 5460

Db	4380	GGTACATTGATCTGCCAGCGGCGACGGCCTCCACGTAGAAGGAGTCCATCTGAGGCAATG	4321	
QY	309	-----	309	---
Db	4320	GGATGACCGATTGAACACTGCGCCAAACCAATAATTGTCAATAATCAGACTGCGCTACCGTTTA	4261	---
QY	310	-----Leu-----	310	---
Db	4280	ACAAAGCCACGGCCTGAAACGGTTTGGCAGTCTGTATGAATAGAGGCAGAGCCTGATGC	4201	---
QY	311	PheGly-----	312	---
Db	4200	TTCCGGTTGCGATGCGCCCTGCAAGSAAACGAGGATGTCAAAACCCCATCTTCGCGAGGAC	4141	---
QY	313	-----Pro-----Gly-----	314	---
Db	4140	GTGACTGAGCCTTGCCGGTGTGTACAGATATAAAATTTATCGTCGTCTCTGACCGAACCC	4081	---
QY	315	-----Ala-----Val-----	316	---
Db	4080	AGTCTGATTAGCAGTCACGTTGAGCACCGGTGAACAATTTGTCGGAATTCAGAGTTTCA	4021	---
QY	317	Ser-----	318	-----Glu-----
Db	4020	TCAGTATCCGATGACATCATCCACAATTCGGAGGCGATGAATACAGCGTAGGCA	3961	---
QY	319	Val-----Ser-----Asn-----	321	---
Db	3960	GTCTAGGGTAATTCGACAAGAAATCCACGATAGCCATGCGGTGCCGTGTCTCCACAC	3901	---
QY	322	-----Gly-----Thr-----SerArg-----	325	---
Db	3900	TCCTAATGTGCGATTTCGTATGTGACGTAACTCGTCACTTCAAAGCCGCTGACCC	3841	---
QY	326	-----ArgAla-----Gly-----Cys-----	329	---
Db	3840	ATTGGTCGGACCTGCCCGGAGGGGTGTCCTGTGCAAAGGATGAATGTAGTCAGCGT	3781	---
QY	330	-----Val-----Trp-----LeuLeu-----Pro-----	334	---
Db	3780	CYTCAATCGCCTAGTGTGCGAAGGGTTGGTATATCTTTGGCCCTTTGGCCAGGTTGAG	3721	---
QY	335	Leu-----Leu-----	336	---
Db	3720	CTAGACCTTCGCTAGCTTGAGCCATTCTCACCCACTGTGTGTTTCAAACAAGAAGT	3661	---
QY	337	Val-----Leu-----His-----LeuLeu-----Leu-----	342	---
Db	3660	GTTTCCCGCTTTCATATAATCAGCGACTGAACCTTCTTCAGCTCCAAAGGATGTCCAG	3601	---
QY	343	-----Lys-----Phe 344		
Db	3600	GCTCGTTCTCAAGAATGACCTCGAGAACGGCTTTGATT	3562	---

RESULT 20
 US-08-222-617A-26
 ; Sequence 26, Application US/08222617A
 ; Patent No. 5882879
 ; GENERAL INFORMATION:
 ; APPLICANT: Veenstra, Annemarie E.
 ; APPLICANT: Martin, Juan F.
 ; APPLICANT: Garcia, Bruno D.
 ; APPLICANT: Gutierrez, Santiago
 ; APPLICANT: Barredo, Jose L.
 ; APPLICANT: Von Doehren, Hans
 ; APPLICANT: Palissa, Harriet
 ; APPLICANT: Van Liempt, Henk
 ; APPLICANT: Montenegro, Eduardo P.
 ; TITLE OF INVENTION: A Method for Influencing Beta-Lactam
 ; TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
 ; TITLE OF INVENTION: Quantities of ACV Synthetase
 ; NUMBER OF SEQUENCES: 27

RESULT 20
US-08-222-617A-26
Sequence 26, Application US/08222617A
Patent No. 5882879
GENERAL INFORMATION:
APPLICANT: Veenstra, Annemarie E.
APPLICANT: Martin, Juan F.
APPLICANT: Garcia, Bruno D.
APPLICANT: Guierrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Von Doehren, Hans
APPLICANT: Palisssa, Harriet
APPLICANT: Van Liermp, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for
TITLE OF INVENTION: Antibiotic Pro
TITLE OF INVENTION: Quantities of
NUMBER OF SEQUENCES: 27

US-10-017-084A-523 (1-344) x US-08-222-617A-26 (1-11444)

QY	1	Met-----LysThrile :::	4
Db	1059	CTCTTCAACGAGGACGATATGCAATTTACGATGCCCTAAACATCTTGTCTGCGCGAA	1118
QY	4	-----	4
Db	1119	GCAGTGATAGGAAGAGTGACCCGGTTGCCGATATCGAACTACTATCCGCGGAGCAGAAG	1178
QY	5	Gln-----Pro-----Lys-----MethHis 	9
Db	1179	CAGCAGCTGGAGAGTGGAAACAACACGATGGCGAGTACCCCTTTCATCAAAAGCGACTGCAC	1238
QY	9	-----	9
Db	1239	CATCTCATTGAAGAGGTGGTTGAACGGCATGAAGACAAATAGCCGTTGTCTCGGACGAG	1298
QY	10	-----AsnSer 	11
Db	1299	CGAGAGCTCACTTACGGCGAGCTCAATGCCCAAGGCAACAGCCTCGCACGCTATCTCCGT	1358
QY	12	Ile-----Ser 	13
Db	1359	TCCATTGGTATCTCTGCCGAGCAGTAGTCGCATTTCTTAGATAAGACGAGAAGCTC	1418
QY	14	-----Trp 	14
Db	1419	ATTGTTACCATCTCTGGCGGTGTGGAATCGGCGCGCCCTACGTGCCCATCGACCCGACT	1478
QY	15	-----AlaIle 	16
Db	1479	TATCCGATGACGAGTGGCGCTTCGTCTGGATGACACCAAGGCAACGGCCATCATCGCC	1538
QY	16	-----	16
Db	1539	AGTAATCAACATGTGAGAGGGTCCACGAGAGGTCATCGCGGATAGAAACCTATGCATT	1598

Db 2679 CTGCCTCGATACATGATTCCCAACGGGTTGGTACAGCTGTCGACATCCCAAGTGAATGTG 2738
Qy 61 Asn-----Arg-----Val-----Thr----- 64
Db 2739 AACGGGAAGCGGACCTACGCGCTTGGCCGCGTCGATATCTCOAATTCACGAGGTG 2798
Qy 65 -----ValAla-----Tip-----Leu 69
Db 2799 CGTTCGACCTTCGAGGCGATACGGAATCGCCCTCGGGGAAATCTGGCCGCGAGTGTG 2858
Qy 70 -----Asn-----Arg-----Ser 72
Db 2859 GGAGCCGCCAGAGATCGCTCTCTCGCAACGACAACTTCTCCGCTAGGAGGCGACAGC 2918
Qy 73 -----Thr-----Ile 74
Db 2919 ATCACTGCATCCAACTGATCGCTCGCATCCGACAAAGAACAGACTCTCGTCAGCATC 2978
Qy 74 ----- 74
Db 2979 TCCGTGAAGATGTTTTGCAACAAGGACACTCTGAGCGCATGGCAGACCTTCTACAGAAC 3038
Qy 75 -----Leu----- 75
Db 3039 AAGCAGCAGGAGAAATGCGACAAACCCCATGAGGCGCGCAGAGACTGCTTTGAGGAGAA 3098
Qy 76 -----Tyr-----Ala-----Gly----- 78
Db 3099 GCAGCAACGGACAAATATCTATCTGCGAAACAGTCTTCAGCAGGCTTCGCTACCAATAC 3158
Qy 79 -----Asn----- 79
Db 3159 CTCAAGAGCATGGAACAAATCCGACGCTATGTAATGAGTCAGTCCGTTCTTCGGTACACACC 3218
Qy 80 -----Asp----- 80
Db 3219 ACATTGCTCAGATCTGTTTCAGAGAGCCCTGGAGCATGACAGCAGTCTTTCCAGCG 3278
Qy 81 -----Lys----- 81
Db 3279 CTGCGGCTCGGTTCTCATGSGAAAGAGAGTTCCTCAACTGCTCGATCAGATCCACCA 3338
Qy 82 -----Trp----- 82
Db 3339 TTGAGCTGGGTTTCTCTACTTCACCGACGTTGCCGCGGTGCTGTCGAGGACCGGAAA 3398
Qy 82 ----- 82
Db 3399 TTGGAAGACTTGGCGGCCAAGACCTTACGAGAGATTCAGCTGGATGTTGGCAGACTG 3458
Qy 83 -----CysLeu----- 84
Db 3459 TTCCGCGTCTATCTGATTAAACACAGCGAATCGCTTCAGCTGCTTTTCAGCTGCCAT 3518
Qy 84 ----- 84
Db 3519 CATGCAATCTCGATGGTTGGAGTCTGCCACTCTTGTTCGAAAAGGTTTCAGACCTAC 3578
Qy 85 -----AspPro----- 86
Db 3579 CTGCAACTGCTGCATGGGACAACTCACTTCGTCCATGATGACCTTACACTCGCACC 3638
Qy 87 -----Arg-----ValVal----- 89
Db 3639 CAGCGGTATCTCCAGCTCACCGTGAGGATCACCTCGACTTTTGGCGGCTGTGTTCAA 3698
Qy 90 -----LeuLeuSerAsn----- 93
Db 3699 AAGATCAACGACGCTGTGATATGAACGCTTGTGTTG-----AACGAGCCGACGCTTACAAA 3755
Qy 94 -----Thr----- 94

Db 3756 GTCCAGCTGCGCAGACTATGACCACTGACAGGCGACACGTCGACAAATGCTCTCTCT 3815
Qy 95 -----GlnThr----- 96
Db 3816 GGAGACGATGGCTAGCAGACCTTCGTTCAGACCTGCTCCGCCAGGTAATACCTACAT 3875
Qy 97 -----Gln-----Tyr----- 98
Db 3876 TCGATTCCTCCAAATTTGTTGGCAGCGCTGCTGACGCTTATGGCGGTGGCACCCACACC 3935
Qy 99 -----Ser-----IleGlu----- 101
Db 3936 ATAACCGCACGACCAATTTCTGGAAGGAACCTGCCCATCTTGGGAATTTGAACGAGCAGTT 3995
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Qy 105 Val-----Asp----- 106
Db 4116 GTGGAATCGGCGCTTTTGCAAAAACCGACTTAAAGCAGCGAATTAATTCGATTCCTTATTC 4175
Qy 107 Val-----Tyr-----Asp----- 109
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Qy 110 -----Glutly-----Pro----- 112
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RESULT 21

US-08-222-617A-1
; Sequence 1, Application US/08222617A
; Patent No. 5882879
; GENERAL INFORMATION:
; APPLICANT: Veenstra, Annemarie E.
; APPLICANT: Martin, Juan F.
; APPLICANT: Garcia, Bruno D.
; APPLICANT: Gutierrez, Santiago
; APPLICANT: Barredo, Jose L.
; APPLICANT: Von Doehren, Hans
; APPLICANT: Palissa, Harriet
; APPLICANT: Van Liempt, Henk

APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12364 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
FEATURE:
NAME/KEY: CDS
LOCATION: 264..11600
OTHER INFORMATION: /function= "enzyme"
OTHER INFORMATION: /product= "ACV Synthetase"
US-08-222-617A-1

Alignment Scores:
Pred. No.: 5.75e-25 Length: 12364
Score: 1718.20 Matches: 300
Percent Similarity: 10.03% Conservative: 40
Best Local Similarity: 8.85% Mismatches: 2
Query Match: 71.35% Indels: 3048
DB: 2 Gaps: 257

US-10-017-084A-523 (1-344) x US-08-222-617A-1 (1-12364)

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QY	4		-----	4
DB	1119	GCAGTATAGGAGAGTGACCCCGTTGGGATATCGAACTACTATCCGGGAGCAGAAG	1178	
QY	5	Gln	-----Pro-----Lys-----MetHis	9
DB	1179	CAGCAGCTGGAAGAGTGAACAACACGAGTGGCGAGTACCCTTCATCAAGCGACTGCAC	1238	
QY	9		-----	9
DB	1239	CATCTCATTGAAGAGGTGTTGAACGCGCATGAACAACAAATAGCCGTGTCTCGGACGAG	1298	
QY	10		-----AsnSer-----	11
DB	1299	CGAGAGCTCATTACGGCGAGTCAATGCCCAAGGCAACAGACCTCGCAGCTATCTCGGT	1358	
QY	12	Ile	-----Ser-----	13

DB	1359	TCATTGGTATCTCTGCCCGAGCAGCTAGTCGCATTTGTTCTAGATAAGAGCGAGAAGCTC	1418	
QY	14	-----Trp-----	14	
DB	1419	ATGTGTACCATCTCTGGCGGTGTGGAAATCCGGCGCGCCCTACGTGCCCATCGACCCGACT	1478	
QY	15	-----Alaile-----	16	
DB	1479	TATCCGGATGAGCGAGTGGCTTCGTGCTGGATGACACCAAGGCGCGCCCATCATCGCC	1538	
QY	16	-----	16	
DB	1539	AGTAATCAATGTGTGGAGAGGCTCCAGCGAGAGTTCATCGCGATAGAAACCTATGCAAT	1598	
QY	17	-----Phe-----	17	
DB	1599	ATCCGCTCGAGGCCCTTGTGTGGCCTCCCTTGTCTCAGGATTCCTCAAAATCCCGCGCAT	1658	
QY	17	-----	17	
DB	1659	AACTTGGACGACTACCCCTCACAAGCCAGAGCTGCCTATGTGACTTACACCTCTGGG	1718	
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DB	1719	ACCCTGTGTTCCAAAGGCGCATATTTAAACAACACACCAATGTGTGTAACAGTATTACC	1778	
QY	20	-----Leu-----Ala-----Leu-----	23	
DB	1779	GACCTGTCTGCAAGGTACGGGTGGCGGGGAGCACCAGAGCCATCTGTTTTCTCG	1838	
QY	24	-----CysLeuPhe-----Gln-----Gly-----	28	
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QY	33	-----Ser-----Gly-----	34	
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QY	35	-----Asp-----	35	
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DB	2079	CTGGCGCTGCGCGCGGTTCAAGAAATCGCATCTCAAGAGTATGGTTTTACCGAGTCA	2138	
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DB	2199	GGGAGACCGGTGCGCAACGCTCAAGTGTACATCTCAATCCATCCCTTAAACGTGTCCG	2258	
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DB	2379	CAGCTCGGATCAACAGCTTGTATGTATCAAGACCGGTGACCTGGCCCGCTTCCGAAC	2438	
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QY 60 --- 60
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Db 5193 GGGGACAAAGAGGACTCTACAGATACATTGAGNAGAACCGAGTGACCTACTTGTCTGGC 5252
QY 156 Thr----- 156
Db 5253 ACCCATCCGTGTCCTCATGTACGAATTTAGCCGTTCAAGGACCATCTACGCCGTGTG 5312
QY 157 -----CysIle-----Ala-----Thr----- 160
Db 5313 GACTGCTGGGGAGGCGTTTCAGCGAACCGGTCTTCGACAAGATCCGCGAAACGTTCCAT 5372
QY 161 -----Gly-----Arg----- 162
Db 5373 GGCTCGTTATCAACGGCTACGGCCCACTGAAGTTTCCATACCACCACCAAGCGGCTC 5432
QY 163 -----ProGlu----- 164
Db 5433 TATCATTTCCAGAGCGCGGAATGGACAAAAGTATTGGCCAAAGGTTCACAAATAGCACG 5492
QY 165 -----Pro----- 165
Db 5493 AGCTATGTGTGACGAGGACATGAAGCGCACCCCATAGGGGTGTTCGGCGAGCTCTAC 5552
QY 166 -----Thr----- 166
Db 5553 CTGGGTGTGAAGGTGTAGCGGGATATCAATCGCGCAGTGTGACCCGCGAGCGT 5612
QY 167 -----Val----- 167
Db 5613 TTTATTCTTAATCCATTCAGTCGGAGAGAGATAAGCGAAGGTGCTTAACCTCCCGTTG 5672
QY 168 -----Thr-----Trp----- 169
Db 5673 TACAGACCGGTGACCTGGTACCGTGGATTCCTCGAAGACGCGGGAGGTTCGAGTATCTA 5732
QY 170 -----Arg----- 170

Db 5733 GGTCTGAATGACTTCCAGGTCAAGATTTCGGGACTCGCATCGAAGTAGCGAGATTGAG 5792
QY 171 -----His----- 171
Db 5793 GCCATCTATATCGTCTTATCACGGAATCAAAAGTCTGTGGTGAATGCCAAGGATTGACA 5852
QY 171 ----- 171
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QY 172 -----Ile 172
Db 5913 GCCATTTCGGCGCTTCATGCAGTCTCGGCTCCCTGGCTACATGTGGCTCTCGCTCTCAT 5972
QY 173 -----Ser-----Pro-----Lysala----- 176
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QY 178 -----Gly----- 178
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QY 186 -----LeuGlu----- 187
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QY 237 ----- 237
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QY 238 -----Lys-----Gly----- 239
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QY 265 -----Gly-----LysLys----- 267
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QY 268 -----GlyVal-----Lys-----Val----- 271
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QY 275 -----ProPhe----- 276
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QY 277 Leu-----SerLys-----Leu----- 280
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QY 309 -----Met----- 309
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QY 310 -----Leu-----Phe----- 311
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QY 313 -----Pro----- 313
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QY 321 -----Asn-----Gly-----ThrSer----- 324
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QY 332 -----LeuLeuPro-----Leu----- 335
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QY 340 -----Leu----- 340
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QY 341 -----Leu----- 341
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QY 342 Leu-----Lys-----Phe 344
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US-08-859-694-1
/ Sequence 1, Application US/08859694A
/ Patent No. 6001613
/ GENERAL INFORMATION:
/ APPLICANT: Donis, Ruben O.
/ APPLICANT: Vassilev, Ventzislav B.
/ TITLE OF INVENTION: A plasmid bearing a cDNA copy of the genome of bovine
/ TITLE OF INVENTION: viral diarrhea virus, chimeric derivations thereof, and
/ TITLE OF INVENTION: method of producing an infectious bovine viral diarrhea
/ TITLE OF INVENTION: virus using said plasmid
/ FILE REFERENCE: UNVNS1110
/ CURRENT APPLICATION NUMBER: US/08/859,694A
/ CURRENT FILING DATE: 1997-05-21
/ EARLIER APPLICATION NUMBER: 60/018,246
/ EARLIER FILING DATE: 1996-05-24
/ NUMBER OF SEQ ID NOS: 1
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 14578
/ TYPE: DNA
/ ORGANISM: bovine viral diarrhea virus
US-08-859-694-1

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Pred. No.:	1.21e-24	Length:	14578
Score:	1717.50	Matches:	293
Percent Similarity:	10.79%	Conservative:	44
Best Local Similarity:	9.38%	Mismatches:	7
Query Match:	71.32%	Indels:	2780
DB:	3	Gaps:	248

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QY	6	-----Lys	-----Met	-----His	9
Db	229	GTCGTGAGTGGTTCGACGCCCTTGGAAATAAAGTCTCGAGATGCCAGCTGGACGAGGGCAT	288		
QY	9	-----Pro	-----Met	-----His	9
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QY	10	-----AsnSer	-----Ile	-----Ile	12
Db	349	GTTACGATACAGCGCTGATAGGTGTCTGCAGAGCCCACTGTATTGCTACTAAAAATCTC	408		
QY	13	-----SerTrp	-----Ile	-----Ile	14
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QY	15	-----Ala	-----IlePhe	-----IlePhe	17
Db	469	AAACCCGTGCGGGTGGAGAACCTGTTTATGATCAGCAGGTGATCCCTTATTGGTGAA	528		
QY	18	-----Thr	-----Gly	-----Gly	19
Db	529	AGGGGAGAGTCCACCCTCAATCGACGCTAAAGCTCCACACAAGAGAGGGGACCGCAT	588		
QY	20	-----LeuAlaAlaLeu	-----Cys	-----Cys	24
Db	589	GTTCCAAACCAACTTGGCATCCTTACCACAAAAGAGGTGACTGCGAGTGGTAAATAGCAGA	648		
QY	25	-----LeuPhe	-----Gln	-----Gly	28
Db	649	GGACCTGTGAGCGGGATCTACCTGAAGCCAGGGCCACTATTTTACCAGGACTATAAGGT	708		
QY	29	-----Val	-----Pro	-----Val	30

709	CCCGTCTATCACAGGGCCCGCTGGAGCTCTTTGAGAGGGATCCANGTGTGAAACGACT	768	
Qy	31	-----Val---Arg-----Ser---Gly-----Phe-----	34
Db	769	AAACGGATAGGAGAGTAACCTGGAAGTGCAGGAAGCTGTACCACATTTATGTGTGTATA	828
Qy	35	Asp-----AlaThr-----	38
Db	829	GATGGATGTATAATAATAAAAGTGCACAGAGAAGTTACCAAAGGGTGTTCAGGTGGTC	888
Qy	39	-----Pro-----Lys-----	40
Db	889	CATAATAGGCTTGACTGCCCTCTATGGTCACAAGTTGCTCACACACGAAGAAGAGGGA	948
Qy	41	Ala-----Met-----	42
Db	949	GCAACRAAAAAAACAACAGAAACCCGACAGACTAGAAAGGGGGAATGAAAAATAGTG	1008
Qy	43	-----Asp-----AsnValThr-----	46
Db	1009	CCCAAGATCTGAAGAAGCAGCAAAAATAAACCTCCGGATGCTCAATAGTGTGGAA	1068
Qy	47	-----ValArg-----Gln---Gly	50
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Qy	53	-----Ala-----Thr-----	54
Db	1189	GCGTGGCAATAATAGCTATAGTTTGTTCAGTTTACAATGGGAGAAACATAACACAG	1248
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Qy	56	---Arg---Cys-----	57
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Qy	58	-----ThrIle-----Asp-----Asn	61
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Qy	62	-----ArgValThrArg-----	65
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Qy	66	---ValAla---Trp-----	68
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Qy	129	-----	129	Qy	166	-----	166
Db	4069	AAATGGTTACAGTGCATTCCTCAGCCCTGGTATCTCGGGTGTCTTGATPAAGAGCCTAATA	4128	Db	5149	GCAGAGTCGACATGTTGGCCCTCAAAATCACCTACTTTTGGCTGATGATGAAGAGTG	5208
Qy	129	-----	129	Qy	167	-----	170
Db	4129	TACCTAGTAGAATCGAGATGCCAGAGTAACCTATCCAAACTGGAGACCCTAACTTA	4188	Db	5209	TATGATATCACAGAGTGGGCTGGATGCCAGCGTGTGGGAATCTCCCCAGATACCCACAGA	5268
Qy	130	-----	132	Qy	171	-----	176
Db	4189	ATACTATTATTATTTGATCTCAACAACAATTGTACAGAGTGGAGAGTTGACGTGGCTGC	4248	Db	5269	GTCCCTTGTGCATCTCATTTGGTTCACGGATGCCCTTCAGGAGGAATACAATGGGCTTT	5328
Qy	133	-----	135	Qy	177	Val	179
Db	4249	CTATTGTGCAATGTGTGCTTATCTTATTTGCTGTGTCAACCTTGTGGCGGACTTCTTA	4308	Db	5329	GTACAAATATACCGCTAGGGGGCACTATTCTCAGAAACTTGCCTGCTACTGGCAACTAAA	5388
Qy	136	-----	137	Qy	180	-----	182
Db	4309	ACCTAATACTGATCCTGCCTACCTATGAATTTGTTAAATTAATCTGAAACTGTT	4368	Db	5449	TGGATCCTAAGGGGGCTGCCGTGTGTAAAGAGATCACAGACACGAAATAATGCCACATT	5508
Qy	138	-----	142	Qy	183	-----	185
Db	4369	AGGACTGATACAGAAAGTTGGCTAGGGGGGATAGACTATACAGAGTTGACTCCATC	4428	Db	5509	AATATACTGATAAACTAAACCGCATTTTCGGGATCATGCCAAGGGGACTACACCCAGA	5568
Qy	139	-----	140	Qy	186	-----	188
Db	4429	TACGACGTGTATGAGAGTGGAGGGCGTATCTTTTCCATCAAGGCAGAAAGCACAG	4488	Db	5569	GCCCCGTGAGGTTCCTACAGACTTACTAAAAGTGAGGAGGGTCTGGAGACTGGCTGG	5628
Qy	141	-----	144	Qy	189	-----	191
Db	4489	GGGAATTTTCTATPACTCTTCCCTTATCAAGCAACACTGATAAGTTGCTGCGCAGCT	4548	Db	5629	GCTTACACACACCCAGCGGGATAGTTTCACTGCACCATTAACCGCCGGGAAAAGATCTA	5688
Qy	143	-----	146	Qy	192	-----	195
Db	4549	AAATGGCAGCTAATATACATGAGTTACTTAACCTTTGGACTTTATGTACTACATGACAGG	4608	Db	5689	CTGGTCTGTGACAGCATGGGAGCACTAGAGTGGTTTGCCAAAGCAACACAGAGTTGACC	5748
Qy	145	-----	149	Qy	196	-----	199
Db	4609	AAAGTTATAGAGAGATCTCAGGAGGTACCAACATAATATCCAGTTAGTGGCAGCACTC	4668	Db	5749	GATGACAGAGTATGCGCTCAAGACTGACTAGGTGCCAGCGTGCACAGCGTGCAGATGTTAT	5808
Qy	147	Ile	152	Qy	199	-----	201
Db	4669	ATAGAGCTGAACCTGGTCCATGGAAGAAGAGAGAGCAAGGCTTAAAGAAAGTTTATCTA	4728	Db	5809	GTGTTAAATCCAGAGCGGTTAACTATACAGTATCAAGGGGCGAGTCGTTCACTCCAA	5868
Qy	150	-----	153	Qy	200	-----	204
Db	4729	TTGTCTGGAAGTTGAGAAACCTTAATAATAAACAATAAGGTAGGAATGAGACCGTGCT	4788	Db	5869	AAGACAGGTGGAGAAATTCAGCTGTGTCAACGATCAGGCACACCGGCTTCTTCGACCTA	5928
Qy	153	-----	162	Qy	202	-----	204
Db	4789	TCTTGGTACGGGAGGAGGAAGTCTACGGTATGCCAAAGATCATGACTATAATCAAGGCC	4848	Db	5929	AAAACTTGAAGAGTGGTCAAGCTTTCCTATATTTGAAGCCTCCAGCGGAGGCTGTT	5988
Qy	154	Ser	163	Qy	204	-----	204
Db	4849	AGTACATGAGTAAGACAGCACTGCATAATAATGCACTGTATGTGAGGGCCGAGAGTGG	4908	Db	5989	GGCAGAGTCMAAGTAGGGAAGATGAAGAGTCTAAACCTTACAAAATAATAGTGGGAATC	6048
Qy	163	-----	165	Qy	205	-----	207
Db	4909	AAAGGTGGCACCTGCCAAATGTGGAGCCATCGGAAGCGGATAACGTGTGGATGTGG	4968	Db	6049	CAGACCGTCTCAAAAAACAGACAGACCTGACCGAGATGGTCAAGAGATAACACGACATG	6108
Qy	163	-----	165	Qy	208	-----	209
Db	4969	CTAGCAGATTTGAAGAAAGACACTATAAAAGAATCTTTATAGGAAGGCAACTTTGAG	5028	Db	6109	AACAGGGGAGACTTCAAGCAGATTACTTTGGCAACAGGGGCGCAAGCAAAACCCAGAACTC	6168
Qy	164	-----	165	Qy	210	Pro	215
Db	5029	GGTATGTGACCGCATGCCAGGGAAGCATATAGGAGTTTGAATGGACCGGAACTTAAG	5088	Db	6169	CCAAAAGCAGTTATAGAGGAGATAGGAAGACACAGAGAGTATTAGTTCTTATACCTTAA	6228
Qy	165	-----	165				

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Db 6229 AGGCGAGCGGAGAGTCTACAGTATATGAGATTGAACACACCCCAAGCATCTCTTT 6288
QY 220 Asn----- 220
Db 6289 AACCTAAGGATAGGGGACATGAAGAGGGGACATGGCAACCGGATPAACCTATGCATCA 6348
QY 221 -----Tyr-----Pro----- 223
Db 6349 TACGGGTACTTCTGCCAAATGCCCTCAACCAAGCTCAGAGCTGCTATGTTAGTAATCTCA 6408
QY 224 Tyrlle----- 225
Db 6409 TACATATTCTTAGATGAATACCAATTGTGCCACTCTTGAACAACCTGGCAATTATCGGAG 6468
QY 226 -----SerGlu-----AlaLys-----Gly----- 230
Db 6469 ATCCACAGATTTTCAGAGAGTATAAGGGTTGTGCCATGACTGCCAGCCAGCAGGGTGG 6528
QY 231 -----ThrGly-----Val-----Pro-----Val----- 235
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QY 236 -----Gly-----Gln----- 237
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QY 238 ---LysGly---Thr----- 240
Db 6649 ATGAAGGCAATATGTTGGTTTGTACCAACGAGAAACATGCCAGTAGAGGTAGCAAG 6708
QY 240 ----- 240
Db 6709 AAGCTAAAGCTAAGGCTATAACTCTGGATATAATTACAGTGGAGAGGATCCAGCCAT 6768
QY 241 Leu-----Gln----- 242
Db 6769 CTGAGAGTTGTGACATACAAATCCCTTATGTAACTGTGCTACAAATGCTATTGAATCA 6828
QY 243 -----CysGlu----- 244
Db 6829 GGAGTGACATACCAGATTGGACACGGTTATAGACACGGGTTGAATGTGAAGAGG 6888
QY 245 -----AlaSer-----AlaVal----- 248
Db 6889 GTGAGGTTATCATCAAAAGATACCTTTCATCGTAACAGCCCTTAAGAGGATGGCGGTGACT 6948
QY 249 -----Pro----- 249
Db 6949 GTGGTGAGCAGCGCAGCGTAGGGGAGAGTAGGTAGAGTGAACCCCGGAGGTATTAT 7008
QY 250 -----Ser-----Ala----- 251
Db 7009 AGGAGCAGGAAACAGCAACAGGGTCAAGAGCTACCACATGACCTCTTGAGGCACAA 7068
QY 252 -----Glu-----PheGln----- 254
Db 7069 AGATACGGGATGAGGATGGAATCAACGTGACGAATCTCTTAGGGAGATGAATTACGAT 7128
QY 255 Trp-----Tyr----- 256
Db 7129 TGGAGCCTATACAGGAGGACAGCTTAAATACCAGCTGGAAATATAATAATATCTA 7188
QY 257 -----LysAsp-----Asp----- 259
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QY 260 -----Lys----- 260
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QY 261 -----Arg----- 261
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QY 262 -----Leuile-----Glu----- 264
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QY 265 -----GlyLys----- 266
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QY 267 ---Lys---Gly---Vallys----- 270
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QY 271 Val-----Glu-----AsnArg----- 274
Db 7548 GTATGTGGTTTACAGGCTCTCTCAAGAGGATGTCCCAATGATAACAGACATATATAC 7607
QY 275 -----Pro----- 275
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QY 276 ---Phe---Leu--- 277
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QY 278 -----Ser-----Lys----- 279
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QY 281 ----- 281
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QY 282 ---Phe---Phe----- 283
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QY 285 ---SerGlu---HisAsp--- 289
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QY 290 ---Tyr---GlyAsn----- 292
Db 8323 ATTGTGGGTACGGGGATAAGTGCAGCCATGGAATCTCTGTACAAAACCCAGTATCGGT 8387
QY 293 ---TyrThrCys---Val---Ala----- 297

Db 8398 AGGTATATCTGTGATGTTGGGGGTAGGGGCAATCGCTCGCACACACGCTATTGAGTCCAG 8447
QY 298 -----Phe 344
Db 8448 TGAACAGAAAAGGACCCTACTTATGAAGGTGTTGTAAAGAACTTCTTGGATCAGGCTGC 8507
QY 299 Asn -----Lys 300
Db 8508 AACAGATGAGCTGTAAAGAAAACCCAGAAAATTTATATGGCTTATTGAGCAGT 8567
QY 300 ----- 300
Db 8568 CCAGCAATGTGTAACCCCTGAGACTAATATACACCTGTATGGGTTTACTACAAAG 8627
QY 301 LeuGly -----HisThr-----Asn 305
Db 8628 TTGGGAGCCCAAGAACTATCTGAGAGGACAGCAGGAGAACTTATTACATTCATAT 8687
QY 306 Ala-----Ile----- 308
Db 8688 GTTTGAGCCTTCGAGTTATTAGGATGAGCTCAAGGGAAATAGGAACCTGTCGG 8747
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QY 314 ---GlyAla---Val---Ser-----Glu 318
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QY 319 -----ValSerAsn----- 321
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QY 321 ----- 321
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QY 322 -----GlyThrSer----- 324
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QY 325 -----Arg-----ArgAla----- 327
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QY 327 ----- 327
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QY 328 ---Gly---Cys-----Val 330
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QY 331 ---Trp---LeuLeu-----Pro-----Leu----- 335
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QY 336 ---Leu-----Val---Leu 338
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QY 339 -----HisLeu----- 340
Db 9348 TGACCTGACCATCTCCAATCTGACAGGCTCATCGAACTAGTACACAGGAACAATCTTGA 9407
QY 341 -----Leu----- 341
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QY 342 -----LeuLys----- 343

Db 9458 AGACGTAGGACTATAAAACCAGTACTAGGAGAGAGATATCCCGACCCTGTAGTTGA 9527
QY 344 -----Phe 344
Db 9528 TATCAATTT 9536
RESULT 23
US-09-341-461-1
; Sequence 1, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 1
; LENGTH: 11272
; TYPE: DNA
; ORGANISM: rat
; FEATURE:
; OTHER INFORMATION: nucleic acid sequence of rat cubilin
US-09-341-461-1
Alignment Scores:
Pred. No.: 4.1e-25 Length: 11272
Score: 1717.20 Matches: 283
Percent Similarity: 11.96% Conservative: 46
Best Local Similarity: 10.29% Mismatches: 12
Query Match: 71.31% Indels: 2409
Gaps: 4
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QY 1 MetLys-----Thr-----Ile-----Gln 5
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QY 6 -----Pro----- 6
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QY 7 ---LysMet-----His-----Asn 10
Db 3055 TCAATAAAGCTGATATTGTGCTGACTCGCCCTTCCACCAAGGCTTTCCATAAAT 3114
QY 11 -----SerIle----- 12
Db 3115 TATGAGCAATCGATGATCATCATGATGTTTATATGACTATACAGATATTTGGGATG 3174
QY 13 -----Ser---Trp----- 14
Db 3175 CTCTCTCCCGAACTTCCCAATAATTACCCAGTAATCGGGAGTGCATCTACAGATC 3234
QY 15 -----AlaIle-----PheThr----- 18
Db 3235 ACTGTGGGACTCAACCAACAGATTGCAATTTCACAGACTTTCACCTTGGAGGACTAT 3294
QY 18 ----- 18
Db 3295 TTTGGGTACAGTGTGTAGATTTTGTAGAAATCAGACGAGGCTACGAAACGTCGCG 3354
QY 19 -----Gly----- 19
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QY 20 -----Leu-----AlaIleLeu----- 23

Db 3415 CTCTGGCTAAAGTTTAAAGTGAACGCGCACTACAGGCAAAAGGGTTTCTCAGCGTACTGG 3474
Qy 23 -----Val-----Ala-----Trp 68
Db 3475 GACGGATCATCAACAGGCTGTGGAGGTAATCTCACACCCCAACAGGTGCTCACAATCGCCC 3534
Qy 24 -----Cys-----LeuAsn-----70
Db 3535 AACTACCGATGCCTTACTACCAAGCTCCGAAATGCTACTGGCGGTGGAAGCCAGTCAT 3594
Qy 25 -----Leu-----PheGln-----SerThr-----73
Db 3595 GGCAGCCCTTCGAGCTGGAAATCCAAAGACTTCACCTGGAAACACACCCAGCGTCTCT 3654
Qy 28 -----Gly-----Val-----LeuTyr 76
Db 3655 CTGGATTACTTGGCGCGTGTGTGAGCGCGACTACCAACTCCCGACTGATAGATAAATTG 3714
Qy 30 -----ProValArgSer-----Asn-----79
Db 3715 TGTGGGATACGACACCTGCTCCCATCCGTTCCAAATAAGACGTCGTGTAATTGTTAAAAACT 3774
Qy 34 -----Gly-----Asp-----80
Db 3775 GAGGAATGATGCAAGTCAAGTCAAGCGTGGCTTTGAGATCAACTTCCGGCAGAGATGT 3834
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Qy 39 Pro-----Lys-----Ala-----Cys-----83
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Qy 42 -----Met-----Arg-----87
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Qy 43 -----Asp-----Val-----Val-----Val-----89
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Qy 45 -----Val-----Thr-----Val-----Val-----92
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Qy 48 -----ArgGln-----GlyGlu-----94
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Qy 52 -----Ser-----LeuLeuSer-----95
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Qy 53 -----Ala-----Asn-----98
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Qy 54 -----Thr-----Leu-----99
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Qy 56 -----Arg-----Cys-----Tyr-----Ser-----57
Db 4375 TCTCCAAAGATAGCCCACTGTGTTCCCAATCAACCGTCAAGCAACCCATGAGGTCTCC 4434
Qy 58 -----Thr-----Ile-----Asp-----60
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Qy 61 -----Asn-----Arg-----Val-----ThrArg 65
Db 4495 TTCAATGCTCGTGGCGAGCAGTCCCTGGAGGTTGTGGTGAATTTATCCAGCTTTCCAGA 4554

Qy 66 -----Val-----Ala-----Trp 68
Db 4555 GGAGAGATTCTTCTCCAAATTTACCCCAACTACAGAGCTAAACACAGAGTGTCTCTGG 4614
Qy 69 -----LeuAsn-----70
Db 4615 ATCATTCAAGTTGAGCGACATCACCGTGTCTCTTGAATATACATGACTTGTGACCTTGAA 4674
Qy 71 -----Arg-----SerThr-----73
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Qy 74 -----Ile-----LeuTyr 76
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Qy 77 -----AlaGly-----Asn-----79
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Qy 80 -----Asp-----80
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Qy 81 -----LysTyr-----82
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Qy 89 -----Val-----Val-----Val-----89
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Qy 90 -----LeuLeuSer-----92
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Qy 93 -----AsnThr-----94
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Qy 95 -----Gln-----95
Db 5275 CATCCAAATGCAGAAATGTCTGTGAAACATTCGCACTCCCTGGCAACCGCTGCAACTG 5334
Qy 95 -----95
Db 5335 TCCTTCCTATCCTTCAATTTGGAGAAATCTCTAAACTGTAAACAGGATTTTGTGAAATC 5394
Qy 95 -----95
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Qy 95 -----95
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Qy 96 Thr-----Gln-----97
Db 5515 ACTGCGATGGGCTTCCAGGCCAGGTTCAAAATATATTTGCAATAATAATATTGTGGGA 5574
Qy 98 -----Tyr-----Ser-----99
Db 5575 ACTCATGGGAAATCGCATCTCCCTTCTGGCCTGGAAATACCCCTACAACTCCAAATAC 5634

QY 99 ----- 99
Db 5635 AAATGGGTGTAATGTGGAGCATATCATATATCCACGGTAGAATCTTAGAGATGGAC 5694
QY 100 IleGlu----- 101
Db 5695 ATAGAACCCACACGAACTGCTTTTATGACAGTTTAAAGATTATGATGGATTGACACT 5754
QY 102 -----Ile-----Gln----- 103
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QY 104 Asn----- 104
Db 5815 AACTATCTGACATTCACGTTTTCTTCCGACTCTTCTGTGTGAGGAAGGGGATTCTCTTCTG 5874
QY 105 -----ValAspVal----- 107
Db 5875 GAGTGGTTGCGATAGATGTTTCTGATAGACCCCTCCACCATCGCTCCAGGAGCTTGT 5934
QY 107 ----- 107
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QY 107 ----- 107
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QY 108 -----TyrAsp----- 109
Db 6055 CTCACATTCTCTCTGGACATCGAACCGGAGCAGTCATCGAATTATGACAGCTGATC 6114
QY 110 -----Glu----- 110
Db 6115 GTAAAGACGAGACAGTACTTATCCACAGCTGGCTGTCTGTGTGGGTAAAGCCT 6174
QY 111 --GlyPro----- 112
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QY 112 ----- 112
Db 6235 GTCGGGGGACAGCTTCAAGCCTCTTTTCAAGAGCTGTGTGGATATTTGCATGCA 6294
QY 113 -----Tyr-----Thr-----Cys 115
Db 6295 GATCAGGAGTTATCACATCCCCCAAGTATCCAGACACCTACCTTCCCAACCTCAACTGC 6354
QY 116 Ser-----ValGlnThr----- 119
Db 6355 TCCTGGCATGTTCTGGTCCAGACTGGTCTGACCATCGCCGCTCCATTTTGACGACGCTTTC 6414
QY 119 ----- 119
Db 6415 CAGATTCAAAACAGAGACTCTTTTTCAGTCAGGGGATTTACTTGGTGTCTAAGAAACGGA 6474
QY 120 -----AspAsnHis-----Pro-----Lys 124
Db 6475 CCAGATAACCAATCTTCCACCACCTGGGACCTTCTGGAAGAAATGTGCTTTCTGGGAATG 6534
QY 125 -----ThrSer----- 126
Db 6535 TACGACGTCCTACTGTGTTCACTCGGCAATGAAATGTTTGTTCAGTTCACTCGGAC 6594
QY 127 -----Arg----- 127
Db 6595 AGTAGTAATGTGGACAAGGGTTTAAAGATCAGATGAGGCAAGAGATTTAGCTCGGG 6654
QY 128 -----ValHis-----Leu----- 130
Db 6655 GGCACGTGTACATCCATGATGCTGACTCTGACGGATACCTGACCTCCCCCAACTACCT 6714
QY 131 -----Ile----- 131

Db 6715 GCTAATTATCCCAACATGCGCAATGCAATTTGGATCTTAGAGGCGCCTCCAGGAGAGC 6774
QY 132 ValGln-----Val-----SerPro----- 136
Db 6775 ATACAGCTCCAATTTGAAGATCAATTCATATTTGAAGACACACCACAACTGTTCTGTGAGC 6834
QY 137 -----LysIle----- 138
Db 6835 TATCTTGAATTCGTGACGGACCACTCGAATGCACTGTGGTTTCCAAAGTTGTGTGGC 6894
QY 139 -----Val-----Glu-----Ile----- 141
Db 6895 CACACTGTGCTCATAGCTGGTATCTCTCGAGAGACGAATATATCTTGAAGTTTCACACT 6954
QY 142 -----SerSer----- 143
Db 6955 GACGGTGGTTCCAGCTACATGGGATTCAGGCCAAAGTACTCTATAGCTTCTCTGTGGAGA 7014
QY 144 -----Asp-----Ile-----SerIleAsnGluGly----- 150
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QY 151 -----AsnAsn-----Ile----- 153
Db 7069 TATGAAACAATGTTTGTTCAGTGGTTTATCCGAGGCTCCCGAGCACACTACCTCACT 7128
QY 154 -----Ser-----Leu-----Thr-----Cys----- 157
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QY 158 Ile-----Ala-----Thr-----GlyArg-----Pro 163
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QY 163 ----- 163
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QY 164 -----Glu----- 164
Db 7309 ACTGCTCAGATTTAGCTGCGAGTTTAACTCCAGCAGACAGAGTGTGTGGGGATTTA 7368
QY 165 -----Pro-----ThrValThr----- 168
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QY 169 -----Trp----- 169
Db 7429 ATCTGTAGTGGACGATCACTGTACAAGAGGAAGCGGATCGTCTCTGACGTTTACCAAC 7488
QY 170 -----Arg-----His-----Ile 172
Db 7489 TTGAGGCTGATACCAGCCCATCTTGTAAAGTGCAGTCACTCATCGTATTTCAATGGCATT 7548
QY 173 -----SerPro----- 174
Db 7549 AGAAGCAACTCGCCCTACTACAGAAACTGTGCGAGCGGTGTGAATGTGACCAATGAATTC 7608
QY 175 -----Lys----- 175
Db 7609 AAATCTTCAGAAACACCACTGAAAGTGGTATTTTTCATGATGGCTCCCGGCGGTATGGA 7668
QY 176 -----AlaVal-----GlyPhe----- 179
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QY 180 ValSer----- 182
Db 7729 GTCTCCGGTGAACCTTTCTTCTCTGGCTATAATAGGATCCGTGATATGCCAGAAC 7788
QY 183 -----Asp-----Glu-----Tyr 185

Db 7789 CTAGACTGTGAATGGACTCTCAGTAATCCAAATCGGGAATAATTCATCCATAAGTATCTAT 7848
Qy 186 ---LeuGlu---Ile---Gln--- 189
Db 7849 TTTCTAGAACTTTCCATGTGAAGTCAACAGACTGTACATTTGATGTCCCTTGAGTTTCGA 7908
Qy 190 ---Gly---Ile---Thr--- 192
Db 7909 GTAGGGGATGCTGATGGGCCCTGTATAGAGAGTTCTGTAGCCTGTGCAGCAACACAGCG 7968
Qy 193 ---Arg---Gln--- 195
Db 7969 CCCTTGCTATCCCTTACCCTCAGGTGTGATAGCTTCTGTACGAATGAGCGGTAGAA 8028
Qy 196 ---Ser---GlyAsp 198
Db 8029 TATAGTGAATTCATATAGAGTACTCTTTACAGATTTGTGGTGAATACGACAGGTGAC 8088
Qy 199 ---Tyr--- 199
Db 8089 AATGGAGTGTCTCAAGTCTCACTAATCCAACTTTGTACAGTGTGATGGACCCACTGTCA 8148
Qy 199 --- 199
Db 8149 TGGCTGTGAAGCCCCAGAGGGCACACCATCTCTCACATCAGTGTACTTTCTTC 8208
Qy 200 Glu---Cys---SerAlaSer---Asn---AspValAla--- 208
Db 8209 GAGGCTCATCAACTTGTCACTTCAGACTCCTGTCAGTGTGAGTGTGAC---TCCCCA 8265
Qy 209 ---AlaProValVal---Arg---ValLys--- 216
Db 8266 GGATCGCCCTGATAGACACTGTGGACAGTGTGCCAGTGTCCCAAGCGCATACAGTCTGTGT 8325
Qy 217 ---ValThrValAsn---Tyr 221
Db 8326 TCCAAACCACTTATAGTACTTTTACACAAACATCAAGGGCAAACTCGTGGATTTTAT 8385
Qy 221 --- 221
Db 8386 GCAACATGGACCAACAAACGCTTTAGTGTGGGGAACATTCCTCACTCAGCTAATGTGTACA 8445
Qy 222 ---Pro---Pro---Tyr--- 224
Db 8446 ATCAATCTCTCCTCAGTGGCTTCAGACATTTCCAGAAAACAGCAGATGCTCTCGACAGTG 8505
Qy 225 Ile---Ser---Glu--- 227
Db 8506 ATCACTCAGCATAGTAAACACTGGGAGATTAGCTTTGACAGCAATTTCCGAATCCCCAGC 8565
Qy 228 ---AlaLys---Gly--- 230
Db 8566 AGTGACAGCCAGTGTGAGAACAGCTTCGTGAAGGTTTGGGGAGCGAGGTGTGATGATCAAT 8625
Qy 231 ---Thr---Gly---Val---Pro---Val---Gly 236
Db 8626 AAGACCTGTGTAGCCAGAGCTGTGAGATGTGGTCCCAAGTCCCATTTGTACATCAGGG 8685
Qy 237 ---Gln--- 237
Db 8686 AACATTTTCACTGCTGTCTTCCAATCTGAGAGATGGCAGCCAGGGCTTCTCTGCATCC 8745
Qy 238 ---LysGly--- 239
Db 8746 TTCATTAGCGGTGCGGACGACATTCATACCTCCCTGGTGTGACATCATCTCTCCAAAC 8805
Qy 240 ---Thr---Leu---Gln 242
Db 8806 TTCCCGAAGCAATACGACAAACATGAATGACCTACCTCATATAGACGCTGACCCCTCAG 8865
Qy 242 --- 242
Db 8866 TCTCTGGTCACTCTGACTTTTGTGCTCTTTCATTTTGGAAAGATCGCTCAGCTATACCGGA 8925

Qy 242 --- 242
Db 8926 ACCTGTGATCATGATGGCTTGGACATCATCAAAGSTCGTAACCTCTCTTCCATCCTCTC 8985
Qy 243 ---Cys---Glu--- 244
Db 8986 GTGACCATAATGTGGTTCGAAACTTTGGCTCCCTCACCTGTGGACGGCCAGTTGTGCTC 9045
Qy 245 ---Ala---Ser---Ala--- 247
Db 9046 AACTTCTATTTCTGATGATACACACAGACTTTGGCTTCAAGATTTTCTTACAGAGCCATC 9105
Qy 247 --- 247
Db 9106 ACCTGTGTGGGATCTACAAATCCTCTGGAATCCTTAGGAGCCCTTCTTACTACTATAC 9165
Qy 247 --- 247
Db 9166 AGCAACTACCCCAACAACCTCTACTGTGTCTACAGCCTCCATGTTAGAGCAGCAGAGTG 9225
Qy 248 ---Val---ProSer---Ala--- 251
Db 9226 ATAATAATTAGTTCAAATGATTTTCGATGTGGCTCCTTCCAACTTTGTGCAATGATCTC 9285
Qy 252 ---Glu---Phe--- 253
Db 9286 CTGGAGGTGTTGTGATGGTCCCAAGCATTTGGAATTCATCTCTTTGGAAAGTTCTGTGTTCC 9345
Qy 254 ---Gln--- 254
Db 9346 ACGCGTCCACAAACTTTAAGAGCACCATAAGCAGCCTGACCTGTGTTCAGACAGAT 9405
Qy 255 ---Trp--- 255
Db 9406 TCTTCTCAACACAGAGAGGTTTGGAAATAATTTTCCGGAGACAATAGGGCCACAGCAG 9465
Qy 256 ---Tyr---LysAsp---AspLys 260
Db 9466 GGATGTGGTGATACCTGACCGAGGACCAACAGAGCTTTGTGTCTCTGATTTCTGATTCG 9525
Qy 261 ---Arg---Leuile--- 263
Db 9525 AATGGACGCTATGACAAAGGCTCTCAGCTGATATGGTATCATAGTTGCACCTGAAACAAA 9585
Qy 264 ---GluGlyLys---LysGly--- 268
Db 9585 CTGGTTAAGCTCACCTTCATGTGTTCCTCTGGAGGAGCCATCGTCAGCTGGAGCTGC 9645
Qy 269 Val---LysValGlu---Asn--- 273
Db 9645 GTCTATGATTAATGTGCAGATAGCAGATGGCGCAACATTAACATCATATTAGTGGAAAA 9705
Qy 274 ---Arg---ProPheLeuSerLys---LeuilePhe--- 282
Db 9705 TTCTGTGCTCCGATGCTGCTGCCCATTTATCTCTCCGGTACTTCTTACGTTTACG 9765
Qy 283 ---PheAsn---Val--- 285
Db 9765 TTTGTCTCTGAGTAACTGTGTAATGAGGGGATTTAATGCAACATATACCTTTTGTGGAC 9825
Qy 285 ---SerGluHis 288
Db 9825 ATGCCTTGGGGGAAACATATAACGCAACCTCGACACCTCAAATCGCTCATCCTCAT 9885
Qy 288 --- 288
Db 9886 TTATCCAAATCGGAGCGCCATCTTCCACCTGTACTTGGGTATCGCAGCTCCGCCACAG 9945
Qy 289 ---Asp--- 289
Db 9946 CAGCAGGTTCAATACACTGTGTGGGACTTACAGTGTGCCCTCACAAGACTGTGTCAAAAGC 10005

QY 12 ----Ile-----Ser--- 13
Db 46508 ACACATCTGATCATAGCCATCAATTACCTGCACAGGTGCTCTCCCTCAGATGCACTTGA 46449
QY 14 Trp----- 14
Db 46448 TGGACAGCAGGTACTCTCTTCCACCAATAGGTTTTATGACTTAATTTTGGATTCTCC 46389
QY 14 ---- 14
Db 46388 TTTAACAACAATATACACAGTCAACAGATTGGTTCTGAGTGAGCTCTCAAGGCTACTT 46329
QY 15 ----AlaIle----- 16
Db 46328 GGCTGATGCGCGATCAATGATGAATGGCTGGACAGAACCTTTTATAGCTCCTTTTCC 46269
QY 16 ---- 16
Db 46268 CCGCCACAGCTTCAGTATTTCCCAATTCCTTCCATAGCCCTCTGTAGAAATGTCTGAT 46209
QY 17 ----Phe-----Thr----- 18
Db 46208 ATCCACCAATTTTTTTTTTTTGGATGGAGTCTCACTCTGTCAACCAGGCTGAGTGCAG 46149
QY 19 ----Gly----LeuAlaIleLeu-----CysLeu 25
Db 46148 TGGTGGATCTTGGCTCACTGCAAGCTCTGCTCTCTGAGTTATGCAATCTCTCGCTT 46089
QY 25 ---- 25
Db 46088 AGCCTCCCAAGTAGCTGGGACTATAGCAGGCACACAGCCGCTGGCTAATTTTTTGGCT 46029
QY 26 Phe-----GlnGly-----Val-----ProVal 31
Db 46028 TTTTAGTAGACAGGCTTCACTGTGTAGCAGGATGATCTCGATCTCCCGACCT--- 45972
QY 32 Arg-----Ser---GlyAsp----- 35
Db 45971 CGTGATCCGCCACCTCAGCCTCCCAAGTGTGGGATATACAGGCGTGAGCTACCGCGC 45912
QY 36 AlaThr-----Phe-----Pro----- 39
Db 45911 CTGACCAATGTCTGCTATCAATTTTTCAGGGCTCAGGCTGCCATCCAGATCAGCCTT 45852
QY 40 ----LysAla----- 41
Db 45851 AGACATAAGGCTGATGATGGCTCCAGGCTGCCATGAGCCAGCCCTCTGCTCCAGAGAGA 45792
QY 42 ---- 42
Db 45791 ACNACCTCAGGCTGCCCTCCAGCAGCACACAGTCTCTGTGCCAACCTTTGCAATGGTT 45732
QY 42 ---- 42
Db 45731 CTTTCAGATGCCACTCTCTCTCTTTAACTCTGCCTCTCCAAATTCACCTCTTAGGCC 45672
QY 42 ---- 42
Db 45671 CCACCCACTCTTCCATAAATACCCGCTACCTGCTCATTCTGCTCATCTTGGCTCTGTG 45612
QY 43 ----Asp-----Asn----- 44
Db 45611 CACCTACAGGCTTACTCTATGATTTTATGTTTATACATGTCTGCTCGTCAATTCACCACTTA 45552
QY 45 ----ValThr-----Val----- 47
Db 45551 TAAGTAGAACTGCATATGCAGAAAGATAGTGGTTATATATGATTTTATTTTGG 45492
QY 48 ----Arg----- 48
Db 45491 GGACAGGGCCTCCCTCTGTGTGCCAGGCTGGAGTGCAGTGGGAAATACAGTTTCACAGC 45432
QY 49 ----Gln-----Gly----- 50

Db 45431 AGCTTCAACCTCAGCTCCCAACTCGCCCTCTGAGTAGCTGGACTACAGCAATTGGC 45372
QY 51 ----GluSer----- 52
Db 45371 ACCATGACCCACTAATTTTTTAAATTTTGTACATATGAGAGTCTCATTTATGTTGCCAG 45312
QY 53 ----Ala----- 53
Db 45311 GCGGTCTCAAACTCCTCGGGCTCAAGCGATCCTTCTGCCTTGGCCTCCCAAAATGCTAGG 45252
QY 54 ----ThrLeu 55
Db 45251 ATTACAGGCATGAACATGATGAGTAGGGTTTTAGAGTCAGATTTTCAATTTTATTCTTTA 45192
QY 56 ----Arg-----Cys-----ThrIle----- 59
Db 45191 TTTTGTGAGACCGAGTCTTGTCTGTATCCAGGCTGGGTACAGTGGCACAATCATGG 45132
QY 59 ---- 59
Db 45131 CTCACCTGCAGCCTTTAGCTCCTAGCTCAAGCAATCCTTCTGCTTTAGCCTCCCAAGTAGC 45072
QY 60 ----Asp-----Asn----- 61
Db 45071 TAGGACTACAGGTGCAACCAACCATGTCGGCTAATTTAAAGAGAGAGAGAGAGAGAG 45012
QY 62 ArgVal----- 63
Db 45011 AGAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 44952
QY 63 ---- 63
Db 44951 TGT 44892
QY 63 ---- 63
Db 44891 GGCTCTCAAACTCCTAGGCTCAAGCAATCCTCCACCTCAGCCCTTTCAAATTCCTGGATT 44832
QY 64 Thr-----ArgVal----- 66
Db 44831 RCAGGCATGAGTACCGTGCAGCCAGCTAGAGTACAGATATTTAAATTAATTCGTCTGCCCTG 44772
QY 67 ----Ala----- 67
Db 44771 TAATAGTACGTGACTTTGGATGAGTACTTAACTTCTCTGTACAGGGGTAAATAAAGA 44712
QY 68 ----TriLeu----- 69
Db 44711 AAGTATGAACGTGATATGTTTGGCTCTGTATPCCCAACCAATCTCACCTTGAATTGTA 44652
QY 69 ---- 69
Db 44651 ATAATCCTCATTTGTCAAGGTTGGGCCAGCGTGGAGATACTGAATCATCGGGTGGTTT 44592
QY 69 ---- 69
Db 44591 CTCCCATACTATTTAATGTAGTAGTAACTCTCACAAGATCTGATGTTTGTAAATA 44532
QY 69 ---- 69
Db 44531 GGAGTTCCTCTACACAAGCTCTCTTGCCTGCTTCAITGTAAGGCATGACTTTGTCTCTCC 44472
QY 70 ----Asn----- 70
Db 44471 TTTGCCTCTGCCATGATTTGTGAGGCCCTCCCGAGCATGTGAAACTGTGCGTCTATTACA 44412
QY 71 ----Arg----- 71
Db 44411 CCTCTTTTCTTATAAATTACCCAGTCTTGGGTATGCTTTTATTAGCAGTATGAGCA 44352
QY 72 ----Ser-----Thr 73
|||

44351	Db	GACTAATACAGTATGTGAAAGCTCTAGTTTCATGGCCCTGGCAACAACAACTGAATTGCACC	44399
74	Qy	Ile-----LeuTyr-----	76
44291	Db	ATACATTCAATTTGACTTATATGAATTTAATCTGTATGCACCTGGGTGGGGAAGAGAGAG	44332
76	Qy	-----	76
44231	Db	AGAGATCAATTTGACGAGCATGGTAGTCTCTACTCAATGAGTGTGTGGCCAAGTGCATGTG	44172
76	Qy	-----	76
44171	Db	GGATGGGAGACAGCTGTCTCAGTGCCTGCGAGCTTCTCCTAGGAGAGCATTCAGGGCAC	44112
76	Qy	-----	76
44111	Db	TGAGTGTGTTCTTAGTGTTTCAATAGCCATGTCTCTTCTTACAACTGGTTTCCAAACA	44052
77	Qy	---AlaGly-----Asn-----	79
44051	Db	CAGGCTGGCTATTTCATGTGAAGCTCTCTGGAAGACAGTGAATCTGTGCCAACTCTAGA	43992
80	Qy	Asp-----Lys-----Tyr-----	82
43991	Db	GACCTCTGGGAGATGGAGATGAATTTCCAAATGGCGCCTTAAGAGATTTTAAAG	43932
82	Qy	-----	82
43931	Db	AATCAGTTCAACTGCACTCAGATTTTGGCTTAAATAGCCTTTAGAACCTTACCCGTCAGA	43872
83	Qy	-----Cys-----	83
43871	Db	GAGTTGAAAATAATGCTAGTGTGTGGTGTGTTTTTCCCACTTCTGGCGATGAACCTT	43812
84	Qy	-----LeuAsp-----	85
43811	Db	ACACTCATTTTGACCTTCTGCAATCTAATCCAGCTCTGTCTTAAAGTTGGCCACTCAATAA	43752
86	Qy	-----Pro-----	86
43751	Db	ATATGTATTGAGTGATTCATGAAGGAACAATCAATAAGTACTTTTAAATAGCCATTC	43692
87	Qy	---Arg-----ValValLeu-----	91
43691	Db	CTGAGAATCTCAGATATCCTTATATCTGTGTAGTCTCTCATAAACCAATAAACTGA	43632
92	Qy	---SerAsn-----	93
43631	Db	AGCTCCAATGAGGCTGACAGCTTCCCTATTAATAAAGAGTCTACATGATTAATCTCTAT	43572
94	Qy	-----Thr-----	94
43571	Db	GATAAAACCTTATCTTTCTATAAGGAATCATTACTTTTAATACCAGCTCAATTTAGTT	43512
95	Qy	-----Gln-----Thr-----	96
43511	Db	AGCTCTAAATCGATAGAACAAATGTTTCCCTAGAGAATGAATTTACCTGTGTTCTCTC	43452
96	Qy	-----	96
43451	Db	CCCATCTTCTTCAATTTCTTTTCATGTGCTGGTACTGTGGCGPATTTTCCTCTAAC	43392
97	Qy	-----GlnTyrSer-----	99
43391	Db	TGCTTCCAATATTCTCGGAAAGCAACCAATCCAGAACTTTAAATGTTTATGAACACC	43332
100	Qy	-----	101
43331	Db	ATAACAAAATAATCTTCTTGCGCCTACAATTTCAAAGTGTGTAATATAAATAAGGT	43272
102	Qy	-----Ile-----	103
43271	Db	TAGAAAATAATGTGCTCTAAAGATGAATAATCTGCCTTATGTTTGGCTGCAGTACTTC	43212

QY	104	----	-----AsnVal	105
Db	4321.1	ACTCCTGTGAGACAGTGGCTTTAGCTACAGAGCTCAATTTTATATATAACCCAAATGTG		43152
QY	105	----	-----	105
Db	43151	TTCATGATGTACACTTACTTTTATAAATCCCACHTTTTATATATAACCCCTCTTATGCACCTGA	43092	
QY	105	----	-----	105
Db	43091	AGTTTTTCTCCTCCCAAAAGAGATATGTTGAAGTCTTAACCCCCAGTGCCTTAGAATGT	43032	
QY	106	Asp---Val-	-----Tyr-----Asp-----Glu	110
Db	4303.1	GAACCCATTTGAAAACAGGGTCGTCGACATGAGACTACTTAAAGATGAGATCATACCAGT	42972	
QY	111	GlyPro-	-----Tyr-----	113
Db	4297.1	GGGCCCTTAGTTCAATATGATGCTCTTGCAGAAGATGCCCATGTGAAGACACGGGA	4291.2	
QY	114	-----Thr---Cys	-----	115
Db	4291.1	CACACAGGAACACGATGTGATGAAGCAGAGATGGAGTGAATGCGACTGCGAAGTAAA	42852	
QY	116	-----Ser-	-----Val--	117
Db	4285.1	GAATGCCAAAGATTGCCAGTCAGCCACGACAGCTAGGAAGAGGCAAGGAAGATTCCC	42792	
QY	118	---Gln-	-----Thr-----Asp-----	120
Db	4275.1	CTACAGGTTTCAGAGGGCACTTGGTCTCTGTCACACCTTGATTTTCTATTTCACACTCTTC	42732	
QY	121	---Asn-	-----His-----	122
Db	4273.1	CAGAATTGTGACACAATACATTCTATTGTTGTAAGCCACCTAGTTGTTGAACCTCTGTT	42672	
QY	123	-----ProLys-	-----Thr-----	125
Db	4267.1	ACAGAGCCCGAGAAACTAATAACAAATCCAAACCTGTTACTGATGACAGATTACTCTAT	4261.2	
QY	126	---SerArg-	-----Val--	128
Db	4261.1	GAATCTCAAGGTGAAAAGCTTTATGAACTTAGCCATATCGCATATCTGAGAAAGTGAAA	42552	
QY	129	-----	-----His--	129
Db	4255.1	TACCTAACTGTATCCCTATAACACTCAGCATGGTGTGACATATTCAGGGGCACGTG	42492	
QY	130	-----Leu---Ile---ValGln-	-----	133
Db	4249.1	AGGAANTAGAGTAACCTCCATTACAGTACAAAAGACAGTAATACAAAGAAATACAAGG	42432	
QY	134	Val	-----Ser-----Pro-----Lys--	137
Db	4243.1	GTAGCCCTGGAATTAACAGTTTTTAACTGTCTCTCTCATTTTCGTTTTTCTTAATGGCA	42372	
QY	138	-----Ile-	-----Val--	139
Db	4237.1	GCTCTGGAATCTAGGCTCTTCCCATTACTTCTTAGCTCTTGCTCTGTTGTAATTG	42312	
QY	140	-----Glu-	-----	140
Db	4231.1	GCTCGGACAGAGTGGACGACAGACCCCTATTATTGAATGAATAATTTATAATGCATCT	42252	
QY	141	---Ile-	-----SerSerAspIle-----	147
Db	4225.1	TTGATTCGGAAACATCTCTGATTTGACATGACTTTTCTCTATAAATAAGAAATTATAT	42192	
QY	148	-----Asn-	-----GluGly-	151
Db	4219.1	CACTAAGCAAACTCAGTATTTGGGAGTTTTTTTGTGGTAAAGTAGTAGAATTTCTCTAAT	42132	

Qy	152	-----AsnIle	-----SerLeuThrCys	157
Db	42131	TATAAAGCAATTAAAAAATATATATATTTTTTCGTGTTGAGAGCGTCTCACTC	-----TGTCAAC	42075
Qy	157	-----	-----	157
Db	42074	CCAGGCTGGAGTACAGGGGCATGATCTTGGCTCACTGCAGCCTCCAACCTCTAGGCTCAA	42015	
Qy	158	---Ile	---AlaThr	160
Db	42014	GCAATTGCTCTGCTCAGCCTCCGAGTAGCTGGGACTACAGGCACCCGCCACACACCC	41955	
Qy	161	-----	---Gly	161
Db	41954	GGCTAATTTTTGTATATTTTCAGTAGACAGGGTTTCAGTGTTAGCCAGATGGTCTC	41895	
Qy	162	-----Arg	---Pro	163
Db	41894	AATCTCTGACCTCGTGATCTGCCGCCCTTGGCCTCCCAAAGTCTGGGATTACAGGCAT	41835	
Qy	164	GluPro	---Thr	167
Db	41834	GAGCCATCAAGCCAGCCTTCTTTTTTTTTTTTTTTTAAACAGACAGTCTCACTGTCTC	41775	
Qy	168	Thr	---TrpArg	170
Db	41774	ACCCAGCTGGAGTACAGTGGCGCACTTTAGCTCACTGAACCTTTGCCCTCCCAAGCTT	41715	
Qy	171	-----	---His	171
Db	41714	AAGCAATCCTCGGCCCTCAGCCCCCTCAGTAGCTGGGACTACAGGCACACACCACAACAC	41655	
Qy	172	-----	---Ile	172
Db	41654	CTGGTAATTTTGTGTTTTTTTGGTAGATAAGGTCTCATTAAGTTGCCTAGGCTAGTC	41595	
Qy	173	---Ser	---ProLys	175
Db	41594	TCGAATCTCTGGGCTCAAGCAATCCACCACCTCAGCCTCCCAAGTCTGGGATTACAG	41535	
Qy	176	---AlaVal	---Gly	180
		:::		
Db	41534	GCATGAGCCATAATATCTGGCCTAATCACTTTTGTGTTGGTTTTTGTGTTTTTGTGTT	41475	
Qy	181	-----SerGlu	-----	182
		:::	-----	
Db	41474	TTTTTTGACACAGAGTCTCGTTCTGTGCGCCAGGCTAGAGTGCAGTAGGGCGATCTCGGC	41415	
Qy	182	-----	-----	182
Db	41414	TCATGCAACCTCCTCCTCCTGGTTCAAGTAATTTCTCTGCTCAGCCTCCCAAGTAGC	41355	
Qy	182	-----	-----	182
Db	41354	TGGGATTACAGGTGTCACCATCATGCTCGGCTAATTTTGTATTTTGTAGTAGACGGG	41295	
Qy	183	-----	---Asp	183
Db	41294	CTTTCCACATGTTGGTCAGGCTCATCTTGAACCTCTGATCTATGATCCGCCACCTTGG	41235	
Qy	183	-----	-----	183
Db	41234	CCTCCAAAGTCTGGGATTACAGGCATGAGCCACCGCACCTGGCCCTTGTACATTTT	41175	
Qy	184	-----Glu	---Tyr	185
Db	41174	TTAATGTGAGCAGAATCTTTAAACAAATAGAACCAAGCACTACAGCACTGCAAGGAAA	41115	
Qy	186	-----Leu	---GluIle	189
Db	41114	TTTGAAGCTCATCTACTCTAAAAATTGTCATTTATAGAAAAAGGAATTAAGGCTCAGATA	41055	
Qy	189	-----	-----	189

41054	GGCTGAATGAACTGCTCAAGGTCCCAAGAAGAGATAGACCAAGAGAAACCGGACTG	40999
QY	190	---Gly---Ile---Thr192
Db	40994	CTAAGGGGTGATTCAAGCGCTGTTCCCATATATTTATTAGCTATTAAAACTGGGACT40935
QY	193	Arg---193
Db	40934	CGGGCCAGGTGCAGTGGCTCAGCTGTGTAAACCCAGCACTTTGGGAGCCCTAGTGGGTG40875
QY	193	---193
Db	40874	GATCAACCCAGATCAGGAGTTCGAGACACGCTTGGAACAATGGTGAACCCCTGTCTCTA40815
QY	193	---193
Db	40814	CTAAAAATACAGAAGTTAGCTGGCGTGGTGGCGGCTGTAAATCCAGCTACTCAGG40755
QY	194	---Glu---194
Db	40754	AGGCTGGGAAGGAAATTTGCTTTGAACCTGGGAGGCAGAGTTGCAGTCAGCCAAATCA40695
QY	195	---GlnSer---196
Db	40694	CACCACTGCATCCAGCCTGGTGCACAGACGGAGACTCTGTCTCAGAAAAACAACAACA40635
QY	197	---GlyAsp---198
Db	40634	ACAACAACAACAAAAACAAAAAACTGGGCACTAGTAGAGAGTATTTCTTGACCTTC40575
QY	198	---198
Db	40574	TGGTGAATGAACCTTTGACTTGAAATCTGTGAACAGAAAACTATTAGGAAATTCCTAA40515
QY	199	---198
Db	40514	TTGCTCCCATATTGGTATTTTACTTACCAATTCCTCTCCACTTCACTTATATTGT40455
QY	199	---Tyr---GluCysSerAla203
Db	40454	TGAGCTTCAAAATTTTCTCTGAAGTACTCAGCAGCGCTTAGAAAAATAGAAATGTTCACT40395
QY	204	---SerAsn---205
Db	40394	TAAGTAGAAACTTGACGAACTTTAGGCACCAATTTGACGAGTAATTTTCAGTTTAGTAA40335
QY	205	---205
Db	40334	TGAGATTCACAATTCACAGTGGCTTGAAGTTCCAAGTTCAAGMAGTAGTTACAGATTAC40275
QY	205	---Asp---206
Db	40274	AGATCTTTACATTTGGAAAAGAAAAATTTTGGAAATCAAAAGGAAAAAGGATGAAGATAA40215
QY	206	---206
Db	40214	CAAGTGGGATACAGGAGAGGATTAAACAGAAAAATATTTCTTATCCAGTGATTTTCTTC40155
QY	206	---206
Db	40154	AGGACAAGATTTCAGTCTTCCATTCTCTATAATATGTTTGGGGAGGAAAAACAGACCCAC40095
QY	207	---ValAla---208
Db	40094	ACCAGAAGTTCTCAGCGTTTGTGTAGTGTCCTAATGTACAGGTTGTCTCTCTGATTTA40035
QY	209	---Ala---Pro---210
Db	40034	ACAATAGTGGCTAGATGTGGTGGCTCACACCTGTAAACCCAGCACTTTGGGAGCGGAGG39975
QY	211	---Val---ValArg---Arg---Val215

Db 39974 TGGGTGATCAGAGGTGAGAGTTCAGATTCAGCTGGCCAAACATGGTGAAACCCCGTC 39915
QY 216 -----Lys-----ValThrVal-----Asn----- 220
Db 39914 TCTGCTAAAAAATTTAGTGGGGGTGGTGGTGGCCACCTGTATCCAGCTACTGGGA 39855
QY 220 ----- 220
Db 39854 GGCTGACGAGGAGCAGAGGTTGACGTAAGCCAAATCGCACCTGCACCTCAGCGCTG 39795
QY 220 ----- 220
Db 39794 AGTCAGAGTGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAA 39735
QY 221 -----Tyr-----Pro----- 223
Db 39734 AGAATGCTGCATATCTGTTTCTGCACCACTACTGAGCTCCCTGAGAGCAGATGTGT 39675
QY 223 ----- 223
Db 39674 CCCTCCATCCATCCCTTTATCTCGCACATAAATGCTTAATGAGAAAGAAATAATGGTT 39615
QY 223 ----- 223
Db 39614 TAGCTGTCTCCAAATGTTAAGGTATTTTCCAGCACAAATTTAGTCAATTTCCAGTCA 39555
QY 223 ----- 223
Db 39554 AACAAATTTCAAGTTTATACTACATTTATATGATCTTTTTTTTGGCAGAAATTTCTGTGA 39495
QY 224 -----Tyr-----IleSer----- 226
Db 39494 AACAAATTTCTGTAATTTATGGTTGCTAAATPAAAAACCGCATTTTCAGACCATAAGTTTTT 39435
QY 227 -----Glu-----AlaLys----- 229
Db 39434 GGAATACGAGTAATCTAAGGCTCCAAAGACAGAACTGTAAATTCAGAAATAACTCCTT 39375
QY 230 -----GlyThr-----Gly 232
Db 39374 TAGGAAGAACATCATGATAAGCATCCCAATTTACAAAGAGCAAGTTAATAATCAGG 39315
QY 233 -----ValPro-----Val----- 235
Db 39314 ATTTAGAAATAGATGAATGACAGCTAAAGCTTTTGTAGTCTTAGTCTTCTCAGCTGTAA 39255
QY 236 -----Gly-----GlnLys-----Gly----- 239
Db 39254 AGTGGCATGGTACCATTTCACAGGAATTTGATACGAGGATTAGAGAGATTAGGCTGTG 39195
QY 240 -----Thr-----Leu-----Gln-----Cys----- 243
Db 39194 AAGTGCTGCACACACAGATAGTTCTTGAATCAATGAGGTAATTTAGTACCTCATCTG 39135
QY 244 -----Glu----- 244
Db 39134 TCTCATAGCCTAACTGGGCATGATCAATATCTTCATGAGAAAAATGATTCACACACC 39075
QY 244 ----- 244
Db 39074 CAGGGCTGTCCAAAAGACATTTCTCTCTGTCTACCTATTCCCTCTCCACCCCCC 39015
QY 245 -----AlaSerAla----- 247
Db 39014 AAATCCTATACAAATTCCTCTTCTCGCGCGGCATGGTGGCTCATGCTGTAAATGCCAG 38955
QY 248 -----Val-----ProSer----- 250
Db 38954 CACTTTGGGAGCGCGGGGTGGATCAAGGTCAGGAGATTGAGACCTCTCTGTG 38895
QY 250 ----- 250
Db 38894 ACACAGTGAACCCCTGTCTCTTCTTAAAAATACAAAAAATTAACGAGGTGCTGGCAGG 38835

QY 250 ----- 250
Db 38834 CGCTGTAGTCCCGAGCTACTCTGGAGACTGAGGCAGGAGAAATGGTGAACCCAGGGGGC 38775
QY 251 -----Ala-----Glu----- 252
Db 38774 GGAGCTTGCACTGAGCCAAGATCGCGTCACTGCCTCCAGCTGGGGGACAGAGCAGAC 38715
QY 253 -----Phe-----Gln-----Trp----- 255
Db 38714 TCTGTCTCAAAAAAATAAATTCCTTTTCTCCATCCCATGCCCTGTAAATGGACCTCC 38655
QY 256 -----Tyr----- 256
Db 38654 AGCAGACAGAAAGCTGGGAGTGGAGAGTATACAAAGAGGAGGGTTACCAGGCATCAA 38595
QY 257 -----LysAsp----- 258
Db 38594 GGGGCATCCAGGAAGAGAGGACCTTCTCTACTGTTTCATGTGAGAGCTTGGGAGATAT 38535
QY 259 -----Asp-----Lys----- 260
Db 38534 AAAATCACATGTGGTCAAAATAATTTGATAGCTTGACAGCTCTCAAAATCTAGACAAAGAGT 38475
QY 261 -----ArgLeuile-----Glu-----Gly----- 265
Db 38474 GGAAGATATATTTTCCAGTGGTGGAGAAAGAGAGGAGTTTGTGGCTGCTCCAGT 38415
QY 266 -----Lys-----Lys-----GlyVal----- 269
Db 38414 TCTTCTGTAATAATCTATGCTCCCTCACTAATTTGAGTCCCAATATGATATTTGAAATTTGAAC 38355
QY 270 -----Lys-----ValGlu-----Asn-----Arg----- 274
Db 38354 GGACAGACACATACTTTTGTGATAATTTGGAGATAAATTAATAATTTGTTATGAAGATCG 38295
QY 275 -----Pro----- 275
Db 38294 ATAAAAACCAACAGTGCCTCAATATCTTTAAGATAAAACATATGCTTTCCCGTTATA 38235
QY 276 -----Phe-----LeuSer-----Lys 279
Db 38234 TGTTCCTGAAGAAATTTCTCTTATCTTATCTTGTCTTATCTCATTTTCACTATTAATGAG 38175
QY 280 -----LeuilePhePhe----- 283
Db 38174 ATTGCCATCCCATAGTATCTTGTGTTTTTTCATAATTCATCCAAAATTTCAACATAAACA 38115
QY 283 ----- 283
Db 38114 ATCAGAGTCGCCAAAGTAACAAATTTTAACTCTTAACTGAAACAAAAAATTTGATGACAAAAACA 38055
QY 284 -----Asn-----Val-----Ser 286
Db 38054 TTTTAAAAATAGAACTCTTAGACTTTAGTCTTCCAGGCTCTGTTAGGTGTCAATATTCT 37995
QY 287 GluHis----- 289
Db 37994 GAAACAGGAATGTCAACATCATGTGAAAAAATTTGAAAAATTTGTAGATCTGCAGAA 37935
QY 290 -----TyrGly----- 291
Db 37934 ATCTATTATGGAGTAAATTTTGTGAATCTACCATAAGACCAATTTAAGATACTATTT 37875
QY 291 ----- 291
Db 37874 TCTTTTAAATGTCCATATTTTGAATAATCCCTAGAACATAAATCCGAATGAAATATAT 37815
QY 291 ----- 291
Db 37814 CTTATTTCTCAAAATGTCTCAATGATCATTTTGAATGATTTTAAATGATTTCAATTTGATTCAT 37755

QY 292 -----AsnTyr-----ThrCys-----Val 296
Db 37754 ATTAGTAACCTCTTGAGAAATGAATATACACAACTATTTTTCACCTGCCATATAGTG 37695
QY 296 ----- 296
Db 37694 GAATTAGTAGGAGGAAGAAGAAATATTAAAGAGCAAGGGATGGTCTGTGCTACAG 37635
QY 297 -----AlaSer-----AsnLys-----Leu-----Gly----- 302
Db 37634 TTAAGCAGCTCTATGATATAAGAAATAAGCTAGATCAGACTTGAGATGAAGAGGGTTAC 37575
QY 302 ----- 302
Db 37574 AGGAAAAGAGAGATAATTTATCAATTACTTATCAATTGTAATAATCTATCAACACATTTA 37515
QY 302 ----- 302
Db 37514 TTGCTTTAATTATCAAGACTTTGTACTCTGTAGGCTAAATTAATATAATACATTAC 37455
QY 303 -----His-----Thr----- 304
Db 37454 ATCAATAATTACACACTTCTCAGTACATGTAAATCCACAGTAATTTATAAGAACACGT 37395
QY 305 Asn-----AlaSer-----Ile-----MetLeuPhe----- 311
Db 37394 AATTGTTATAAGCTTGAGATGTCAACAGATTTGTAATTGTGTAAATATATGACATTTCTGA 37335
QY 312 -----Gly----- 312
Db 37334 TGGAAATTAACAAATCTTTCTAACAAAAAAGAAAGAGCTGGGATAGTGG 37275
QY 313 -----Pro-----GlyAlaValSer-----GluVal 319
Db 37274 CTCTTGCTGTAGTCCAGCACTTTAGAGGCCAAGGCAGGTGGA--TCACATGAGGTC 37218
QY 320 Ser-----Asn----- 321
Db 37217 AGTGGCTGCTGGTAGAGGGTACCTGAGATTTGAAGAACCAACTAAACAAGCAGGTATA 37158
QY 322 -----GlyThr-----Ser 324
Db 37157 GGGCTGACATAGAAGAGGACTAACATGGCCAGGCATGGTGGCTAGCTGCTGTAATCC 37098
QY 325 -----ArgArgala----- 327
Db 37097 CAGCACTTTGGAGGCTGAGCGGGCGAGATCACCTGAGTCAGGAGTTCAAGATCAGGTT 37038
QY 327 ----- 327
Db 37037 GGCACACATGGTGAACCTGTCTTTACTAAATAATATAAATCATGTTGGGCATGGTGGT 36978
QY 327 ----- 327
Db 36977 GCACGCTGTAGTCCAGCTACTGAGAGCGCGAGCAGCAATCGCTTGAACCTCAGNA 36918
QY 328 -----GlyCys----- 329
Db 36917 GGCAGAGGTTGAGTGAGTGTAGATTGCGCCACCGCACTCTAGCCCTAGGCATCAGAGTGA 36858
QY 329 ----- 329
Db 36857 GACTGCTACAAAAGCAACAAAGAAAGAGTCAAGGAACATATGTGTTAAATGAAG 36798
QY 330 ValTrp-----LeuLeu----- 333
Db 36797 AATTGGAAGATCTCTCTGGATTATTGTTAGGAGAAATTTGGATTTCAGATATAATAA 36738
QY 333 ----- 333
Db 36737 TGTTAATATAAAGATATTTTATGATTAACCAAGCTTAAGCTAGACCAACAATATTACC 36678
QY 334 -----Pro----- 334

Db 36677 ATTGACTGGGATGGACCATGCCTGTTTCTGAGCCGTAATCTCACTCCAGTATTTT 36618
QY 335 Leu-----LeuVal----- 338
Db 36617 CTTGAGGAATAGGTGATAACTTTGGTTTGTGGGCTCTCCTCCTCAGCATATCAAGTTGAG 36558
QY 339 -----His----- 342
Db 36557 CATATAATAATCAATAATGTCCACAGACAGCAGCAATTTTGGGTCTTCTCTATCATTTT 36498
QY 343 -----Lys-----Phe 344
Db 36497 TCTGAAGAAACAAGAGGGGATGTTT 36471
RESULT 25
US-09-453-702B-242
; Sequence 242, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31880
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-702B-242
Alignment Scores:
Pred. No.: 3,97e-23 Length: 31880
Score: 1714.90 Matches: 304
Percent Similarity: 11.31% Conservative: 34
Best Local Similarity: 10.17% Mismatches: 3
Query Match: 71.22% Indels: 2648
DB: 4 Gaps: 256
US-10-017-084A-523 (1-344) x US-09-453-702B-242 (1-31880)

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Qy	54	Thr-----Leu-----Arg-----Cys---	57		
Db	20378	ACAGTGGGATTTGAACATATATCTAAATTTGTATGTCCGCAAACTATTGATGCATGTTTT	20437		
Qy	58	-----Thr-----Ile-----Asp-----	60		
Db	20438	GAACATTTCTGGCAGTGGGACATCTCCGGTCTCAAGACGAGATTGAGAGCGAGGAAAA	20497		
Qy	61	-----Asn-----Arg-----Val-----Thr---	64		
Db	20498	TTAAAGTTTGTATGGAACACATCTGGCCACCGTCTCGATTAAATAGTATCGCCACTCAT	20557		
Qy	65	-----ArgVal-----AlaTrp-----	68		
Db	20558	GAGCTAGATTATTTGCTCGTCTATATGACAGGAAGAACCCAGCCTGGCAGGCACGT	20617		
Qy	69	-----Leu-----	69		
Db	20618	TTGCCAGCCTTACATGCTAAACAACTTGTGTCTGTACTTGGAAAAAGTTTGTAAATCAGCG	20677		
Qy	70	AsnArg-----SerThrIleLeu-----Tyr	76		
Db	20678	AATAGATTAGTGATTTGCAGGGGCGAGTATTTTCAACGGTTATGTCGTGATCAAAACATAT	20737		
Qy	77	Ala-----	77		
Db	20738	GCTCAGAGGATGGGACAATTTACGGCGAGACTCAATTCCTCAAGATTCATCAATGG	20797		
Qy	78	-----Gly-----	78		
Db	20798	GTACTGCTGGCCCTCATTTCTTGTGTGGAGCGCGTCTACAGACTCCGGCGAAAAAC	20857		
Qy	78	-----	78		
Db	20858	TGTACGTTAAACAGCGAATTATGACTGCCTGGAGTTGCTAACTCTGCCTGACGACTATCTG	20917		
Qy	79	-----Asn-----Asp-----Lys-----	81		
Db	20918	CCGGCAGCTAACTACATTCGGCGATGTGATGCACAGGAGTATGCAAAACGTAATCCATGC	20977		
Qy	82	-----Trp-----	82		
Db	20978	GTTACATGGAGCTGAACCTGCTGAAGATGAACCGAAGAGGTAAACAGATTATTCGCTTA	21037		
Qy	82	-----	82		
Db	21038	GCTATCAGAGCCATGTGGCTCAATCGGGGGAACGACACTAAATTAGTGTATTTATCCG	21097		
Qy	82	-----	82		
Db	21093	CCAGAAATAAGTCACATGAACGCGATACGTTCTTACTGCTATAGCTCAGAAATCTGTTA	21157		
Qy	83	-----Cys-----	83		
Db	21153	CTCGAACATTCAGGTATGTTTTTTCTTACCTTTTGATTTTATTGTAATCTACTGGC	21217		
Qy	84	-----LeuAsp-----ProArg-----	87		
Db	21218	AAGGCAACTTACATCAGATGCTTGATGTTTCTCATACGTATTATTCAATCCGAGACAA	21277		
Qy	88	-----Val-----ValLeu-----	90		
Db	21278	AAGGCATTATTAATCTAGTATATCATATAAATCTGTAAATGATGATATGCTGGC	21337		
Qy	91	Leu-----Ser-----AsnThrGln-----	95		
Db	21338	CTTTGGCAATCTGCTACACCCGACCTTCAACACCCAGCGCTTGGAGCGGGATCTCCCG	21397		
Qy	96	-----Thr-----Gln-----	97		

Db 21398 CAGCTCCCCCAGGATTCTTCCGCCAAACTGACCCAGAGTGGCAGCGTAACCTGCGCTTTA 21457
Qy 98 -----TyrSer-----Ile----- 100
Db 21458 CGCTCTGACTACAGTCTGTCGAGGCGTGGTGGAAATCGACGTATTGGTGGCGCAGGCG 21517
Qy 101 -----Glu-----Ile----- 102
Db 21518 CTGGGGTTAACTCTCGAAGAGCTGCTTACCATTATTCGCGTTTCAGTTCCCGGTGATGCGC 21577
Qy 103 -----Gln----- 103
Db 21578 CAGTACGAGCGGATACCTGCTAGCATCAAAACGGTCGCAATTATCTTTACCCCAAGCAAA 21637
Qy 103 ----- 103
Db 21638 GGGCTGGTGGCGTTGGCTTTCCTCGCAGCGCGTAAAGCTGACCTGAAAAACGGCTTT 21697
Qy 104 -----AsnValAsp----- 106
Db 21698 GTCTTTAACTGACAGCCCGGAGTGAGCCGGCGTGACTGACCCGATCAAGCTATCGGT 21757
Qy 107 -----Val-----Tyr----- 108
Db 21758 TGGGATGATGCAAAACATCTTAAACCGGTACCGTCAGCGTCACCTTTGATGATTATACC 21817
Qy 109 -----AspGluGly----- 111
Db 21818 CGCAGCGAAGAGTGAGCGCGTACCGTCACCTGCGAGCGTCCGTTTATCAAGCCAGAT 21877
Qy 111 ----- 111
Db 21878 CGCGAAGATGACTACAAAGTGGCTGGCGTCTTTGGCAAGATGAAGAGCGCGCTGA 21937
Qy 112 -----Pro-----Tyr----- 113
Db 21938 TGTGTCCGTCCGTTGTCAGTGGCAGGTCCGCGACAGCGTTGCGGCTTTTACGGGCGG 21997
Qy 114 -----Thr-----Cys-----SerVal-----Gln----- 118
Db 21998 CGTCCCGCTAAACAGCCCGCTGTTTAAACGGTGAGAATAACGATATGTCATGCTGG 22057
Qy 119 -----Thr-----AspAsnHis-----Pro----- 123
Db 22058 AGCAATTTCTGGCCAGCGCGAAACGCTGCTGAAGGAC---CATACCTTCGCGCCAGT 22114
Qy 124 -----Lys-----Thr-----Ser 126
Db 22115 TGCCGTTTCGTAAAAGTGACTTACCGCTGAATTTTTCCTTAATCTGACGCTGCGCTTCC 22174
Qy 127 -----ArgVal-----HisLeu----- 130
Db 22175 CGCCGACCGGCTCAGGCCCGGCGATTTTACGGTCTGGGAAGCGACGCGCCACAGCCGA 22234
Qy 131 -----Ile-----Val----- 132
Db 22235 CGCTGTCGCAACCGGTACCGCTCCGCTGAAACAGATGTTTATGTTCCGCTGTCTCA 22294
Qy 132 ----- 132
Db 22295 ACCACTGCGCGGCGCGTCAAAAGCGGGGTTAAAGCGATTATCATCTACCGATGAACG 22354
Qy 133 -----Gln-----ValSerProLys-----Ile----- 138
Db 22355 CCCTGGCAACCGATCAGGCCAGCCGCTTTCGCCAAACCAATCGCCAGCGATCCACAACTGC 22414
Qy 138 ----- 138
Db 22415 ATGCAAGGTGACCTGCGCGCTGTTTGTGGCGAGCGCAATCGAACCCAGCAAAAAA 22474
Qy 139 -----Val----- 139
Db 22475 TGTGGCGAAGAAAGTCTATTACCTGTTAAGCACAGCTGCGCGAAGAGCGCGGACATCC 22534

Qy 140 -----Glu-----IleSer----- 142
Db 22535 TGTGTACCAACTACAAAATGCTCGACTACTGCTGAAGCGCCCTGGCGATCAGCCGCTCT 22594
Qy 143 -----Ser----- 143
Db 22595 GGGTTTAAACACAGCCCGGTTTCATTGCGTTTACTGTCGTGGATGAATTGCATACGTTTG 22654
Qy 144 -----AspIle-----SerIle----- 147
Db 22655 ATGGCGCGCAAGGCTGGGATCTGGCGCTGCTGGTGCAGCTTTGAAGCATCACATAGTGG 22714
Qy 148 -----AsnGlu-----Gly-----Asn----- 151
Db 22715 TGGATAACCAAGATTGCGCTCGCGGACATCAGCTACCGTCGGCGAGCAATGGGCG 22774
Qy 152 Asn-----Ile-----SerLeu----- 155
Db 22775 AACTGCTGATTACGCAAAAACAATCTTTGACCAGCGTTTACCGATGAGCGGTTATTTC 22834
Qy 156 -----ThrCys-----IleAla-----Thr----- 160
Db 22835 GCGAAGATCGTACACGCGCAGCGAGTACTTGCAGAAATTACGCCATTGCGTACAGTCACT 22894
Qy 161 -----GlyArg-----Pro----- 163
Db 22895 ATCCGGGCGCGAGGTGCGTTCGGCCCTGGAGCCCGCAGAGTTACGCTACCCCGTAGCGT 22954
Qy 164 -----Glu-----ProThrValThr----- 168
Db 22955 ATCTTAAAGGCAATCCCTTTGTGTTCCCGCAGACGACTTGCACACTCCCGGAGATC 23014
Qy 163 TrpArg-----His----- 171
Db 23015 TGGAGAGCGACGAGCGGCGTGAAAAGCGTATTGCGCTGGGGTCACTGTTCACGCGCCACA 23074
Qy 171 ----- 171
Db 23075 GCGTGATGATGCTTACTTCCATGATCTGCAAGCGGGGATCTCTCTGAACGAGAGTGT 23134
Qy 172 -----IleSer-----Pro-----Lys 175
Db 23135 TGGAAATCTCCAGTCTATGCTGGCAGAAAGCGCGACCATGTCGCGACGCGTGTGCAA 23194
Qy 176 Ala----- 176
Db 23195 GCATTCGGCACTGATCGCGCAGGACGCTCTCGAAGTACCGGAAACGGAACACGATCGGC 23254
Qy 177 -----Val----- 177
Db 23255 AAAAAGCTCTCCAGCGAAGAAAGCGGTCGCGTGTGCTGCGGTTTGTGCAACTGCGCTCC 23314
Qy 178 -----GlyPheValSer----- 181
Db 23315 AGTTGTGCTCTCGTAG-ATGCGTGTCTGTGTCGCCAGCGTGGCGGAAAAACGCCCGACTG 23373
Qy 182 -----GluAsp-----Glu-----Tyr----- 185
Db 23374 GTGTTTCCCGATGATGTGGCGGTGGAAAGATCGCGAACACTATTTCGCGGTTATCCACTGC 23433
Qy 186 -----LeuGlu 187
Db 23434 CGTGACTGCCACGCAACTGCTGGCGCAGCGCTGGTTCATGGGCAAGCGTTTCAGTTGGAA 23493
Qy 188 -----Ile-----Gln-----Gly-----Ile----- 191
Db 23494 ACAGACTCGACGCGCATTTATCGCCAGTCTTTTGAAGAAAGGGCGCTCCATCGTCTTGCT 23553
Qy 192 -----Thr----- 192
Db 23554 TTCCCGGATAACACGNAAGAGCGGTGCTGCGCGCACACGAGAAACTGTGTCTTACCTGT 23613

QY 193 -----ArgGluInSer-----Gly----- 197
DB 23614 CTGAACTGAACCGA-----CAGTCAGCGTCCAGTGTGGACATTCGGGTGCATACGGAACGTG 23670
QY 198 -----Asp-----TyrGlu----- 200
DB 23671 TTGCAGGTACTGATCCCGGATATGCTCAAGAGCGTTAAGACGAGCTGGAGTTTGCTAAT 23730
QY 201 -----Cys----- 201
DB 23731 GAATGCCGCTACTGCAACAGCAACAGGGGATTCGATTCTGGGTCAACGGCTGCCAGT 23790
QY 202 -----SerAla----- 205
DB 23791 CTGTCGGCGGTGATGATTCACAGCTTTATGGCAGCCGCGCATCGTGCAGCTTCTTACTGCCGT 23850
QY 206 -----Asp-----Val-----AlaAla----- 209
DB 23851 ATTACGTTTTCTGACTCGGTACAGAGCGCGCGCATCGTGCAGCTTCTTACTGCCGT 23910
QY 210 -----Pro-----Val----- 211
DB 23911 ACCTGCCGCTGATGATTCGTGGGCAATCGCCAGTGTCTTAGCGAAGAAAGACATTA 23970
QY 212 -----Val-----Arg-----Arg----- 214
DB 23971 CGCTGGATCGTTCCGGCGCGGTGTTGCGCAACAAACGCGTGAACGTTCACCGGACGAT 24030
QY 215 -----Val----- 215
DB 24031 GCTCATTTTCAGCAACAGCTATCGCACCAATATGACGTGGCTGAATGATATCAGACG 24090
QY 216 -----Lys----- 216
DB 24091 CTGAAAAATGAAGGCAACTGGCGGAGAACTCCGATCTGCGGAGCTGTTCCCTGCCG 24150
QY 217 -----Val----- 217
DB 24151 CTCGACTGGAGGTGTACAGCAATTTACCTCGCGCGCGGTATCGGAGTACGAGTGGAA 24210
QY 218 -----Thr-----Val-----Asn----- 220
DB 24211 GCCACCGGTTATGCCGTTGCCGGAGTGGATAAAGATCGCTTCATCCGCAATTACCGCC 24270
QY 220 ----- 220
DB 24271 CTGCATCAACAGCTTTGTGAAGAGCTGGGTGATGAGANGTCTGGTGTGAGCGTCGAGCAG 24330
QY 220 ----- 220
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QY 220 ----- 220
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QY 221 -----Tyr-----Pro----- 222
DB 24451 ACCTCGGCTATATGCTTCTATCGGTTCGAAAAACGCGTAAACCGGCTTATGCGTCTTT 24510
QY 223 -----Pro-----Tyr----- 224
DB 24511 GAAAAAATTAATGTTTCCATCGCTGATTGGCGGAAGTCTAACCCGAGTTGGTATCAG 24570
QY 225 -----IleSer-----Glu 227
DB 24571 CATTGGATCAATTCGACCGCTGAGTAACGCAATAATCTGTTTATCAGTAGCGTTTCGGAA 24630
QY 228 -----Ala-----Lys-----Gly----- 230
DB 24631 ACAGTGTACGCGCTGTTTACGGCGTGTGAATAATAGCGGAGTAGTAAAGATTTTGAC 24690
QY 231 Thr -----Gly-----ValPro-----ValGly----- 236

DB 24691 ACCAAAGGGCGTGAAGCTCGGGACTGGTCTCGGCGTGGTGGAGCCGTGACGTC 24750
QY 237 ---Gln-----Lys-----Gly----- 239
DB 24751 GTTCAGCTTAATTTGCTCATGTTCCGCTGAGGTGTCCGGCTCCGGCCGATCAAGGCTGG 24810
QY 240 -----ThrLeuInCysGlu----- 244
DB 24811 CAGTGGGTAAATGCGGCTTGTCTCTCTTTACGTTGTGAAGTCTGTATCCAGGAAGTCGAC 24870
QY 245 -----Ala----- 245
DB 24871 AATACGGCAGCTGGCGTTTGGGAGACATGACATCGCGCGGTACAGGGCGGAGAACAC 24930
QY 245 ----- 245
DB 24931 ACGGGCTCTTAGCGTGAAGATCGGAAGTCAACGAAAAATCGTTCTACCGCGCAAC 24990
QY 246 -----SerAla----- 247
DB 24991 CAACCGTGAATATCAACCTGTTGTCCGCAACACACGACGCTGGAGATGGGTATTGACGTT 25050
QY 248 -----ValPro----- 249
DB 25051 GGGGATCTTTCCACCGTTTACTCTGTTCTGTCTCCACCTGCTCAGGCCAACTACTTGCAG 25110
QY 250 -----Ser-----AlaGlu----- 252
DB 25111 CGTATTGTCGCGCGCTGTAAGATGTAACGCTTAAACATTACCGTGGCAGAAAGG 25170
QY 252 ----- 252
DB 25171 AACCCGACGATCAGTTTCTTTTGAAGAACCACTGGAGATGATGAGGGCCAGGTGCAG 25230
QY 253 -----Phe-----Gln----- 254
DB 25231 GCTCTGGCGTCTTCTTAAATGCAACGGCTATTCTCGAACGCCAGCTGSCAGCTTTTGT 25290
QY 255 -----Trp----- 255
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QY 255 ----- 255
DB 25351 ATGCTGGATGAGTGGAGTTCGGGCGTAAATCGGGTTTTCGTATTAACCTACTGCGATAT 25410
QY 255 ----- 255
DB 25411 ATCGAACAGCATCATGCGGAGATTGCTCGCAATTTACGGCAATCTTCCCGATCTTCC 25470
QY 256 -----Tyr----- 256
DB 25471 GCAGAACTCCCAACAGCTGTTGTCTTATCTTCAGGGCGCGCAGGACAAACGTCGCTG 25530
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DB 25531 GTGCAGCGTATCGAAGAAGCGTTAAACTGCTGCTGGAGATCGCAATCTTTGGGCTCA 25590
QY 258 -----Asp-----AspLys----- 260
DB 25591 CGCATCGATAAATCAAGCGCAGTATCGATAAATGGAGAACGCGCGCGGATCAAAAC 25650
QY 261 -----Arg-----Leu----- 262
DB 25651 TTTGATAGCATATGCGGAGTTAACTTCGGAACGCGAGGCGCTGATGGCGCTGTCAAT 25710
QY 263 -----Ile-----GluGly----- 265
DB 25711 CAATCAACRAATAGCAACGCTGAATTTCTCTCAGGATGAGGTCTGCTCCCTAACTAC 25770
QY 266 -----LysLysGly----- 268

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QY 268 ----- 268
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QY 269 -----Val----- 269
Db 25891 GCTGAGTGGCTCGGTGAATAATTTCTATCGCGTGGGCATAAAGTTGAATTTGAGCAG 25950
QY 270 -----LysVal-----GluAsn---Arg----- 274
Db 25951 ATAGACCTGAAGTCTCTGAGCCGGGAGAACTGGCGTATCTGTAGCCACTGTAACTACAGC 26010
QY 275 -----Pro----- 275
Db 26011 GAAATATGACAGACGCGCGCAGCAGATAAATATTGCCCGAATGTGSCACACCGGGG 26070
QY 275 ----- 275
Db 26071 TGGCCGATCCGGACAAAACACACGCTGCTGAACTTCGCCAGGTTTATGCCCGGCC 26130
QY 276 -----Phe----- 276
Db 26131 AGCGCAGTGATACCCAGATCACGAGCAGAGCGACGCGTGAACCTGCTTCTCCAG 26190
QY 277 -----Leu---Ser-----Lys----- 281
Db 26191 CGTCAGCTATTGTTAGTTTCGAAAAGAAGATGTATCGCGGCATACCGGATTGAGGAA 26250
QY 282 -----Phe----- 283
Db 26251 GCGGAGTCCGTTGGTTGGTTGAAATTTTAAGCAAAAGTCACCTCGCGGATATCAACTTC 26310
QY 284 -----Asn----- 284
Db 26311 GGCAAAATGCGCGATGATGCCAATGAGTTGATGTTCCGGAGAACGGAAGCGAAC 26370
QY 284 ----- 284
Db 26371 GGGTTAAAGTTTGCTCGGGTSCGCGATGGTSCAGCGTCTCGCATCATGAACCACT 26430
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Db 26431 CATGATTCAGCTGCAATATCCACGGAACCGGAAGCGGAAGTTGCAAGATTATCTC 26490
QY 285 -----ValSer----- 286
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QY 287 -----Glu----- 288
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QY 290 -----Tyr-----Gly----- 291
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Db 26731 CTTAAGAACTGATGGGCACCTCCGACAAATTTGCTGAATTAATTAAGTGGCCATCAG 26790
QY 294 -----Thr----- 294
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QY 296 ----- 296
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QY 296 ----- 296
Db 26911 CTGGCGAAATTTTGCAGGCAAGAGATTGATACGGGTAATTGATTCATCAAAAACATT 26970
QY 297 -----Ala-----Ser----- 298
Db 26971 TCCTCGAAGCCATGATGGCAGTGAGCTGGAAAACGGTTTTATTAGCTGCGCTGCAAGAA 27030
QY 299 AsnLys---Leu-----Gly----- 302
Db 27031 AATAAAAACCTGATTGTAGTCGCGATTACGCGCATCAGGGCGCTGGGTGGATTATTAAAC 27090
QY 303 -----His----- 303
Db 27091 ACCCGCAGCAACCGATGATGAGCTGGCATCTTAAAGCTCAGGTGGATTAGCGCGTAA 27150
QY 304 -----Thr----- 304
Db 27151 GAGCGGTGGGATCCCTTGTGCGCGGATTACGTGCTATATCCGCTTATGAGTCTGAT 27210
QY 305 -----Asn-----Ala-----Ser-----Ile----- 308
Db 27211 GCCATTAAACCGGTGGCTATTTTCTGATGGCTTTGCGTTCCACAAAATAGCGCTGCA 27270
QY 309 -----Met----- 309
Db 27271 GAGGATGTCAAAACGCCAGCGGATTCGGGATAGCGGTAAATTTCTGGGTGGACATG 27330
QY 310 -----Leu-----Phe----- 312
Db 27331 AGTGGGCGGATCTCAAAGAGCGCGGCTTAAACATGTTACGAGATGCTCTGGGACTGG 27390
QY 312 Y----- 312
Db 27391 CATAAACCGGATATGAACAGCTTAAGTTTATAACCTGTTTCATGATACCAACTTTGCG 27450
QY 313 -Pro-----Gly---Ala---Val----- 316
Db 27451 GCGCTTGAAGCGTCGTTCCGGGAGCGACACAGTTTTCACCTGCTGCTGGATTATCTCGC 27510
QY 317 -----Ser-----Glu-----Val----- 319
Db 27511 GATCGGCGGAAGAACCGAGTTATGGCAGAAATGGCTGCTGCACATGCTCGGTGTGG 27570
QY 320 -----Ser-----Asn----- 321
Db 27571 TTGGATGTGAAGATCACAGACGCGGGAAGAAACAAAAGTATGCTATGAATGAG 27630
QY 322 -----Gly----- 322
Db 27631 GAAAAACGCGCAGCTTGGCGCTAGCAGAGCTTTTTCAGACGACCGCTTTGTCTTTGCT 27690
QY 323 -----Thr-----Ser----- 324
Db 27691 GGTTTACTCGATGCTGAATCATCGCAGCAATTTATTGAGCTGGCTTCGTTGTTACCA 27750
QY 325 -----ArgArg-----AlaGlyCysVal----- 330
Db 27751 CAACAGCCATTAAACCGACACGAGCGTCCCAAAATGCGCAGCTGGCTCGTTGCT 27810
QY 330 ----- 330
Db 27811 ATCTGTTTGAAGATGCTATACGAGGATGACGGTATGAAGCGGAGCTCAATGGCTTC 27870
QY 331 -----Tyr-----Leu----- 334
Db 27871 TGGCGACTGGTAAACCTGTTACAGTTCTCTCGCGATATGACCTTTTACGAGCGGTAAGCC 27930
QY 334 ----- 334
Db 27931 GTGCAITTTACCGAGAAAGGTTGACATAAGTTTTCGGCAACGCCAGGCGAGTACCA 27990

QY 335 -----LeuLeu----- 336
Db 27991 GAGACTGATGAGAGTTGGGCTGAGATTATTGAGTTTGGCTTAATAAGCGCTGAAGAGATC 28050
QY 336 ----- 336
Db 28051 GCGTGTTCAGTCTCATTTCTCTCTCTGCGCGGACTCTCGGCTACGAATTTGCAAAATGAT 28110
QY 337 -----Val-----Leu-----His---Le 340
Db 28111 GAAGGTGAATATTGGGAGCGGATCTCGCTGGCCATCACAATAATGGCAATTTGATT 28170
QY 340 uLeu-----LeuLyS-----Phe 344
Db 28171 ATTGATAATCAAGAAATTTATTC 28192

RESULT 26

US-09-453-702B-50
; Sequence 50, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSER: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION: <unknown>

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.95017

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 38584

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-09-453-702B-50

Alignment Scores:

Pred. No.:	9,06e-23	Length:	38584
Score:	1714.70	Matches:	297
Percent Similarity:	10.1%	Conservative:	37
Best local Similarity:	9.04%	Mismatches:	7
Query Match:	71.21%	Indels:	2943
DB:	4	Gaps:	246

US-10-017-084a-523 (1-344) x US-09-453-702B-50 (1-38584)

QY	1	Met	-----LysThr-----Ile-----Gln-----	5
Db	26158	ATGACGAATGCTGAGCGGTGTAAAGTTCCGCAATAACGTCGGCAACTTTTGGCGGCTT		26217
QY	6	Pro	-----LysMet-----	8
Db	26218	CCTTTCCATTAAACAACTTTTCGACGTAATCCCATGACACACAGACATCAGGATCTCG		26277
QY	9	His	-----	9
Db	26278	GCGCAGCCCGCGGATGTGCGCAGCGGAGTCTGCGGGCTTCTGTGTAAGACACGCGGAG		26337
QY	10	Asn	-----	10
Db	26338	GGGGAAGATATTTCCCTGCGTGAATATCTCCGGTGAGCCGAGCGTATTTCCGTATG		26397
QY	11	Ser	-----Ile-----Ser 13	
Db	26398	TCGCGGAAGACTGGCTGCAGGCAGAAATGCAAGGTGAGATTGTGGCGCTGTCACAGC		26457
QY	14	Trp	-----Ala-----	15
Db	26458	CACCCCGGTGTCTGCGCTGGCTGAGTGAGGCGGACCGCGGCTGCAGGTGACAGTGTAT		26517
QY	15	Ile	-----Phe-----	17
Db	26518	TTGCGTGTGTGGTGTGTCGCGGGGAGATTCATTAAGTTCGCTGTGTGCGCATCTC		26577
QY	18	ThrGly	-----	19
Db	26578	ACCGGGCGCGCTTTTGACACGGGTGACGAGTGTACACGCTGTCGGGATGCTTAT		26637
QY	20	LeuAla	-----	21
Db	26638	CATCTGCGGGGATGAGATGCGGATTTTCATCGAGGATGACTGTGGTGGCTCACGCT		26697
QY	21		-----	21
Db	26698	CAGATCTCTATCTGGATAATCTGGAGGCCACAGGCTGTATCAGGTGCGTGTGTATCA		26757
QY	22	Ala	-----LeuCysLeuPheGlnGly-----ValPro-----	30
Db	26758	GCACAAACCGCGGATGTGCTGTGTGCTGTTT---GGTTCATCGTGCGGATCATGCC		26814
QY	31	Val	-----	31
Db	26815	GCCATTATCTGTGTGATGGCGAGCTGTCACCATATTTCTTGAACAACACTGAGCAACGA		26874
QY	31		-----	31
Db	26875	GAGAGGTATACGACAATGGCAGGACGACACACTCCCTCTGGCGGTACCGGCGATGG		26934
QY	32	Arg	-----Ser-----Gly-----Asp-----Ala-----ThrPhe-----	38
Db	26935	CGCGCATCTGCTTTACGGGATTTGCAACGATTTGGCGCGGATCGACCTTCGTGTAA		26994
QY	39	ProLys	-----	40
Db	26995	AAACGGGGCGCAAGCCATCCGGGCGCTGGCCATGACATCCCGCGTTCGTCAGAAAGC		27054
QY	41	Ala	-----MetAspAsn 44	
Db	27055	TGAGCGAGCGGTGTATCTGTACGGATTGCGGGCGGTGATACAGGTGAAAATG---AAT		27111
QY	45	Val	-----Thr-----	46
Db	27112	TATCTGCGGTTTAATGAGCGGCTGGCAATGTGCGGTGATCCACATCTGCGCGGCC		27171
QY	47	ValArg	-----	48
Db	27172	TGGCGGTGCTAAAGTGGGGTGTGTTTCAGGCGAGTGTGTTTCAGGCGGTGGCGGTGATTGGG		27231

QY 48 ----- 48
Db 27232 TGGCATGGTGAACCCCTGTGGGCTGGCTGGGGCGCGGCTGTATCGGGTATGTATGTCAG 27291
QY 49 GlnGly----- 51
Db 27292 CAGGGCCAGTATGATCCTCGGTGGTGTGGCGCAGATGTGGCACCAGAAAGCCAGAATC 27351
QY 52 -----SerAla-----Thr 54
Db 27352 CCCTGACACAGAACCGGATAACGGCAAAACAAACACCTATTCTCTCACTGGATAACA 27411
QY 55 ---Leu---Arg-----CysThrIle----- 59
Db 27412 TGGTTGCCAGGGCAATGTTCTGCCCGTTCGTACGGTGAATGCGGTGGATCACGTG 27471
QY 59 ----- 59
Db 27472 TGGTTTCTCAGGAGATCAGCAGCGCAGACGAAAGGGACGGTGTGTCAGGTGTGGTGATTG 27531
QY 60 -----Asp-----AsnArg----- 62
Db 27532 GTCGCTGATGCAAAATGTTTATGTGAACCGCCTCGGGCGGTGTTGTCGTTATGGAG 27591
QY 63 -----Val-----Thr 64
Db 27592 CATGACGAATGGTAAGGAAGCAGTAAGGGGCATACCCCGCGCAAGCAAGGACAACC 27651
QY 65 -----Ala-----Arg-----Val 66
Db 27652 TGAAGTCCACGACGTGCTGAGTGTGATCGATGCCATCAGACGAGACCGATTGAAGTTC 27711
QY 67 -----Ala----- 67
Db 27712 CGGTGATGGATTAAAGCGTGTCTCTGAACAGTACGCCGCTGTGGACAGTGAAGGTA 27771
QY 68 -----Trp----- 68
Db 27772 ATACCAACATCTCCGCTGTGTCAGGTGGTGTTCGGGCGCGGTGAGCAGGAGCAGACACCGC 27831
QY 69 -----LeuAsn----- 70
Db 27832 CGGAGGGATTTCGAATCTCCGTTCTGACACGCTGTGGTACGGAGTGAATACGACA 27891
QY 71 ---ArgSer-----Thr---Ile-----Leu----- 75
Db 27892 CGCCGATCACCGCACCATCACGTGCGCAACATCGATCGTCTGCGCTTTACTTTTCGGTG 27951
QY 75 ----- 75
Db 27952 TGCAGGCACTCGGGAAACCACTCAAGGGGGACCGGAATCCGTCGGAAGTCCGCCTGC 28011
QY 76 -----Tyr----- 76
Db 28012 TGGTTTCAGATACAGGTAAATGTTGGTGGTGGTGGGTAACCTCGCGCGCGCCGTTTA 28071
QY 76 ----- 76
Db 28072 AAACACGTGCGATCTGGCTCGTGGTGGTGGTGGATAACTCGCGCGCGCCGTTTA 28131
QY 77 -----AlaGly----- 78
Db 28132 ATATCCGATGCGCAGGATGACCGCGGACAGCAGCAGCAGACCAAGCTGCAGACAAACG 28191
QY 78 ----- 78
Db 28192 CTCTGGTGTATACACCGAAATCATCCATGTTGAACAGTGTACCCGACAGCAGCA 28251
QY 78 ----- 78
Db 28252 CTGGTTGCGTGCAGGTGGACTCGAGCAGGTTTGGAGTGTGAGTGTGAGCGGATTAAT 28311
QY 79 -----Asn----- 79

Db 28312 CATCTTCGGCGGCGCATTCCTGCAAGTGGCGCTCAAACTATGATCCGGAACACGACTTAC 28371
QY 80 -----Asp-----Lys-----TyrCysLeu 84
Db 28372 AGCGGCATCTGGGACGAAACGTTAAACCGGCATACAGCAACACACATGCGCTGTGCTG 28431
QY 85 ---Asp-----ProArg-----Val 88
Db 28432 TGGGATATCTGACCCACCCCGCTACCGCATGGGGAACGCTTTGGTGGCGCGATGTG 28491
QY 89 -----ValLeu-----Leu-----Ser----- 92
Db 28492 GATAAATGGCGCTGTATGTATCATCGCCAGTACTGCGACCACTCAGTACCGGACGCTTT 28551
QY 93 -----Asn-----ThrGln----- 95
Db 28552 GCGGCACGAGCCCGCATCATCTGTAATGGGTACTGACCACGACGCGCAAGCGGTGG 28611
QY 95 ----- 95
Db 28612 GATGTGCTCAGTGATTTCTGTCGGCGATGCGCTGTATGCCGTATGGAAACGCGGACAG 28671
QY 96 ---Thr-----Gln----- 97
Db 28672 CTGACGTTCTGTCAGGACCGGCGCTCGGATAAGTGTGGACCTATAACCGCAGTAATGTG 28731
QY 93 -----TyrSer----- 99
Db 28732 GTGATGCCGATGATGAGCGCGCGTTCGCTACAGCTTTAGCGCCCTGAAAGACCGCAT 28791
QY 100 -----IleGluIle----- 102
Db 28792 AATGCCGTTGAGGTGAATCTGGTACTACCGGCACACGCTGGGACGCGGACAGGCTT 28851
QY 103 ---Gln-----AsnVal----- 105
Db 28852 GTGGAGACACGCGAGCCATTTGCCGTTACGCTGTAACGTACCAAGATGGATGCCCTT 28911
QY 105 ----- 105
Db 28912 GGCTGTACCACTCGGGGGCAGGCAACCGTCCGGGCTGTGGCTGATTAAACGGAACGTG 28971
QY 105 ----- 105
Db 28972 CTGAAACGCGACGCTGGACTTCAGCGTGGCGCAGAGGGCTTCGCCATGTACCGGCG 29031
QY 106 AspVal----- 107
Db 29032 GATGTCAATTGAATCTGNGANGCCGANTTCCGGGGATCAGCATCGGTGGAGTGTGCTN 29091
QY 108 ---TyrAsp----- 109
Db 29092 GCGGTGAACAGCCAGACCCGCAACGNTGACGTTGACGNGTGAATCAAGTCCCATCTCC 29151
QY 110 -----Glu----- 110
Db 29152 GGCACACGCTGATAAGCTGTGTCGGAAGTGGCAATCCGTCAGCGTGGAGTTCAG 29211
QY 111 ---Gly-----Pro-----Tyr 113
Db 29212 TCCGTACCGACCGNGTGAAGGTAAAGTGAAGCGGGTTCTCGACGGTGTGCTGAATAC 29271
QY 114 ---Thr-----Cys---Ser--- 116
Db 29272 AGCGTGGGGCTGAAGCTGCGCAGCCTCGCCAGCGCTGTTCGCTCGGTGAGTATC 29331
QY 117 ---ValGln----- 118
Db 29332 CGTGAGAACGACGACGACGATGATGATCCTGCGCTGAGCATGTGCGGAGAAAGAG 29391
QY 119 ---ThrAspAsn----- 121
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Db 29392 GGCATCGTGATACGGGGCGCACTTTGACGGTGACCGAGCAGCACGGTGAATGTGTC 29451
Qy 122 -----His----- 122
Db 29452 ACGCCGCCAGGCTGCAGACACCTGACCGCGAAGTCTCCGACAGACCGGGGAATATCAG 29511
Qy 123 -----ProLys----- 124
Db 29512 GTGCTGGCGGATGGGACACGCCGGAAGTGTGAAGGTGTGAGCTTCCTGTGGCTG 29571
Qy 124 ----- 124
Db 29572 ACGTGGCAGCGGATGACGGCAGTGACGGCTGTGACGACGCCCGGACGACGGAACC 29631
Qy 125 -----Thr----- 125
Db 29632 ACATACCGCTTACGACGTGGCGCTGGGAACTACAGGCTGACAGTCCGGCGGTAAAT 29691
Qy 126 -----Ser---ArgVal----- 128
Db 29692 GCGTGGGACAGCAGGCGGATCCGGCTCGGTATCGTTCCGGATTCGCGACCGCGACGC 29751
Qy 129 -----HisLeu--- 130
Db 29752 CCGTCACAGATTGAGCTGACACCGGCTATTTTCAGATACCCCGACCGCGCATCTTCGG 29811
Qy 131 -----Val 132
Db 29812 GTTTATGATCCGACGTACAGTTTGAGTTCTGTTCTCGGAACGGGATTCGGATATC 29871
Qy 133 -----GlnVal-----Ser 135
Db 29872 AGCAGGTTGAACACGAGCGCGTTATCTTGGTACGGCGCTGTACTGGATAGCCGCACT 29931
Qy 136 -----Pro----- 136
Db 29932 ATCAATATCAACCGGCCATGATTATTTATATCCGAGTGTGAACACCGTTGGC 29991
Qy 137 Lys-----Ile---Val-----Glu----- 140
Db 29992 AAATCGGATTCGTGAGCGCGTTCGGTCCGGCGAGCGATGATGCGAAGTTATCTGGAT 30051
Qy 141 -----Ile----- 141
Db 30052 TTTTTCAAAGGCAAGTAAACCAATCTATCTCGCAAGAGCTGCTGAAAAAGTCGAT 30111
Qy 142 -----Ser-----Ser----- 143
Db 30112 CTGACGGAGGATAACCCAGCAGACTGGATGAGTTTTCGAAAGATGGAGACGCTAAC 30171
Qy 144 -----Asp----- 144
Db 30172 GATAAATGAATGCCATGTGGGGCGTCAAAATGAGCAGACCAAGACGGCAACATAT 30231
Qy 145 -----Ile-----Ser----- 146
Db 30232 GTCGGGGTATTGGCTCAGCATGAGGACACCGAGGAGGCACTGAGCCAGTTTCTG 30291
Qy 147 -----Ile-----AsnGlu----- 149
Db 30292 GTTGCCGCAATCGTATCGCGTTTATGACCGGCAACGGGAATGAACCGCATGTTT 30351
Qy 150 -----GlyAsn-----Asn----- 152
Db 30352 GTGGCGAGGGCAACAGATATTCATGAACGAGTGTCTCTGAAGCGCTGACGCCGCC 30411
Qy 153 -----Ile-----SerLeuThr----- 156
Db 30412 ACCATTACAGCGGTGGAATCCACCGGTATTTTCCCTGACATCAGACGGAAGCTGACC 30471
Qy 156 ----- 156
Db 30472 GCTAAAAATGGGATATCAGTGGCAGTGTGAATCGGAATCGGAACCTCGGGACGCTCAAACAGTC 30531
Qy 157 -----Cys---Ile-----AlaThr----- 160
Db 30532 ACGTAAATGAAAACTGTACGATTAAAGGCGCATCTGGAGCGCACTCAGGTGAGAGTGAC 30591
Qy 160 ----- 160
Db 30592 TTCGTTAAAGCTGTATCCAAATCATTTCCGAAACAGGCTGGTACGTGGGGTAAACACGGAA 30651
Qy 161 -----Gly-----Arg----- 162
Db 30652 ACACCAACCGGACCGGTTACAGTCACCATCAGCGATGATCATAACTTTGACCGCTCAATC 30711
Qy 162 ----- 162
Db 30712 AYTATTCGCCCATATATCTTTAAAGGAATAGCGTATAGCGATCCGGGAAGTGTATTAAC 30771
Qy 163 Pro----- 163
Db 30772 CCGGAGGTACAGATACACGGGTTATGGTTTGAAGTTCGCAAAACCGGTGATTAAATC 30831
Qy 164 -----Glu-----Pro 165
Db 30832 GCATCCAGAGAACTAAAGGGGCCATTCGCCGTAGCTACAGTCGGTTATTGATATGCCG 30891
Qy 165 ----- 165
Db 30892 AGTGGCAGGGGAAGCGTCACTCTGGAGTTTAAAGGTTTCCATAAAGGCAATCAGCGGCA 30951
Qy 166 -----Thr---ValThr----- 168
Db 30952 GGTAATATCACCGACTGACGGTGTATTTGACCAAAAGACGGCTTCGGGCATCAGTATC 31011
Qy 167 -----TrpArg----- 170
Db 31012 CGTTGAATATTTATPAACCTAATAACGGCGCCAGAAATGCGCGCTTTTATTGCGA 31071
Qy 170 ----- 170
Db 31072 AAATCGGAGGTAATTATGCGTAAAGTTTGTGCAAGAAATTTGTCCGAGCAATTTGTCT 31131
Qy 171 -----His-----Ile 172
Db 31132 GGCCGTATCCGTGTGCTGCATGGCGCTCTGAGCATCAGTCCAGCTGAGCGCAGGATA 31191
Qy 173 Ser----- 173
Db 31192 TCTTCATCCAGTACGACGCTCCCGCAGCGCATGATCTGAACGGGATTAACGTGAATA 31251
Qy 174 Pro----- 174
Db 31252 CGTTATGAGTTTACGACACACTGGGGCTGATTACGTCCTTACGTTATGCAACGCGA 31311
Qy 175 -----Lys----- 175
Db 31312 AGATGACAAAACCGCATTAACGCGATACCGGTGGCATGAGGATTAACGTGCGTAAACG 31371
Qy 176 -----AlaVal----- 177
Db 31372 CTGTTACGCGTGTGCTTACAGCGCTGTGTCGATGATGATGATGATGATGATGATGATG 31431
Qy 178 -----Gly-----Phe----- 179
Db 31432 GATCGCGGTGTGCTTACAGCGCTGTGTCGATGATGATGATGATGATGATGATGATGATG 31491
Qy 179 ----- 179
Db 31492 TGACAAACAGAGGAAACCGCAGCGTGTGTCGCGGAAGTGAACGCTCGCTACAGCA 31551
Qy 179 ----- 179
Db 31552 CACATCTCTGGCGTGGGGGCTGGCGTGCAGTTTAAACCGACCGAATCAGTGGCGGTGA 31611
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QY 179 ----- 179
Db 31612 TGTGCTTATGAAAGCTCCGGCAGCGGTGACTGCGCAGCTGACGGTTTCATCGTGGGTGT 31671
QY 179 ----- 179
Db 31672 CGGTTATAAATTTTGTATTAGTAACAACAGCGTTTATGACAGCCCGCGGTTTCAGCGCGGCT 31731
QY 179 ----- 179
Db 31732 TTTTGTGGANTGGGTATGGCAGCANTACAAATATCANGCGTGTGAAGANGGTGCGNGA 31791
QY 179 ----- 179
Db 31792 AAACCAATACAGAACTGCNCCNTTCAACTGAAGCCAGAGCTAAACAGACCANGGTGGTG 31851
QY 180 -----Val---SerGlu---Asp---Glu 184
31852 GTGAACACCGTGGCCTCTGAAATATCCGATGAGCGAGCGGCTTANAGNATGAGCGTCCGAG 31911
QY 185 Tyr---Leu---Glu----- 187
31912 TATGGTCAGTACAGCTCACTCTGTTGGTGAAGGATTCGCCCATCATCGCCGAGC 31971
QY 188 Ile---Gln-----Gly---IleThr 192
31972 ATCTCGTGTATGAAGATTCTCAACCGGTGAGGATTCGCGTGAATGATTTCTCGTGCATGAGC 32031
QY 193 -----Arg---GluGln----- 195
32032 GAGGATGATGCCGTCGCGAGGCACTGCGTCTGTTTGAACAGATGGTGAAGAGCAGCG 32091
QY 196 -----Ser----- 196
32092 CGTCAGCAGAGGCGGAAGAAGATGCCGAGAAGCAGACGCTCCCGAGGATGCC 32151
QY 197 Gly-----Asp 198
32152 GGCATATCAGCCAGTAAGCGGAGCGAGCGCGCAAAATGCTGATACITTCAGCAGAGGAT 32211
QY 198 ----- 198
32212 GCATCGAGTCAGCCCGCAGCGCGCAGAAAGTCAGCCTCTGCAAAAGATCAGAGAA 32271
QY 199 -----Tyr----- 199
32272 CGGTCTCGTCTCAGCCTCTGAGCGCGCTCAAAAAGCAGTGAATTCATAAAGTCA 32331
QY 200 -----GluCysSer---Ala---Ser---Asn-----Asp 206
32332 ACAGATGCCGATTTGTCAAAAAGACCGCAGAAAGTCAGCGCGTAAATGCAAGCCAGGAT 32391
QY 206 ----- 206
32392 GCAACGACCTCAACAGAAAAAGCCCGGATCAGCAGAAAGCGCAGACAGTCAAGCGAACA 32451
QY 207 -----ValAlaAla---Pro---ValVal----- 212
32452 AGCAGAATAGCGGCGGAAGACGCGGTAAACAGAAATTCACCGCTGGTGGGCGCTCCCGGA 32511
QY 212 ----- 212
32512 CCAAGGGGGAACCGGTCCCGCGGTCTCAGGGGCGGAAGGGAGATAAAGGAGAGCGT 32571
QY 213 -----Arg----- 213
32572 GGAGACACCGTCCCGCAGGCGCAACCGTGAACCGGACCGGGAGGAGATACAGGTCCG 32631
QY 214 -----Arg----- 214
32632 GCAGTCCGAGGGGCCGAAANGCNACANGGACANCGGGANAGACCGGTCTGACGGGA 32691
QY 215 -----Val----- 215

Db 32692 AATGCAAGTCCACAGGGTCCAAAGGGAGACACCCGGGGCAGCAGGCGCGCCAGCCACAG 32751
QY 215 -----Lys---Val----- 217
32752 GGACCGAAAGAGAGAAACAGGTGCGGCTGGCCCGGTGGGGGCAACCGGACCTCAGGGNGC 32811
QY 213 -----Thr-----Val--- 219
32812 AAGGCGACCCCGGGGGAGACACAAATACGGTTCCGTCTGGGGCCGATGAGAATTATTGAG 32871
QY 220 ---Asn---Tyr----- 221
32872 ACAACACGCTATGGCTGGTTCGCCGGGTACAGATGGTGGCTCATCACCGGACGTACCTTT 32931
QY 222 ---Pro----- 222
32932 CTTGACCCCAAGATGCCAGGATGTTAAGGGACTGGATGAAGTGGGCGAGTGATACAGGCAGA 32991
QY 223 ---Pro----- 223
32992 GGTGACGGGCCATGCCAGGATGTTAAGGGACTGGATGAAGTGGGCGAGTGATACAGGCAGA 33051
QY 223 ----- 223
33052 ACTGGAGATGACATGATATTTTGAAGAGCTTATGACAGACTGTGTCGGTTCGCGAAA 33111
QY 224 -----Tyr---Ile----- 225
33112 GCATGATGACTGTGAAGACGAGCGTCACTTACAGACAAATTCGACTGGGACCGGCAGA 33171
QY 226 ---Ser---Glu-----Ala---LysGly----- 230
33172 CATCTGGAGTCAGATGAGAATGCAATTTATCCGAGCAGCAGCAGGGAATATCACACAGT 33231
QY 231 ---ThrGly-----Val-----Pro 234
33232 GGTGATCTGATCGACATGATAAAGCAGATACAGTGTGTGAAGACCGCTGCAATCCT 33291
QY 235 ---ValGly-----Gln-----Lys 238
33292 GCGTCTGACGCGGACGTGGGAAAATATTGGCAAAATGAAGTAACCCGACAGCTTCACAAA 33351
QY 235 ---GlyThr---LeuGln-----Cys----- 243
33352 ACCGAGTCCGACCTCCGTTTGTGTGATGTCGGTGGATGTTGTAGGAAAGCAAA 33411
QY 244 -----Glu---Ala----- 245
33412 GATGGCAAACTGCTGGAGGTTTGTGTGATGAGTATCCCAATATAATTAATAGATTAAG 33471
QY 245 ----- 245
33472 AGTTAGTTGTGAAGAAATATGGATAAACAGGACGCAATGCTTTCACCGATAAGGACA 33531
QY 246 ---SerAla---Val-----Pro---Ser---Ala 251
33532 ACTTCCATTAACACTCAGTAATATAGTGCAGAGTTCACCTGTCAACCGGTTCTTTTSCA 33591
QY 252 -----Glu-----PheGlnTrp--- 255
33592 GGAAGGAATATGAGTTAAAGGTCAATGATGAAAAAAGCGCTATCTTTTTCAGTGGTTT 33651
QY 256 ---TyrLys----- 257
33652 GAACCTAATCCTGAACGATATAAGAAAGATGAGGTTCCAAATAGTTAATACTAAGCAGCAT 33711
QY 257 ----- 257
33712 CCCTATTAGATAATGTCAAAATGCCGAGGATAGAGAGTGATCGATGATAGGTATT 33771
QY 257 ----- 257


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QY 341 LeuLeuLysPhe 344
Db 35989 TATTATAAATTT 36000
RESULT 27
US-09-334-220-4/c
; Sequence 4, Application US/09334220
; Patent No. 6323177
; GENERAL INFORMATION:
; APPLICANT: St. Jude's Research Hospital
; APPLICANT: Curian, Thomas
; APPLICANT: D'Arcangelo, Gabriella
; TITLE OF INVENTION: INTERACTION OF REELIN WITH VERY LOW
; TITLE OF INVENTION: DENSITY LIPOPROTEIN (VLDL) RECEPTOR FOR SCREENING AND
; TITLE OF INVENTION: THERAPIES
; FILE REFERENCE: 2427/0F704
; CURRENT APPLICATION NUMBER: US/09/334,220
; CURRENT FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 11580
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-334-220-4

Alignment Scores:
Pred. No.: 5,79e-25 Length: 11580
Score: 1713.20 Matches: 293
Percent Similarity: 11.09% Conservative: 44
Best Local Similarity: 9.64% Mismatches: 5
Query Match: 71.15% Indels: 2698
DB: 4 Gaps: 256

US-10-017-084a-523 (1-344) x US-09-334-220-4 (1-11580)
QY 1 MetLys-----Thr-----Ile---Gln---Pro 6
Db 9796 GCGGAAGTGTGGTACTAGAGAGACATGGTCAGCAGCTGGATGATTTTCCA 9737
QY 6 -----6
Db 9736 GCTTGAGCTGTTGACAGAGTTGTAGATGGTGGCTTCATGGAAGTGAAGGAGGAGCACC 9677
QY 7 -----Lys-----7
Db 9676 AATGCTGTTAGAGAGGAAGGAAGCACTGGGTCTGTACGAGCTGCCAGGAATCCGATCT 9617
QY 8 -----Met-----8
Db 9616 TGCATCCTTAGTGATTCCAGCATTTACGGATGAAGGTCACCAAGAAGTGGCTTCACA 9557
QY 9 -----HisAsn-----10
Db 9556 ACCCACCACAAATTTAAACTGCATCATGTCTCGGTGTATATGAGTTCTCGGAGGA 9497
QY 11 ---SerIle---Ser-----Tyr---14
Db 9496 GAGAGCAATGTGAGTCTTGTCTCTTTTATTGGCCAATAGAGGTGAAGAGATGATT 9437
QY 15 Ala-----Ile-----LeuAla-----21
Db 9436 GCCACAAAATCTGTGTCCTTACAGCATAGGTAGGTAAAACTCCAGTTTCTTCATGGGA 9377
QY 20 -----21
Db 9376 AGTGCCTTCATCATCAAAAGTGTCCACCAATTGGCTGGGATTGATTCTGTCCACCAAT 9317
QY 22 -----Ala 22
Db 9316 CAAAATGTTGTCAGTGCCCACTGAGCAGCAGCTCCACCCAGAGACCACCAATTCATTGCT 9257
QY 23 -----Leu-----Cys-----24
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Db 9256 GATCACAAGAGCTGCCACAGGAAAGTCGAGTTGTGTGGTGAGGGCATCTTCAGGAAG 9197
QY 25 ---Leu-----Phe-----26
Db 9196 AAGTATGTAGTCTGTCTTAACAGAAATGATTTCTGGTAATCCATCTCATGAGCAAGT 9137
QY 27 -----Gln-----27
Db 9136 CCAGGTAATTCCTCCATCGTAGAGTAGTCCACAGCAAGCGCTTCTCCGGCAGATGG 9077
QY 28 -----Gly-----Val-----ProVal-----31
Db 9076 ACGATGGCAAGAGTCTGTCTCTCACTACCGATCGCGCCCGCATGATTCAGGAACAT 9017
QY 32 -----Arg-----SerGly-----34
Db 9016 TGCACCTCGAGATCCAAATCTTGTAAACCGTGTCTCACAGTGGATCCCGCCAAATA 8957
QY 34 -----34
Db 8955 GAGTCAGTGTCTCGGCAAGAAATTCACACTCAGTGAAGTACTTCCACCTTCTAAGGA 8897
QY 35 -----Asp-----35
Db 8895 CATCCATAAGTCAGGTTGATTTCTCACTGTCAAAAGCGTTCCTTCAGGAAGTCTTCAG 8837
QY 35 -----Ala-----Thr-----Phe-----38
Db 8835 AGTGTGGGTCAAGTAGCAGTTTGGCCCTGAGTATCCCGATCACAGATGCACTGTTCCCT 8777
QY 38 -----38
Db 8775 TAAGCAATCTCCATGGCCCTGCGAGTTGTCCAGCATCCAGGCGCCAGGTAGAAATTATC 8717
QY 39 -----ProLys-----40
Db 8716 GATTGCCACTGCATGCTGAGTACTTCTGATAGAACCTTAACCTTACCGGATTTCCCAAC 8657
QY 41 ---Ala-----Met-----Asp-----43
Db 8656 TAAGCTTTTCAAGAAAGTGGTAGTGATCTCTTCCACCCCTTTAGTTGGAAGAAATACAGA 8597
QY 44 -----AsnValThr-----Val---ArgGln-----49
Db 8596 TGGCTGAGAAAC---ACTTCCAGAGCAATTTGGGTGAGGCAAGCACTGAGGCAAGCAG 8540
QY 50 -----Gly-----50
Db 8535 ATAATTCCAACTCACACCGAAGTCAGTAGAATACTGCACATGAATTTGATTCGGGCAAT 8480
QY 51 -----Glu-----51
Db 8475 TTTTTCAGACACCTTACATCCAACTGAGATCTTGAATTTGCATATATCCAGCCTTCAGTGG 8420
QY 52 -----Ser-----Ala-----53
Db 8419 AGTCAGTCTATGGTCACTGCATACACCTCCCGTCCATCATGATGCTGCCACAGACATCAC 8360
QY 54 ThrLeuArg-----CysThrIle-----59
Db 8359 ACCATCAGGGAGTTCACAGAATCTTCTACTGTACAATCATCATGGAATAGCAGTCTC 8300
QY 60 -----Asp-----AsnArg-----62
Db 8299 ATTCACTGAAGTTTGTCTTCCATAAACATGTCAAAGCGATCTCCGACAGGCGCGC 8240
QY 62 -----62
Db 8239 ATCTGCAGGGAGCGGTCTGTGCTGGGGTACTGGGGCGGTGCTGAAGGTGTCCAGCATAC 8180
QY 63 -----ValThrArg-----Val-----66
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Db	8179	GGTCTTTGGTCAGCAGAGCTGAGATGAGGACATTTGCTCAATGGCCCGAGTGGTCTGATC	8120
Qy	67	---Ala---TyrLeu---Asn---70	
Db	8119	CAGCCCGTCATGCTTGGCTGCCACAGCGGAGTGGCATCTCTTTAGCATCAGG	8060
Qy	71	Arg---Ser---ThrIleLeu---Tyr---76	
Db	8059	AGGAGAGAAGATATTCACAAATCCGGCTTACTGTACTGTCTATGAGAAATCTCCATGAG	8000
Qy	77	---Ala---GlyAsn---Asp---Lys---81	
Db	7999	CAGGTCAGGTAATGCTCCATGACAGATATTCAGAGAACACCTTGGTTACGGTT	7940
Qy	82	---TyrCys---LeuAsp---85	
Db	7939	GTITGGTGAATCAGGCACCCATCATGATGAATGAATGGATGAATCAGCATTAGTGAG	7880
Qy	86	---Arg---Pro---86	
Db	7879	GTITAGATCCACAGTACTAATAATCGACTACAAACCCCACTGAAATGGAGAGCCATTC	7820
Qy	87	---Arg---87	
Db	7819	CGAGGCCAGGCTCCACACTGTACTCAATTTCCCTCCGTTCCAGTCAAGCCAGTTCTG	7760
Qy	88	---ValVal---89	
Db	7759	ACTGGATGAGCTCGATTGAAGTTGTCTTTGAGTTGGTTGGAAGAGAGTCTCGGGGTC	7700
Qy	89	---89	
Db	7699	ATCAGATACAGGCCACCCACCTGTTCATCAGACAGCCAGTTTCCCTGGATGATCTCC	7640
Qy	89	---89	
Db	7639	ATGGCCACTGCATGCTCTATGAGCCATCCCGATATAGACATATCTATTGCCCATGT	7580
Qy	90	---LeuLeu---Ser---Asn---Thr---94	
Db	7579	CTGCTGCTTTCAAAGAGAGCTGGTTGATGATCCAAACGGAACGAGTGGCTTGGACCTGT	7520
Qy	95	---Gln---95	
Db	7519	ATAAGAGGAGAGCGAGTGAATCTAGTCCACTTTGTTGAAAGTGTCTGACACCAAGAT	7460
Qy	96	---Thr---Gln---Tyr---98	
Db	7459	CGTTTGACATGATAGCGACTGATTCACATTTGGTAGGCACACAGTCCCTTACCAATGG	7400
Qy	99	---SerIleGluIle---Gln---Asn---Val 105	
Db	7399	GTGCCATGACATCC---AAGATCTACTGATGATTCCTCAATCGCATACAAAGAGTC	7343
Qy	106	---Asp---ValTyr---108	
Db	7342	TGTGACTGACAGGAGGAGCGAAGTCTATCTGTAGGAGGAATCCTCATTCACGGCAAC	7283
Qy	109	---Asp---Glu---110	
Db	7282	GTCTGTGCTGACCGTAACGGGTGCTGGCTTTTCAATGAAGACCGGCATCACCAGT	7223
Qy	111	---Gly---ProTyr---Thr---114	
Db	7222	AGAGCCACACAGGCGATCTTTGGTCTCTCTGGTGAAGACGCCATTTCTACTATCAAG	7163
Qy	115	---CysSerVal---Gln---Thr---119	
Db	7162	GTTTGTGAATCATCTTCAGACCGTATTAACAGAAATATTTCTCCAAATGAATCTG	7103
Qy	120	---AspAsn---121	
Db	7102	ATCGATAACCCAGGGGCTGTAGAGTGGCCATCTCTCAGAGGTTGCCACCGAGGCG	7043
Qy	122	-----His-----122	
Db	7042	AGTAGAACAGAACGGGCTTTCAAGGTATCTCCAGGGCAATGATACCTGCCACATGCT	6983
Qy	123	-----Lys---Thr---SerArg---127	
Db	6982	GGAAATGTGTAAGAGGAACCTCTGAAAGAGACTCCACAGAGAGGCCACCGTTGAGAGAATA	6923
Qy	128	-----Val-----His 129	
Db	6922	CTGTAGGACACGGGTTGACTCTCTGGGGTTCAGGAAGCGCTTTACCACATCCCATCTCAT	6863
Qy	130	-----Leu---Ile---Val-----Gln 133	
Db	6862	GAAGAACTGCACAAATCTAGCATGTATTAATCCAGGTCTCTGTGTATCAATATGCCAA	6803
Qy	134	-----ValSer-----135	
Db	6802	GCCATCTTCATTGAAAAAGAGGTTGTTTCCACTAGAAAGGATTCACACTTTTCGAGATGG	6743
Qy	136	-----Pro-----LysIleVal---139	
Db	6742	TTTCCACCACTCATTAATAAGAAATCTATCAGATCTTAGCTGACCTTCGAAATCATCTTT	6683
Qy	140	-----Ile-----141	
Db	6682	GAGAAATCAGGATTTTGGTCTTATTTTACAGTTGGAAGCTGAGTAGCCAGGCTCACA	6623
Qy	142	-----Ser---Ser---Asp---IleSerIleAsnGlu---Gly 150	
Db	6622	TATACATTTGGTTCCATTGATACAGCTCCCTGTCTCCATTACACATCTCTCACATGGG	6563
Qy	151	Asn-----Asn-----Ile---Ser 154	
Db	6562	ACCGATGTAGACATTTATCAATGGCCCATGTCTACTGGCTGAGAGCGGAGGTTAAATCC	6503
Qy	155	Leu-----Thr-----156	
Db	6502	CTGGTACCATCTGAACCGACAGATCCAAAGGTGAGTTCCTCCAAAGTGACACCTC	6443
Qy	157	-----CysIle-----158	
Db	6442	CCTCTCCAGCCCTGCATGTTCTCTGCTAGTAGTGTGCTGGGGTGGTGTCTCGTGA	6383
Qy	159	-----AlaThr-----Gly 161	
Db	6382	GCATTAAGAGCTGAGTGGCTGTCTGTGTGTAGCAGAGGGGCGACAGAGGTGCCAGT	6323
Qy	162	ArgProGlu---Pro-----165	
Db	6322	CGCCCGAAGTCCCTTGAAATTCAGTCTCCTGGATCCCGGGATGAGCTATCAGTGA	6263
Qy	166	Thr-----ValThr-----168	
Db	6262	ACAGCAACGTTGATCTCAAATTTGATGATGGTGTCTCTATTACATTTAGTCTACGGT	6203
Qy	168	-----168	
Db	6202	GGTAATGGAATGCTCACCACTTCATTTGAAACAAACACCATAGCTGAATCTTCTTCAGG	6143
Qy	169	-----Tyr-----Arg-----170	
Db	6142	TGCCCCCTTTGAAGAAATATGACAAATAAGAACCGATGTACCACCGATAGAAAAACCA	6083
Qy	171	-----His-----171	
Db	6082	ATTGTCTTCTCGGCCCAAAATCAAATGTATCCAGAGCATCACAGGTTGTTTACATT	6023
Qy	172	IleSer-----173	
Db	6022	ATTTCCATCGAATGAAGTCATCAACATCCAGATTTCTTTCTTCTTACCGTTATTATA	5963

QY	174	----	ProLys-	----	AlaVal-	----	Gly-	----	178
		:::			:::				
Db	5962	AGGTTGCCAGAGCTCGAATCTTGTAAGCATTGGTTGGCAGCTGTATGGCAAGGGAACATT	5903						
QY	179	----		----	Phe-	----	Val-	----	SerGlu
									182
Db	5902	GATGAAAGATATATTTCGTTGTTTGAGGAAAGTAAAAATTCATCCATCAGGTGCCAAGTGAT	5843						
QY	183	----	Asp--Glu-	----		----		----	184
Db	5842	TCCTCCATGATGGAGAATTGTAACAGAAATAGATGAGATCTCTCGGGTACTTTTTC	5783						
QY	185	Tyr-	----			----		----	185
Db	5782	TATAAATCTAAGTGAAAACTGGACATACATTGTATTGTACAATCTAGATCTCTTGAAT	5723						
QY	185	----		----		----		----	185
Db	5722	AAGCATCTTAGTCCCTTCCCTTTAAAAATTTAGAGATGTTCCAGATTTGATGGTTTCACC	5663						
QY	186	----	Leu-	----		----		----	186
Db	5662	ATTCAGATTCCCTCTCTGCAACATACACTTCAGGCCAAAGGTCAGGATGTAAATTCOC	5603						
QY	187	--GluLe-	----	Gln-	----	Gly-	----		190
Db	5602	ATTGAAATCGTCTTTAAGAANTCGAGGCGAGAGGAACAACAGGAACAACATAGGGTCCACC	5543						
QY	191	----	IleThr-	----		----		----	192
Db	5542	AAAGCCCGGTCACACACAGGTCAGCATCACAAATCCCTCGTCTGAGCACATCCA	5483						
QY	192	----							192
Db	5482	AGGCACCCCTGAGGCCAGTACACATTATCAATCGCCAGGAATCAGCCCCACAGTGTA	5423						
QY	193	----	Arg-	----					193
Db	5422	GTTGGCCTGAATCCATCTGAACCGGGTCTCGGAGAAATGGTGGAGAGTGGAGGTAGAC	5363						
QY	194	----	Glu-	----		----		----	194
Db	5362	AGTGATCCGCTTCCAATCTGGAACTCTTCGAGGTGTAAATTGAATTTCCGTGTAATG	5303						
QY	195	GlnSer-	----	GlyAsp-	----			----	198
		:::							
Db	5302	CAGACGCCAAATGGTTGGAGGAACACACTCTTCGGTGAACAAGTGCAGTCCCTTGCATT	5243						
QY	199	----	Tyr-	----	Glu-	----		----	200
Db	5242	GTTTCAGAGAACTGGAGCTGTACACTGGGAGTTGCTGAAGGGTGTGCTACAGCCAT	5183						
QY	201	----	Cys-	----		----		----	201
Db	5182	GCTCATTTCAACTGCAAAAGGTAGATGTCACATGAAATCCAGGTCTCAGCATA	5123						
QY	202	----	Ser--AlaSer-	----	Asn	----		----	205
Db	5122	ACGAGGTTTTCTTAUGTTTTCAGTGAATATCAGAGCAGTATCCATAGAGAGCAGTCAAT	5063						
QY	206	----	Asp-	----	Val-	----	Ala-	----	208
Db	5062	ATCAACTTGACCTCCTTGGAATTCGATACCAGTTGGCTTGCAAAATCTATAGAGCCATCAA	5003						
QY	209	----	Ala-	----		----		----	209
Db	5002	TTTGTCTTGAATCCAGTTTGAGAGCTGTCAATTCATTCCTATAAGAACATCATCCAAAGC	4943						
QY	209	----							209
Db	4942	CCACTGGGCTGAATGCTTCCCATGTTGGGTTGCCACCATCGAAATGCGTTGCGAGTGT	4883						
QY	209	----							209

4882	DB	CTTCGGCTCTGTGGCAGGTCAAATGGAAATGATCTGTGGTTCCAGGAAGGACATGAAGTC	4893
210	QY	-----ProValVal-----	212
4822	DB	CAACTCTCGAAGCAATGCCAGAGATATCCCATTCATCTGATTTTGATATCTGAAACAATAAGCCC	4763
212	QY	-----	212
4762	DB	TTCATTTCTAGTTCTTGTGTTTGATCGAGGTAAATGCCTGAAGTTTGTCTCCAAATTGTTAT	4703
213	QY	-----Arg-----	213
4702	DB	ATAAAAATTGAACAAGTCTGATATATTCCTGGTGTCCAGAGGACCGTCGGGGCTTCCCTTTT	4643
214	QY	---Arg---ValLys---Val---	Asn 220
4642	DB	CCGAGGGCCATTGAAGTAGAGAGATTGCCATCGTTAAGTGTGCCAGCAGGTTCCAC	4583
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4582	DB	CTGGGCACCTGTTATCTTTGTATCTGTATCCACAGAGGGCTGAGCTTCCCTCAAAACCTATCGAACAT	4523
222	QY	-----	222
4522	DB	CTCATTTGTATTGGGACATTTGACACACAGGTTCTTGTGACAGCATATATCCCAGGTC	4463
223	QY	-----Pro-----	223
4462	DB	ACAGAAACACACTCTGAAATGCAGTCCCATGGCCACTGCAGTAACTGGACAGGCTC	4403
224	QY	---Tyr---Ile---	225
4402	DB	GGATATGTACTCCATCTAAACCAAATGAGGCAAGTTTTTCTGTGAGTGTCTCTCTG	4343
226	QY	---SerGlu---Ala---	228
4342	DB	GATCCATCGGAATCTGTCTCTGTGATGCAAGAGACCTTGGATTAACAATGGTGATTC	4283
229	QY	-----Lys-----Gly---Thr-----	GlyVal 233
4282	DB	TGTCATCTTCAAAGTCCCTGTGTGATACATGGTGGGTCTGCTGAGTTCTCTGAGTT	4223
234	QY	-----Pro-----	234
4222	DB	TCCTTCGATCCTTTGCCTGCAGAACCGGGTAAACAGCCTTCTTTCACGAAACCGAGA	4163
234	QY	-----	234
4162	DB	CATACCAGCATCATGAGAGTACTGAAGAAGAACTGGAGCAGTACTGCTGAATTGATTGGC	4103
235	QY	---Val---GlyVal---	237
4102	DB	ACAACTATGTTAGTTGAACTGTAGCACATATCAAGTTTTCAGGGGTCAAATCTCGAGT	4043
238	QY	-----Lys-----	238
4042	DB	TACTGCAAAATCGATCTCCATCTGATTTTCCAAATATCATTTGCTGATGTTGGCAGCACA	3983
239	QY	---Gly---Thr---	240
3982	DB	GAAGGTTTCATTTTAAACCATTCCTTCATTAGCAACATCAACACACACTCATCTGATT	3923
240	QY	-----	240
3922	DB	CATAGGTAATCAAAGCTGGCTTCTCATAAAGTTCTGAGGTAAGTTGGATTGATAAC	3863
241	QY	-----Leu---Gln-----Cys-----	243
3862	DB	TGGGATGATCTGCTTCTCGACAGAATGATGATGTCATCGACTGCCACTGGTC	3803
244	QY	-----Glu---Ala---	245

Db 3802 ATAGTCCTCCCTGAGAACAGGGCTGCCACAGCGGAACCTGGTGCAGAGGGTCTTGGC 3743
QY 246 -----Ser-----Ala----- 247
Db 3742 AGCAGCTGGAAGCTCCAGATAGACAAATCTGGGTTTGTCTGAAGTCTGAAAGTACATCTC 3683
QY 248 -----ValPro----- 249
Db 3682 TGCTAGCAGGTGCCACTGGATGCCCCCATTTGTCTGTACTGAAGGAGAGCGCCCTCCTC 3623
QY 250 -----SerAla-----Glu----- 252
Db 3622 TCTGCTGCAGGCTGTGTGCATGAAGCACTCTCTCCGCTATCTGGATGTAGAAGTGTGAC 3563
QY 253 -----Phe----- 253
Db 3562 AAAGTCCACCAAGAAGTATCCAGTCCCAACTCACCAGCTGTCTTTTCCAGCGCTTGGCT 3503
QY 254 -----Gln----- 254
Db 3502 GAAGTACAGAGATATCCAGAGAGATGACACCAACACCCCTTGTCTGTCTTTTACAATTTC 3443
QY 254 ----- 254
Db 3442 TCCCCCAATAACTTCTTCCAGTCAGACTCCAGCCATTCTGGTTCTCAAAATCTGACAT 3383
QY 255 -----Trp----- 255
Db 3382 AATTGTGACGGAAGGCAAGCTTCTGGGTGGCAATTCAGTGCCTTGGTACCCTTGGTCACA 3323
QY 256 -----Tyr----- 256
Db 3322 CCTGCATATGCCATGATCGCATGAGCCATGCCCACTGCACATGTTGGGGCACTGCTGCC 3263
QY 256 ----- 256
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QY 257 -----Lys-----Asp----- 258
Db 3202 GAAACGGGTAGCACTGGACCAAGTTTCTGGGAGAGCACTATGACTCTCTCCACTG 3143
QY 258 ----- 258
Db 3142 TGTAATACTACTGCTGTAAATACTTGTCTGTATGTAAATTCCTGCAACTTGGCATACT 3083
QY 259 -----Asp-----Lys-----Arg 261
Db 3082 TGGAGGCAATCTTCTTGGACGAGGTGCCAGGTAAAGCCGTGGTGGTTGAGTACTCCAG 3023
QY 262 Leu-----Ile-----Glu 264
Db 3022 CTTCACTGGTGTCCATGTGGGGTGTATTTCTGGCCACATCCCATCACCACCAACTGAA 2963
QY 264 ----- 264
Db 2962 CTGAATCATATAGAGTCTCTATCTGCATGTATGTGTGTTCACATAGCGCATACTGA 2903
QY 265 GlyLys-----LysGly-----Val----- 269
Db 2902 GGCAAGTTTAGAATCTCTGTAAACAAAGGTTCCAGTGTGGCCACAGTATGGCTGAAC 2843
QY 270 -----LysValGlu----- 272
Db 2842 ATTTCCAGGTAGAATPCCAGAGACTGAGTGCCTCCACAGATTGGTAAAGTCAAGACT 2783
QY 273 Asn-----Arg-----Pro-----Phe----- 276
Db 2782 AATGCTGTTGAAGACACAGATGTATGATATATCTCATCAATAGCCCATACATCTTCTCT 2723
QY 277 -----Leu-----SerLys----- 279
Db 2722 CTGGGAAGAAATGATACGGTTGCCACCATCTGAACCTGAATTCACAACTGCTTTGGCATACC 2663

QY 279 ----- 279
Db 2662 TGGTAGTTCTACGAGATTTATTTGGGCTCATGATAGTGTAGATATGAATATGCTCCAG 2603
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QY 282 -----PhePhe----- 283
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QY 283 ----- 283
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QY 284 -----Asn----- 284
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QY 285 -----Val----- 285
Db 2302 CATTTGGGAATGTCTGGGATGCCATCTCAACAGCTGGGCCAGAAAATCCAGGGTCAACATT 2243
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Db 2242 GCAACCATGTCTAGTCACTGTCTCTGCCAGAACAGATTTGAGACATGACGGGCAAT 2183
QY 288 -----His-----Asp----- 289
Db 2182 ATAAACATTTCAATTTGCCCATGTTTCCAGGATTTGCTCTGTCTTGTCTCCAGCGAAT 2123
QY 290 -----Tyr----- 290
Db 2122 CCTGGTGTCCGGTTAGTGTCTGCTGTAGGAAGGGGAATGTTTATTTCCGTTCCACCCACT 2063
QY 290 ----- 290
Db 2062 GTAGTTTTCAGAGGAGTAGACAGTGTGTGGGGAGGTGGGTCCAGACAGATCTCAGG 2003
QY 290 ----- 290
Db 2002 TAAGCATTCAGTGTGAAGGAGGACCAAGGAGGCCCATGGTTGGTAGAAAAATTCCAAGCT 1943
QY 291 -----Gly----- 291
Db 1942 GACACTGTTACCAGGCTGATGGTTCCATCCAGATTTGATGGAAAACTGTATCATGTG 1883
QY 292 -----Asn-----Tyr----- 293
Db 1882 AGACATTTGAGAGGAGAGAAAGGCAAGACATGGAAGTCTACAGCCACACATTCCT 1823
QY 294 -----Thr----- 294
Db 1822 ATTATGCTCTGATGGTTCTTTTGTCCCTGAGACAAAAATTTGGTAGCAGGAGTCTGAAGTTC 1763
QY 294 ----- 294
Db 1762 AGGATTGATGACCACAGAAACCAAGACGGAACCTTATATAGGAATAGGAAGGGTATC 1703
QY 295 -----CysValAla----- 297
Db 1702 CAGTGTATATGCTCTTTCTCTCTTCAATTTTGTGCATACAGGATTTATGTCATTTTCATG 1643
QY 296 -----Ser-----Asn-----Lys-----Leu----- 301
Db 1642 AGAATTTCCAGGGTCACAAAATTCCTCCCATCACAAAGTAAACCTCAGGTTCCCATACC 1583

QY 302 -----Gly-----His--- 303
Db 1582 GGTAGTGTCCATGGAGTGCATATTTCTCTCCATCTTTGAGGAAGACCATGA 1523
QY 304 -----ThrAsn---AlaSer-----Ile----- 308
Db 1522 TAAGCTGATCTATCGTTCACATCTGTACCACTGACAGCTCCCAAGACATCCCATCC 1463
QY 309 -----MetLeu-----Phe---Gly----- 312
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QY 313 -----ProGly-----Ala---ValSer---Glu----- 318
Db 1402 TACATCCCTGGGTGGCAAAATGAATGAACTGCTGCTTCAATTCATGGAATAAATGA 1343
QY 319 Val-----Ser----- 320
Db 1342 GTTCCCATCTGACTGACGATCTTAATCTAGTCTCTGGGAAGAACCCAGTTGCC 1283
QY 321 -----Asn----- 321
Db 1282 TGTGTCCACTGGGTGAGACTATCTTAAACGACTTGTCTGAGCTGAATGATGAT 1223
QY 322 -----Gly-----Thr----- 323
Db 1222 CAAGATGTTATCTAAGCCCGAGGCTTCATACATTCACCTACAGAGATTTTCCTG 1163
QY 323 ----- 323
Db 1162 CTTCCTCAATGAAATGGACATCTCCCTTTGGGCTCTCAGGAAGTAGAGATATGAT 1103
QY 324 -----Ser-----ArgArg--- 326
Db 1102 GATTGTGCTGACATGGAAGGGCTCTAATTTCTCTAGCTGAATCCAGTCCGACAGTT 1043
QY 327 -----AlaGly----- 328
Db 1042 ATTCTTGGCATATACACGATGCTGGGTCTGAATACTAAAGCGACATGAACCTGA 983
QY 329 -----Cys----- 329
Db 982 CCCAATGGAATTTGAGGACAGAGCTGTGTGTATTAAAGCCCTGTGTATCAGTTC 923
QY 330 -----ValTyr-----Leu 332
Db 922 TCGTGGCCATATGGTTACAGAGGTGACGCGATGCGCATGATTAATCGCCACACTG 863
QY 333 -----Leu-----Pro-----Leu---LeuVal 337
Db 862 TTCTCCAGTCTCACAGTTGTTACATTCACCATATATTTGGATTTAATTCAGTTGGTG 803
QY 338 -----Leu----- 338
Db 802 GTAGAGTCAAAGTCACTCTCAGGATATGCTGCTACTATGATTTTACGTAGATGGG 743
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Db 742 GTGCACAGTGCATCTGTGGAGCTCTTGTTCACAACTGCTGGGTAAAGCATCTTT 683

RESULT 28

US-08-471-119A-1/c
; Sequence 1, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Leitner, Ernst
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoerendorfer, Kurt
; APPLICANT: Weber, Gerhard
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation

STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kassenhoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
TELEFAX: 201 503 8807
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 46899 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tolypocladium niveum
STRAIN: ATCC 34921
US-08-471-119A-1

Alignment Scores:
Pred. No.: 2,348-22 Length: 46899
Score: 1712.70 Matches: 291
Percent Similarity: 11.34% Conservative: 45
Best Local Similarity: 9.82% Mismatches: 5
Query Match: 71.13% Indels: 2623
DB: 1 Gaps: 249
US-10-017-084A-523 (1-344) x US-08-471-119A-1 (1-46899)
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QY 5 -----Gln-----Pro--- 6
Db 1489' CGCTTCCTGAAGCTTGGCGGGGTAAAGTTTGGCCCGACGAGGATGAGCTTGTCCCGGG 14838
QY 6 ----- 6
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QY 7 ---Lys----- 7
Db 1477' GCGAAGGTTTGCCTTGAGGATTCGAGAGAACCGGATGATCGTCTCGAAGACCGTGGCGC 14718
QY 7 ----- 7
Db 1471' CAACACCGCATTAACGTGTGCGGAGCTGAAGAACCGGTGAGGAGCCAGCGGACCCCT 14658
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Db 1459' GGAATCGGGTTGATCGAGACCTGCTCTCATGGAACATCAACCAAGGAATCACGAGG 14538

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Qy	96	-----Thr-----	96
Db	12317	ATCCATCTTGGTCGGGCAAAATCAACCCAGGCGCCAGGACTGACTTTGTGTCGGGTTT	12258
Qy	97	---Gln-----Tyr-----SerIleGluLeu-----Gln-----	103
Db	12257	CGCAGATCATTCAGTGGCGCAAAACAGCAGCATACCGATACGACTCAGCTCGTTCTGGC	12198
Qy	104	---Aen-----Val---AspVal---Tyr-----	108
Db	12197	TCGCAATCTCTTGGGAGAAATCTCCAGCTGCTTGATATCTCTACTTGGTCTCGAGGA	12138
Qy	108	-----	108
Db	12137	GSTGAATAAGGCGGATCAACGAGCAGTTCTCTCAGACTCTTCATTCGAACAACCTC	12078
Qy	109	-----Asp-----	109
Db	12077	CGCTTGAATCTCGGCTTTGTTCGCTTATGCCAGTGCATGAACCTGCGGAGCGACAAG	12018
Qy	110	Glu-----Gly-----Pro-----	112
Db	12017	GAATCCCTGTTGATGGCGTGGACCTCATATCAACCAAGAGATACGCTCCAGCCAGG	11958
Qy	113	-----Tyr-----	113
Db	11957	GACCTTGGTAAGATCTGACCAACTGSGCGAGATAGTCTTGACTCGGAAAGTATGAGC	11898
Qy	114	-----ThrCysSerValGln-----	118
Db	11897	GACCGAGTTGACGACGACAAAGACTGC---GTGCAGATCGTCTCCAGCCGGTCCGATATC	11841
Qy	118	-----	118
Db	11840	AGTTGTGTTTCAACTTCAACCGGATCCTATCTCAAGCCAGGGAATGACTTGGCGC	11781
Qy	119	---ThrAsp-----	120
Db	11780	CTTGTGTAACAAACGGGTTGGCGATGGCGATGGCTCTAGGCCAAGTACTTTGCAGACC	11721
Qy	121	-----AsnHis-----Pro-----Lys-----	124
Db	11720	CCCTTCTCTGCGAGGTTGAACAGAACCATGCCAGTCCCTGTACCAACTTCAGTACGTG	11661
Qy	125	ThrSerArg-----Val-----	129
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Qy	130	Leu-----IleVal-----	136
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Qy	137	---Lys-----	140
Db	11546	TCCAAGGCTTGTGATCGATGTGGTGATATCTCGTATGCGATGCGTGTGAGTGAAGT	11487
Qy	141	-----IleSer-----	142
Db	11486	CTGCCATCTTGGACCTGGTGTGCTGATCATCTCTTAACATCAGGCACTCGGGCGGC	11427
Qy	142	-----	142
Db	11426	CACGAATCCAACTCTCCAGTCTTGATTTTCTTGAGTGGGTGACGACTGCCGCAATC	11367
Qy	143	SerAsp-----	144
Db	11366	AGTGACAGGCTGTGGCTTAGAAGACATCTCGACCTCAGCTGTTGATGCGGTGGCC	11307
Qy	144	-----	144
Db	11306	GCGGATCTTGACCTGGTATCGATACGGCCGAGAAATTCGATCTGGAGGTCTTTTGGTGC	11247
Qy	145	-----IleSer-----	148
Db	11246	GTAGCGCACTCGATCTCTGTGCGGTATGCCCTGACTTGTCTGCCATCGATATCAAGTT	11187
Qy	148	-----	148
Db	11186	GATAAATCGACAGTGTGTGAGAGAGAAAGTAGTAGCTTCGAGCAGACCGTCTCCAST	11127
Qy	148	-----	148
Db	11126	CACGATGAGTTCTCCATTTGCACAGAGGGGGGTGATTTGCTGATTTGTTCCATGACAAA	11067
Qy	149	-----Glu-----Gly-----	150
Db	11065	AGCTCCCGAGTTACTGACAGCATGACCGATGGGACACCATTTGATGAAGGGGTCTTCGSC	11007
Qy	151	Asn-----	151
Db	11005	AATGGGATAGATTGTCTCATGACTGTGTTTCCGTTGGGCCGTACGCATTGAAAGCTTG	10947
Qy	152	-----	152
Db	10945	CGTCTGGACGACCCCTTGTCTTGGCAGCATCAGAGCATCTAGCCTATCACCACCAAT	10887
Qy	153	Ile-----	153
Db	10886	ATAGAGAACGTGAGAGTTTGGACAGAGCGGTGAGTTGTCAAGGCATGCTTTTCAGCAA	10827
Qy	154	-----Ser-----	154
Db	10826	GGCTGGAGGAGCAGAGCAACATTGACCGTTGTTGCGAAGAGACCTTCTCGAGCGCTGT	10767
Qy	155	---Leu-----Thr-----	156
Db	10766	GCTCTCCAAGAGATGAATAATAGTCGATACACCAACGTCCTCCATTGAGAAGCGTGT	10707
Qy	156	-----	156
Db	10706	GAACACTTCCACACGAGGATCGAAGGCAAGATTTCGATATGTGGCCATGTGGAAGA	10647
Qy	157	-----Cys-----	157
Db	10646	CTCTGGCAGTTGGATGTGATGTTGGTCTGTCTTTGTAAGCAAGATTCGCGATGCTC	10587
Qy	158	-----Ile-----Ala-----	159
Db	10586	GACCATGACGCCCTTTGGTCACCACTCGATCCAGACGTAAGATTCATACGCAAGGCT	10527
Qy	160	-----Thr-----	161
Db	10526	TGCTGAGTGGGCTGACTCTCGCGCCAGCCGTTGATGTGCTGCTTCTTGGCTCGGCGAG	10467
Qy	162	-----Arg-----Pro-----	163
Db	10466	AATCTCGTATCCGATCGTCTCCGCTTCAGCCATCCCTCCGGAATCCGGGTCTCTGC	10407
Qy	164	-----GluPro-----	165
Db	10406	GCCCAAGGACCAACATCGATCCGACACCTCGAAGAGATGGCTCGAGCCGGGACGC	10347
Qy	166	---Thr-----Val-----	168
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Qy	169	-----Tyr-----ArgHis-----Ile-----	172
Db	10286	CACGATGTCTCGACGAGCGTGGTCCAGGATCGCCACGACGATCTCTCAGAGCGATACC	10227
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Db	10226	TCGCGAGATAGCCAGCAACCCACTTGTATCCGACTTCCGATCCCAAGTCGCAATAGCTCAG	10167

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267 ---Lys---
7946 GTGCCGTTCCAGATAGTCTTGTCTGTAGGATGTGAACACACGATATCTTTCGGGATC 7887
269 ---Val---
7886 TTTGTTCTCTTTCAACAGCCTAGCAAGACCTGTCTATCCATCTGTGGCTTGGAGCGAAGTC 7827
273 ---AsnArgPro---
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276 ---PheLeu---Ser---
7706 CGCAGGATCTCAACATGCTCTATTCTCCGATAGAGATTCTCTGAGACTTGTGAAGAA 7647
279 ---Lys---Leuile---Phe---
7646 GGCAGGTCGACAAAGCAATCTCTCTCAACCGGGCCACCTCTCTGTGTGCAC 7587
283 Phe---
7586 TTTAGATCTGTCACCTGCTCCGTTTGTGTGACCGCGCTGCAACAAAGAAAGTCTTT 7527
285 ---ValSerGlu---
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287 ---
7466 CAGGGCTCAACACCTCGCGAGGATTTCTCGGCTCGGGAATACTGGCCACCGAGTT 7407
288 ---His---
7406 GATGACGATCAGATCGGGCTCAAGCGCTGAGCGCGCCGCTATCCATCGCGTGCAGAC 7347
290 ---Tyr---
7346 ATGTACTTGGGCTTTCCCTCAAGCCCTGGAAAGTTGGGCTGCTGTGTGACGAATG 7287
291 ---Lys---
7286 AACCGGATTTGGGAAGGTTCCAGTCCAAATGTAGCTCTTCAGCCCGAGCTTGACCGAGAT 7227
295 ---Cys---
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297 ---Ala---Ser---
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7106 TCCATCGTACATAGGTCCAGGATGTAAGTCTCGCGGAGCGGTGTTTGTATCAATGGC 7047
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7046 CGTGATGTCGCGTAGGCGGTGTCTGAATGCTCTCCCAATCTCTGAGCTTGGTGTCT 6987
301 ---LeuGly---
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304 Thr---
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307 ---SerIleMetLeuPheGly---
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313 ---Pro---Gly---
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315 ---AlaVal---Ser---Glu---
6746 TGTGCGATAGGCCCTCGAAGTTGGCTCGAGCAATGACATCCACGACCGGTGCGAATC 6687
319 ---Val---
6686 AAGAGCGGGTGTGTAGCCAGAGCCAAACCATCTCCAGTGACTTACAGCTCTCCCAT 6627
321 ---
6626 CACGCCAACGCGACAGCTGTGATTCTGTGTCATCAGTAGACCCAGAGTTGCTAATC 6567
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325 ---Arg---Ala---
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329 ---Gly---CysVal---
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331 ---
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333 ---LeuLeuPro---Leu---
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337 ---Val---
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339 ---His---
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341 ---LeuLeu---Lys---
6146 ACTGGATAGAATGTGTCTGTCTTCAACAGCGCAAGACTCCGCGGTGTGATCATCATC 6087
344 ---Phe 344
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RESULT 29
US-08-646-695-1/c
; Sequence 1, Application US/08646695
; Patent No. 6168943
; GENERAL INFORMATION:
; APPLICANT: Rose, John K.
; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
; TITLE OF INVENTION: USES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

QY 49 ---Gln----- 49
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Db 8537 GAGAAITTTGAAATAGACTGATGAGCCGGTCTGCGACTCCCAAAAAGTCCCTGATTGA 8478
QY 50 -----Gly---Glu---Ser-----Ala--- 53
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QY 53 ----- 53
Db 8417 CTTCTTCATGATCAAAATATATGTTGTCATCTCTTAATCACTCGTTCCTGATGGTTGTC 8358
QY 54 -----Thr-----Leu----- 55
Db 8357 TTGATTTCGATTAGCATTTTAACTCAGTCTTTAAACAAGTTGCGTGGACTCAATCCCA 8298
QY 56 ---ArgCys-----Thr 58
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QY 59 -----Ile-----Asp----- 60
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QY 61 -----Asn----- 61
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Db 7997 APTGACGAAGACAGGATCATGATCATCAACAAGAGCTAGCAATGTCCTCAAAATAT 7938
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QY 77 -----Ala-----Gly-----Asn----- 79
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QY 82 -----Tip---Cys----- 83
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QY 83 ----- 83
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Db 7097 APTCGGTAATTACAAGTATTCTCGCAATTTCCAAGACATTAGGAGAGAAATCTACCTG 7038
QY 89 -----Val----- 89
Db 7037 CCAACTTCAGTTCCTCTCTTTTAAAGACCAATAATTAGATCATCATCTAAAGC 6978
QY 90 -----Leu-----LeuSerAsn----- 93
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QY 93 ----- 93
Db 6917 TCTGCAACACCTTTTACTAGGATAGGAGTGTTCGGATTTCATTCGGACATGTTTCAACA 6858
QY 94 -----Thr-----GlnThr----- 96
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Qy 109 Asp-----GluGly----- 111
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Qy 112 ---Pro-----Tyr----- 113
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Qy 114 ---Thr---Cys----- 115
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Qy 135 -----Ser-----Pro----- 136
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Db 5357 CAAGTTGATTTGGTCCAAACATGAAGAATCTGCTAGCAGGATTTGAGTTACTTTCCAG 5298
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Qy 149 ----- 149
Db 5237 AAGATGGATACCACTCGGAGAACCAAGATAGTCCATGATTAACCCCTATGATAAGAA 5178
Qy 150 -----GlyAsn----- 151
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Qy 151 ----- 151
Db 5117 TTTGGATAGCCCATGATATACCAAAAAATAAACTCTCATCATCAGGAAGTTGCGAAGCAGC 5058
Qy 152 -----Asn-----Ile----- 153
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Qy 154 ---Ser-----Leu-----Thr----- 156
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Qy 158 ----- 158
Db 4877 TGTGTTAGTTCCACTGATCATTTCCGACCATTTCTTGAGAGATTTGGACAGCAATATCGAC 4818
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Db 4757 GGTCTCTGGTTTATAGGAGCAAGATAGCTGAGATCCACTGGAGAGATTTGGAAGACCCGC 4698
Qy 163 -----Pro-----Glu-----Pro----- 165
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Qy 170 ---Arg-----HisIle----- 172
Db 4577 TTCAGGGAATCGGCTCGCAGCAAGAGATCCTTATCAGCCATCTCGAACACAGACACCTGA 4518
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QY 190 ---Glu---GlyIle---Thr 192
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QY 193 ---ArgGlu---Gln--- 195
Db 4157 TTGAGGAGGAGCCTGGATTGACCAAGTCTCTGTTGTTGTTGTTCAATGCTTCTT 4098
QY 196 ---Ser---Gly---Asp---TyrGluCys---Ser 202
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QY 224 ---TyrIle---SerGluAla---Lys---GlyThrGly--- 232
Db 3440 ACCATATTTGAATGCTCTCTGAGTGTCTGTGATATTGAGCATGGAGGGTCTTCCC 3381
QY 233 ---Val---Pro---Val--- 235
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QY 236 ---Gly---GlnLys--- 238
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QY 242 ---Gln---Cys--- 243
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QY 244 ---Glu--- 244
Db 3140 GAAGAATTTCTCATATCTTAATGTATCGGATCATAGGTGTCATCTCGTCAACTCAAA 3081
QY 245 ---Ala---Ser---Ala---Val--- 248
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QY 249 ---Pro---SerAlaGluPhe---Gln--- 254
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QY 255 ---Trp--- 255
Db 2966 AATCTTCTTTRAGGAACATCATGATGATGGATGGGATTAACACTTAGATCGTGATATCTG 2907
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Db 2906 TTACTTTTTTTCATAGTCTACAGAGAAATTTGACTCTCGCCTGATTGTACAACTTTTG 2847
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Db 2845 TATCTAGCCCGAGCAGGATGGCTCTTTATGAGACATTCGTCCGTCACTCCGACAGAG 2787
QY 257 ---LysAsp--- 258
Db 2785 ATGAACCTCTCTCTAGATGAGAACAAATTCATCCAAAGGATATGGTGAGAGGCTGAAGACTT 2727
QY 259 ---Asp---LysArg--- 261
Db 2726 GCTTTCTTGGTTGGAAGTCAATGATGCTTTGAGAGAGACCAACATCTGATACTGT 2667
QY 261 --- 261
Db 2666 TCTGATTTGGAGGATGTGTGTTCACTGAGTGAACCTTATATACATCCGGATTTATC 2607
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Db 2486 CCACTTAAACCTCTGGGATGTCAACGGTAAGTCTTTCCATGCTGCTCAGATTCAAGC 2427
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Db 2426 TCAGGCTGTTTCCAGTCCGAAGTAAATACAACTCCACTTCTCATCTGATAGTCACT 2367
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QY 272 Glu---Asn--- 273
Db 2246 GAGGGCTTAGTATGCTCTTCCATCCATCTCTTGGAACTCACTCATTAATTTGGACTTTCA 2187
QY 274 ---Arg---Pro--- 275
Db 2186 GCTGTTGCTTGGATCTCACTATCTCTCCAGCCCTGATCCAGACAGAAATAGGAC 2127
QY 276 ---Phe---LeuSerLysLeu---Ile---PhePhe--- 283
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QY 289 - - - - - Asp - - - - - 289
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QY 290 Tyr - - - - - 290
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QY 291 - - - - - Gly - - - - - 291
Db 1886 ACCACATCTCTGCTTGTGGGGTGCATTAGTCTCAATCTCCGGTACTATCATCTGGA 1827
QY 293 - - - - - Thr - - - - - 293
Db 1826 GTGTATTTGTATCTCCACACAAACTGTGTGCCAAGTCGGCAGAGGATCTCTACTGCA 1767
QY 296 - - - - - Val - - - - - 296
Db 1766 TAAGCGTACAAACCTGCTGTAGTAGAGATGTATCTCAATGTATCAGGCTGTGCG 1707
QY 297 - - - - - Ala - - - - - 297
Db 1706 GCATCTCTGCTGTGGATCTGAGCAGAGAGCTGTCAATTTGCCCCAGAGAGTGAAG 1647
QY 299 - - - - - Ser - - - - - 299
Db 1646 GCAGGGTTTTTGACGGAAGATATGGAGACTTAGAGACAATCCAAAGTCGATCAATAA 1587
QY 301 - - - - - Leu - - - - - 301
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QY 302 - - - - - 302
Db 1526 TCTGCAACTTCTCGGTTCAAGTCCAGGTGTTACATCTTCTGTAGACATTCGGTTATT 1467
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QY 303 - - - - - HisThr - - - - - 303
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QY 306 AlaSerIle - - - - - Met - - - - - 309
Db 1346 GCGCAATTTTGTGTATTAATGTCATTTCCCCACACATCAAAATGTACAGACCTTCT 1287
QY 310 - - - - - Leu - - - - - 310
Db 1286 GGCACAGAGGTTCAAACGTGTTCAATGTATCATTTTGTCAATGATTTGTACGCCATCCATG 1227
QY 311 - - - - - Phe - - - - - 311
Db 1226 AGCTTTTCTGTATTCAGGCATTTGTGTTCTGCCCACTCTGTATAGCAAGTAGATAC 1167
QY 312 - - - - - Gly - - - - - 312
Db 1166 AAAGCAACCAATTTGTATCTCGGTGTTCTGGAAGCATCCGATACCTCATCTGGAAGT 1107
QY 315 - - - - - Ala - - - - - ValSer - - - - - 317
Db 1106 ACGCGTCCAGGCTTCAAGGATACAAGGTCAAATATTCCGATTGTATCCCTGCTTTC 1047
QY 317 - - - - - 317
Db 1046 CCGATGTTTATCCGAACTTGACCAATCTTTATCCAACTTACCCGGATGCTTTAAT 987
QY 317 - - - - - 317

Db 986 GCTCCATACAAGTAGCTGTTGACATGTATGATGATACATTTCCGGATTTCCAGCCTTGG 927
QY 317 - - - - - 317
Db 926 TAGACATATCCTCTTAGATCTGACAAACTTTTGTAGTATTGATGTAAAGAGAACTCTCC 867
QY 317 - - - - - 317
Db 866 TTTGATTTTCTGAAGTAATCTGCGGGGTATTCACCTGGATCCTCATTTGCGAGGAAGTTT 807
QY 317 - - - - - 317
Db 806 GGAATATGACTGTGTGTCAATGATTTCTTGACTGTAAACAGACATTTTGATTACTGTT 747
QY 318 GluValSer - - - - - AsnGly - - - - - 322
Db 746 AAAGTTTCTCCTGAGCCTTTTAATGATAAATATGTTTGTCTCTGCTCCCTATAGTG 687
QY 323 - - - - - ThrSerArg - - - - - Arg - - - - - 326
Db 686 AGTGTATTACAACTCGAGGGGGCGGTACCCCAATTCGCCCTATAGTAGTCTGATT 627
QY 326 - - - - - 326
Db 626 ACAATCACTGGCGTCTGTTTACAACTGCTGACTGGGAAACCCCTGGGCTTACCCAAC 567
QY 327 - - - - - Alagly - - - - - 328
Db 566 TTAATCGCCTTGACAGCATAATCCCTTTCCGACGCTGGCGTAAATAGCAAGAGGCCGCA 507
QY 329 - - - - - Cys - - - - - 329
Db 506 CCGATCGCCTTCCCAACAGTTTGGCAGCCTGATGCGGAATGGAGCGGCCCTGTAGCG 447
QY 330 - - - - - ValTrp - - - - - 331
Db 446 GCGCATTAAGCGCGGGGTGTGTGTTACGCGAGCGTGACCGCTACACTTGCCAGCG 387
QY 332 - - - - - LeuLeu - - - - - 333
Db 386 CCTAGCGCCCTCTCTTTCGCTTCTTCCCTTCTTCCGACGTTTCGGCGGCTTTC 327
QY 334 Pro - - - - - Leu - - - - - LeuValLeu - - - - - 338
Db 325 CCGGTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTCGTTTACGGCACC 267
QY 333 - - - - - 338
Db 265 TCGACCCCAAAAACCTTGATAGGTGATGTTACGTAGTGGGCATCGCCCTGATAGA 207
QY 333 - - - - - 338
Db 205 CGTTTTCGCCCTTGAGCTGGAGTCCAGTCTCTTAAATAGTGGACTCTTGTGTCCAAA 147
QY 339 - - - - - His - - - - - LeuLeu - - - - - Phe 344
Db 146 CTGGAACAACACTCAACCTATCTCGGTCTATTCTTTGATTATAAGGGATT 93

RESULT 30

US-08-646-695-7
; Sequence 7, Application US/08646695
; Patent No. 6168943
; GENERAL INFORMATION:
; APPLICANT: Rose, John K.
; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR
; TITLE OF INVENTION: USES
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

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; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,695
; FILING DATE: On Even Date Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEFAX: (212) 869-9741/8864
; TELEFAX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-646-695-7

Alignment Scores:
Pred. No.: 1,51e-24 Length: 14311
Score: 1712.20 Matches: 293
Percent Similarity: 10.13% Conservative: 43
Best Local Similarity: 8.83% Mismatches: 4
Query Match: 71.10% Indels: 2978
DB: 3 Gaps: 253

US-10-017-084a-523 (1-344) x US-08-646-695-7 (1-14311)

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QY 3-----Thrile-----4
Db 4338 TGGATAGACATCTCAGATAACCAATATGTAATAATGTGATCTGTATTTCCCTTTT 4397
QY 5-----Gln-----Pro-----6
Db 4398 CAATTAGACGGCATTTGATTTGAAGTAATTTCTGACAAATCACCCCATATCACGGTTGC 4457
QY 6-----Lys-----Met-----HisSerIle-----12
Db 4458 TTGTCGGATAGAGGTTGGGATCTTGTGGGATCGTTTCTAATTCGTCTCTAATAGGTC 4517
QY 7-----Lys-----Met-----HisSerIle-----12
Db 4518 CTGATCTAGTAAGAAAGGAATGAGGTGATACAC---TCAATTATCAATCAAGTAA 4574
QY 13 Ser-----Trp-----Ala-----Ile-----PheThrGly-----19
Db 4575 TCAACCTCCGTACACTCGTTGGCGCCCTCTTCAATAGAGCCAGACTTCTCGGTGTA 4634
QY 20-----LeuAlaLeu-----23
Db 4635 TTACTTGGCAGCACTTCTCTATTATTCGTCTAGCAACCTTTTAAAGAACTCGAC 4694
QY 24-----Cys-----Leu 25
Db 4695 CTCTAATACGACCTTGTATAGATAGAGGAATAGAGAACTGTCTCGGCATGATGATT 4754
QY 26 Phe-----26
Db 4755 TTCTATAGCCCAAGTCTCCATATAGAAAACCTATACATCTGCCGACTTGTAGGATTGCT 4814
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QY 28 -----GlyVal-----29
Db 4875 CCCAGCAACCTTCCCAATTTCCCTCCATGTTTCCAGCACATGGGATACATCTGGGGGGTGT 4934
QY 30 -----Pro-----Val-----Arg-----32
Db 4935 AGTCATATCTGAGTCCAGGGGTGATCTCTCTATGGGTCTCAACACAGGACTTACAGGAA 4994
QY 33 -----Ser-----33
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QY 34 -----Gly-----Asp-----35
Db 5055 GAGCATAGAGCAACGTTGCTTGGATAAAAGTCGAAATTTCTGATCTCCAGATCCCTCA 5114
QY 35 -----Thr-----35
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QY 35 -----35
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QY 37 -----Thr-----37
Db 5295 CTAGTTTAGTGGGTTTCAACAAACCAAGAGATAGCATCTCTAAGAGCTGTAGTCTTTT 5354
QY 38 -----PheProlys-----40
Db 5355 TAATCAGTGGGACTTTGTTTCCCTTTCCCAAGGCTGCAAAATAGATGTAGATTCAGATG 5414
QY 41 -----AlaMet-----42
Db 5415 TTTTAGACCTTAGATAAGCAGGCAATGGTCCCGTGAACCTAAGACGTCATGGATCCGT 5474
QY 43 ---AspAsn-----44
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QY 47 -----Val-----Arg-----48
Db 5655 TACATGATCCCTTCTCAAAATGAAGTTTCCCTAAATGTGTCAAAAGAGGATACCTCACTCC 5714
QY 49 ---Gln-----49
Db 5715 TCAAAATCAATCAATCCATTCCTATGATACATCTTTTCTTAAGAGGATTCGGAATAGTAC 5774
QY 49 -----49
Db 5775 GAGAAATTTGAAATAGACTGATGAGCCCGTCTCGGACTCCCAAAAAAGTGCCTGATTTGA 5834
QY 50 -----Gly-----Glu-----Ser-----Ala-----53
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QY 53 -----53
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Db 5895 CCTCTTCATGATACAAATATATGGTTGCATCCTTAATCACCTGGTTCCTGATGGTTTGTG 5954
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QY 56 ---ArgCys-----Thr 58
Db 6015 TAGCGATGTTGAGAGAGGTTGGATCTTCTACTAGCTTGCTCTATGTGAGTTATTGCAAACT 6074
QY 58 ----- 58
Db 6075 TGGCTATCTCGGGGTTCCAAATACTGCATCATCTCTCTTCAGATGCTCACTTCGAGCAT 6134
QY 59 -----Ile-----Asp----- 60
Db 6135 GTACATGATGAATCTCCAGAATGAGAGACTTTCTGTACGGATCTGGGAGGCTCTAA 6194
QY 61 ----- 61
Db 6195 TCMAAAACCTGGACAAAGACATGCCGACACTCTCCAATGGAAGGTCCTCAAAATACAACA 6254
QY 62 ---Arg-----Val----- 63
Db 6255 TGGCGTATTGAAAGTAGAACTGTGCAAGCCGGTATCTTATCTTGAACCTTACAAATG 6314
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Db 6315 ATTGACGAAGAGCAGGATCATGCATCAACAAGAGCTAGCAAAATGTCCAAATAT 6374
QY 66 -----ValAlaTrp-----Leu-----Arg----- 71
Db 6375 TGTACTGTATCATGGCATTTGATTGGTTCTCAGCAAAATGAGCTACGGTGAGAGCATTTG 6434
QY 72 ----- 72
Db 6435 TGGAACTGAGCTCAATTATATAGACAAGTGGTATTTGGTCATTTGGTGACACAAGTCA 6494
QY 73 -----ThrIle----- 74
Db 6495 CTCGTGACCATCTCTTGGTCTCTAACCTCTAATCATCTCCAGAAAATCGGTATTTTC 6554
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Db 6555 CATAAATCAAGTAATCTGCAGATTCATAGTCTCATCTGCTATTAATCAAAAGTCTTAAT 6614
QY 74 ----- 74
Db 6615 TCCCTGTCCCTATTTTGTATTCGATGATATATTTCTCATTTATAGAACCAATTTGATGA 6674
QY 74 ----- 74
Db 6675 GAGCACCTGTAATCTTACACAGTTCTTCGATTTCTCGTTTATATCTGTGTGCAATAA 6734
QY 75 Leu-----Tyr----- 76
Db 6735 CTTGATTAATCACTTTGTGCCAAGACTTTGACAGCAGTGTCTTCTGATTTTAGCCTCTCTT 6794
QY 76 ----- 76
Db 6795 GAATAACCAAGTAGATTGAGGATGATCCATCTTTTGGCGTAGACCTTCCAGTCCACCT 6854
QY 77 -----Ala-----Gly-----Asn----- 79
Db 6855 CTTGTCTTGCACAACAACCTCGTTGGGAGGTGTAATTTGATCAGTGTGTGTGTGAACAC 6914
QY 80 ----- 81
Db 6915 GCATCAAGTCTGCTCTTCCATTTGATGATATAGACTTTTCTCAAAAATTCATGAGTTC 6974
QY 81 ----- 81

Db 6975 TCTCGATTAAAGTAGGATAACCTAAGAACTGGCCCAATACTCGGAACACTGGGCGGTTG 7034
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Db 7035 ATAACTTCCTTTGGTGTATTTCCATTTTCGTAATCAATGTGATGGCTATGCAAAATG 7094
QY 83 ----- 83
Db 7095 CCTCATATGATCTCAATCCTTGGCCGGATGAGGAATCTAAATCTTTTAAATGACTGAG 7154
QY 84 LeuAsp-----Pro----- 86
Db 7155 TTAGATCGTCGGCCATTTGTTCAGGCCITTAACATAGAGCAAAATGAGTCTTTATCAAAT 7214
QY 87 -----Val-----Arg-----Val----- 88
Db 7215 ATTGGGTAATTAACAAAGTATTTCTCGCAATTTCCAAGACATTAGGGAGAAAAATCTACCTG 7274
QY 89 -----Val----- 89
Db 7275 CCAACTTCAGTTCCTCTCTCTTTTAAAGCAAAATTAATTAGATCATCATCTAAGC 7334
QY 90 -----Leu-----LeuSerAsn----- 93
Db 7335 CCTTCTCATCAATCTCTTTAAAGAAATTTCTTCCAATTTGGTAGCTTTGTGTCACAAATG 7394
QY 93 ----- 93
Db 7395 TCTGCAACACCTTTTACTAGGATAGGAGTGTTCGAAATTCATTCGACATGTTTCAACA 7454
QY 94 -----Thr-----GlnThr----- 96
Db 7455 CCTCTGACCTATTCATTTGAATGACTTTTGTGAGAGTATATTATCGATGGGTCTAGTAAAT 7514
QY 96 ----- 96
Db 7515 CGGGTATTTCAAAACATTTAATCAGCGAAGTTTCAGCCATTTATCTCCAAATCTTGAA 7574
QY 97 -----Gln-----Tyr----- 98
Db 7575 CTTGAGACCTGTGGCCATGTATTTCTTTAAACATGACTTTTAAAGGATGATCATGAG 7634
QY 99 -----Ser-----IleGlu----- 101
Db 7635 GGAGCAAGTCTCCATTCACGAACTTTTATGATCATTTGAACCTTTGAAATAGAACAA 7694
QY 101 ----- 101
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QY 103 -----Ile-----Gln-----Asn 104
Db 7755 TTACTTGGGAATGTATTTTCTAGTCCAGTAAATAATCTATAAAGGATGACCCCAAT 7814
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Db 7815 GTCTGAACGATCCATAATCACCAGTGTGAGATCCACTGTTTTCACACTCATTTCTGAT 7874
QY 107 -----Val-----Tyr----- 108
Db 7875 CATGGAGAAATCTTATACCTCGGTCAATTTTGGCCCTTCATCAACAGAAGTCTTGATAT 7934
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QY 112 ---Pro-----Tyr----- 113
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QY 114 ---Thr---Cys----- 115
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QY 116 ---Ser---ValGln----- 119
Db 8175 CATCTTTGACCAATTAAACAGAAAGTTTGGTCCATTAGAAATATCAAGTTTCTTGAAGTAAG 8234
QY 120 ---Asp----- 120
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QY 121 ---Asn----- 121
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QY 122 ---His-----ProLysThr----- 125
Db 8355 CCTCAGACAGCAATTTAAGATTAAATCTCAACTTGTGTAGTTCAAAACCTTTTGGACACA 8414
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Db 8415 AATAAGCGAGAAATTTGAATGAGTCAGTCCTCATCTTCTTTTGAATGATTAATCAATGGTT 8474
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Db 8475 TGTGGCCCGAGCGGATGAAGTCTCCACCAGTCCTCAAAATGTTATTTCTGCCCTCTTTGT 8534
QY 128 ---Val-----His-----Leu----- 130
Db 8535 CCACCTTCAATGATAAAACTATACCTTGTAGTCGATCATGATATCAGACATTAACCAAC 8594
QY 131 ---Ile----- 131
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QY 131 ----- 131
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Db 8775 CATGATTCAAGTACGTATGCGCTCATCGGATTCAGGAATTCCTTGTGGCATAGTCAT 8834
QY 135 -----Ser-----Pro----- 136
Db 8835 CTTCAATGAATCAATGAACCTGCTGGTCTCAAAATCGTGACCTTCCATGATGCTGTTA 8894
QY 137 ---Lys-----IleValGlu-----IleSer----- 143
Db 8895 GTTTTTTCAFAAAATTAATAAACTCAAAATATATTAATGAGGCTCTTTGAGCATGATATCA 8954
QY 144 ---Asp-----Ile----- 145
Db 8955 CAAGTTGATTTGGTCCAAACATGAGAAATCTGGGTAGCAGGATTTGAGTTACTTTTCCAAG 9014
QY 146 Ser-----IleAsn----- 148
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QY 149 -----Glu 149
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QY 150 -----GlyAsn----- 151
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QY 152 ---Asn-----Ile----- 153
Db 9255 GTCTTGAATGTGAGGATGTTGGAACACCTGAGCTTTGAGCTAAGATGAAGATCGGAGTC 9314
QY 154 ---Ser-----Leu-----Thr----- 156
Db 9315 CAACATACCATGTCCCAATCATGTATAAAGAAACTTATATCTCTGAACCTGCTCTCAGAAC 9374
QY 157 -----Cys-----Ile----- 158
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Db 9435 TGTGTAGTTTCCACTGATCATTCGACCATCTCTTGAGAGGATTTGGAGCAGCAATATCGAC 9494
QY 159 -----Ala-----Thr 160
Db 9495 TCTGATGATCTGGTCTCAAGTATTTTAGGTTACCATGATTATGTTGTAAGCAGGACC 9554
QY 161 Gly-----Arg 162
Db 9555 GGTCTCTGGTTTTTAGGAGCAAGATAGCTGAGATCCACTGGAGAGATTTGAAGACCCGC 9614
QY 163 ---Pro-----Glu-----Pro----- 165
Db 9615 TCTGATTTTGTCTCCAGGTTTCTTGGCAGAGGAAATATCCAAGATCCTCTCAACCTCTG 9674
QY 165 ---Thr---Val-----Thr-----Trp----- 169
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QY 170 ---Arg-----HisIle----- 172
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QY 173 ---SerProLys---AlaVal-----Gly-----Phe 179
Db 9795 TGGAGTCTGACTCCCAATGCTTGCAGTATTTGCATTTTGCAGGCTTGCCTCCAGTTTC 9854
QY 180 ValSer----- 181
Db 9855 ATAAGCAAGTAGTTACTTCTGAACCCCTGTGCCCTCTTCCAGGATGATAGTCTCC 9914
QY 182 ---Glu---Asp-----Glu----- 184
Db 9915 GTCCTCTGAGAAGAGGTGATGCCATGGAATGAGGTAGATCATACATAGCCCTTTGAC 9974
QY 185 -----Tyr----- 185
Db 9975 CTTATAGTCAGAAATGCCAGGTTGTAGAGTTATGACAGTGGGCAATATTAATTGCTGA 10034
QY 186 Leu-----Glu-----Ile-----Gln----- 189
Db 10035 TTTTCCGTTGATGAATCTGAATCAACCCATCTCCTGTGTATTCATCAACACAGCATG 10094
QY 190 -----GlyIle----- 192
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QY 193 ---ArgGlu-----Gln----- 195
Db 10155 TTGAGGAGGAGCCCTGGATTCAGCAAGTTCTTGTGTTTGTTCATGCTTTCTT 10214
QY 196 -----Ser---Gly---Asp---TyrGluCys-----Ser 202
Db 10215 GCATTTCTTACAGATGGAGTGAAGATCGGATGAGCTG---TGTTATATATCTTCGGTCC 10271
QY 203 ---Ala-----Ser----- 204

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QY 205 ---Asn---
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Db 10392 ATGCCAATTTAAATCTGAGCTTGACGGGCAATAATGGTAATTAGAAGCAACATTTTCCA 10451
QY 217 ValThr---Val---AsnTyr--- 221
Db 10452 GTTTCCTTTTGTGTGGGAAACTATGGTGAACCTTGCATTCACCCCAATGAATAA 10511
QY 221 --- 221
Db 10512 AAAGCTAAGTACAAAAGGCATCTCATAGTACGCGTAAACACATCGATCTCTGTAGTT 10571
QY 221 --- 221
Db 10572 TTTTTCATAGGATAGAAAAGACAGATATTAGTTGTTTCGAGAGGCTGGAATTAAGAGAG 10631
QY 221 --- 221
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QY 222 ---Pro--- 222
Db 10692 GATAGAAATCCAGGACCCAGCTCCAGATGCTTTTCTCGCAATCAGGCCAAACATTA 10751
QY 223 --- 223
Db 10752 GGCCTTCTCTGAAATCAGAAAATTTGGAAGATTGAATGATCCAGATCATAGGAGC 10811
QY 223 --- 223
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QY 236 ---GlyThr---GlnLys--- 238
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QY 242 --- 242
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QY 244 ---Glu--- 244
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QY 249 ---Pro---SerAlaGluPhe---Gln--- 254
Db 11292 GGGTGTGGATCCCTAATTTCTTAGATTCTTACC---TTTCCCTTCAGACCGAG 11345
QY 255 ---Tyr--- 255

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QY 255 --- 255
Db 11406 TTACTTTTTTTTCTATAGTCTACAGAGAAATTTTGACTCTCGCCTGATTTGACAACTTTT 11465
QY 256 Tyr--- 256
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QY 261 --- 261
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QY 261 --- 261
Db 11706 TGGCGCTCTTTCATAATGACCCCTTCTCCGATGCTTCAAAATGTGCATCTGCCAGATTC 11765
QY 263 ---LeuIle---Glu--- 264
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QY 265 ---Gly---Lys--- 266
Db 11826 CCACTTAAACCTCTGCGGATGTCAACGTAAGTCTTTTCCATGCTCTGCAGATTCAAGC 11885
QY 266 --- 266
Db 11886 TCAGGCTGTTTCCAGTCGAAAGTAAATAACAATCCACTTCTCTCATCTGCATAGTCACT 11945
QY 267 LysGly---ValLys--- 270
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QY 271 ---Val--- 271
Db 12006 TGATGTCTTCAATTTCTGTTTCAAGATTCGTGTGTCAGAAATCATCTGCTGCTGAAATAA 12065
QY 272 Glu---Asn--- 273
Db 12066 GAGGCTTAGTATGCTCTTCCATCCATCCTCTTGGAAACAACATCATTAATTGGACTTTTCA 12125
QY 274 ---Arg---Pro--- 275
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QY 276 ---Phe---LeuSerLysLeu---Ile---PhePhe--- 283
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QY 291 ---Gly---Asn--- 292
Db 12426 ACCACATCTCTGCTTGTGGCGTGCATTAGTGTGTCATTAATCTCCGCTACTATCATCTGGA 12485

[illegible]

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		:::				
Db	13625	AGTCGATTACAACTCGAGGGGGGCCCGGTACCCAAATCCGCCCTATAGTAGTCGTATT				13685
QY	325	-----				326
Db	13685	ACAATCACTGGCGCTGTTTACAACTGTAATGGGAAACCTTGGCGTTACCCAAC				13745
QY	327	-----				328
		-----AlaGly-----				
Db	13745	TTAATCGCCTTCGACACATCCCCCTTTTCGCCAGCTGGCGTAAATAGCAAGAGCCCGCA				13805
QY	329	-----Cys-----				329
		:::				
Db	13806	CGATCGCCITCCCAACAGTTGCGCAGCCTGAATGGGAATGGGACGCGCCCTGTAGCG				13865
QY	330	-----ValTrp-----				331
		:::				
Db	13866	GGCATTAAAGCGCGCGGGGTGTGTGGTTACGCGCAGCTGACCGCTACACTTGCACGG				13925
QY	332	-----LeuLeu-----				333
		:::				
Db	13926	CCCTAGCGCCGCTCCTTTCGCTTCTTCCTTCCTTCGCGCAGTTGCGCGGCTTC				13985
QY	334	Pro-----				338
		:::				
Db	13986	CCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGATTAGTGTCTTACGCACC				14045
QY	338	-----				338
Db	14046	TCGACCCCAAAAACTGAATTAGGTGATGTTTACGTAGTGGGCCATCGCCCTGTATAGA				14105
QY	338	-----				338
Db	14106	CGGTTTTTCGCCCTTTGACGTTGGAGTCCAGGTTCTTTAATAGTGACTCTTGTTCCTCAA				14165
QY	339	-----His-----				344
		:::				
Db	14166	CTGGAACACACTCAACCCATCTCGTGTCTATCTTTTGGATTATTAAGGATTT				14219

Search completed: May 28, 2004, 15:40:16
Job time : 715 secs